Identification of Six Complementation Classes Involved in the Biosynthesis of Glycosylphosphatidylinositol Anchors in *Saccharomyces cerevisiae*

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Abstract. Glycosylphosphatidylinositol (GPI)-anchored membrane proteins are synthesized by the posttranslational attachment of a preformed glycolipid to newly made glycoproteins. α-Agglutinin is a GPI-anchored glycoprotein that gets expressed at the cell surface of *MATa* cells after induction with type a mating factor. Mutants affecting the biosynthesis of GPI anchors were obtained by selecting for the absence of α-agglutinin from the cell wall after induction with a-factor at 37°C. 10 recessive mutants were grouped into 6 complementation classes, gpi4 to gpi9. Mutants are considered to be deficient in the biosynthesis of GPI anchors, since each mutant accumulates an abnormal, incomplete GPI glycolipid containing either zero, two, or four mannoses. One mutant accumulates a complete precursor glycolipid, suggesting that it might be deficient in the transfer of complete precursor lipids to proteins. When labeled with [2-3H]inositol, mutants accumulate reduced amounts of radiolabeled GPI-anchored proteins, and the export of the GPI-anchored Gaslp out of the ER is severely delayed in several mutant strains. On the other hand, invertase and acid phosphatase are secreted by all but one mutant. All mutants show an increased sensitivity to calcofluor white and hygromycin B. This suggests that GPI-anchored proteins are required for the integrity of the yeast cell wall.

Many glycoproteins of lower and higher eukaryotes are attached to the plasma membrane by means of a glycosylphosphatidylinositol (GPI) anchor covalently linked to their carboxy terminus (15, 41). These anchors have the conserved core structure protein-CO-NH-(CH2)2-PO4-6Man~l-2Man~l-6Man~l-4GlcNH2-mylo-inositol-PO4-lipid. Anchors are synthesized by stepwise addition of sugars and phosphoethanolamine to phosphatidylinositol (PI) to form the complete precursor (CP) glycolipid. The transfer of CP's onto proteins is effected by a yet unidentified enzyme complex that recognizes a GPI signal sequence in the COOH-terminal 30–40 amino acids of GPI proteins. This enzyme complex cleaves off most of the GPI signal sequence and replaces it with the preassembled CP. Although all biosynthetic reactions required for GPI anchor biosynthesis have been reproduced in microsomal in vitro systems and are quite well understood (11, 13, 24, 25, 37–40, 42, 43, 45), the identification and study of individual enzymes are still far from complete. Four genes required for GPI biosynthesis have been cloned by complementation of mammalian somatic cell mutants deficient in the biosynthesis of CP's (29–31, 46). These mutant cell lines were isolated by selecting for the loss of surface expression of GPI-anchored proteins, and show normal growth in tissue culture (28). Of the four genes isolated by complementation cloning, two are required for the addition of GlcNAc to PI (30, 46), one for the addition of the third, i.e., the α1,2-linked mannose (31), and one for the addition of phosphoethanolamine (29). In contrast to mammalian cell lines, GPI anchoring seems to be essential for yeast cells (33). Nevertheless, several conditional *Saccharomyces cerevisiae* mutants have been obtained in a screen for the absence of [2-3H]inositol incorporation into proteins at 37°C (33, 56). Mutants belonging to three complementation classes were deficient in the addition of GlcNAc to PI, and one other mutant did not add mannose to the GlcN-PI intermediate. To obtain additional yeast mutants, we tried to develop a selection for GPI biosynthesis mutants in yeast.

*S. cerevisiae* contains numerous GPI proteins, some of which are very highly glycosylated, but the function of

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Materials and Methods

corresponds to 1-2.5 x 10⁷ cells, depending on the strain. Reagents were salts, vitamins (but no plates (9), and were cultured in salt/dextrose (SD) medium containing ura3 bar1-1). Dynabeads M-280 coupled to sheep anti-rabbit-IgG from Milan fordshe, UK); 0.2-mm-thick silica gel 60 plates (20 x 20 cm) from Merck suspensions was measured in a 1-cm cuvette at 600 nm; 10D600 U of cells S. cerevisiae procedure based on this assumption.

Materials, Growth Conditions, and Materials

S. cerevisiae strains were W303-1B (MATa ade2-1 can1-100 ura3-1 leu2-3, 112 trpl-1 his3-11, 115), X2180-1A (MATa), HMS174 (MATa sec13-1), CA (MATa leu2-3, 112 ura3-52 gni40) and RH932 (MATa end2-1 leu2 ura3 bar1-1). Cells were grown on yeast extract/peternone/dextrose (YPD) plates (9), and were cultured in salt/dextrose (SD) medium containing salts, vitamins (but no myo-inositol [Ins]), trace elements, and 2% glucose as a carbon source; SDC medium is the same, but in addition contains 1% casein hydrolysate. SDUA and SDCUA are SD and SDC media supplemented with uracil and adenine, each at 40 μg/ml. The OD of dilute cell suspensions was measured in a 1-cm cuvette at 600 nm; 1 OD₆₀₀ U of cells corresponds to 1-2.5 x 10⁷ cells, depending on the strain. Reagents were obtained from the following sources: anti-rabbit-IgG/alkaline phosphatase conjugate (A2506) from Sigma Chemical Co. (St. Louis, MO); Amberlite XAD-2 resin from Serva Fine Biochemicals (Heidelberg, Germany); Dynabeads M-280 coupled to sheep anti-rabbit-IgG from Milan Analytical AG (La Roche, Switzerland); ENHANCE from NEN (Hertfordshire, UK); 0.2-mm-think silica gel plates (20 x 20 cm) from Merck (Darmstadt, Germany); mixed bed ion exchange resin (AG-501-X8; BioRad Laboratories, Richmond, CA) ammonia in methanol (7 M; Jansen Chimica, Beerse, Belgium); phosphatidylinositol-specific phospholipase C (PI-PLC) from Boehringer Mannheim GmbH (Mannheim, Germany). GPI-phospholipase D (PLD) purified 1,000-fold from bovine serum was a kind gift of Dr. U. Brodebeck, University of Bern, Bern, Switzerland. α-Factor was isolated by incubation of cells with Amberlite XAD-2 resin, and quantitated as described (73). A polyclonal antiserum was raised against α-agglutinin in a rabbit by repeated s.c. and i.v. injection as described (79).

Isolation of GPI-deficient Mutants

Mutants were obtained using the scheme depicted in Fig. 2. Ethyl methanesulfonate mutagenesis was performed as described (34), and cells were allowed to recover by an overnight incubation at 24°C in SDCUA, buff- ered to pH 5.0 with 0.05 M phosphate. Before immunoselection, 3 ml of Dynabeads M-280 suspension (6-7 x 10⁸ beads per ml) were prewashed, once with 25 ml PBS, twice with 25 ml PBS containing 5% FCS, and once with 25 ml PBS containing 1% FCS and bovine serum albumin (BSA) (1 mg/ml). Finally, 8 ml of prewashed 10D600 U of phosphatase were added to the cells and incubated at 24°C for 2 h in the presence of 25 ml PBS and 1% FCS. The cells were then washed and incubated in 25 ml SDCUA for 20 min at 37°C. The cells were then washed with 25 ml PBS at 37°C, resuspended in 4.5 ml PBSF, and 0.5 ml anti-α-agglutinin rabbit anti- tisera was used. Cells were incubated 90 min at 37°C on a slowly rotating wheel. Cells were then washed with 20 ml of PBSF, and re suspended in 10 ml PBSF. For the first round of immunoselection, 5 ml of prewashed Dynabeads (coated with sheep anti-rabbit-IgG antibodies) was added to the cells, and was incubated with the cells for 90 min at 24°C on a wheel. The tube was then placed for 5 min against the magnet, and the medium with the unbound cells was collected in a recipient vessel. At this stage, the magnetic beads were washed five times, by each time removing the tube from the magnet, resuspending beads in fresh PBSF (15 ml), placing the tube next to the magnet for 5 min, and collecting the free cells into the recipient vessel. These washings were necessary to recover the cells that display a normal, constitutive expression of α-agglutinin at 24°C. Cells pooled in the recipient vessel were then centrifuged, resus pended and subjected to a second and a third round of immunoselection by adding fresh Dynabeads and incubating another 90 min for each round. Finally, that cells that were not firmly bound to Dynabeads during three rounds of selection were resuspended in PBSF, plated on YPD plates, and incubated for 3-4 d at 24°C. YPD plates were replicated, and replica plates were incubated for 2 d at 37°C to allow for selection of clones that are temperature sensitive (ts) for growth. It is mutants were tested for acid phosphatase secretion by replica plating clones grown at 24°C onto phos- phatase-free SDCUA plates, and incubating the replicas at 37°C for 1-2 d. Replica plates were then processed for the detection of secreted phos- phatase as described (21). Mutants able to secrete acid phosphatase at 37°C were picked to be further screened for GPI defects.

Radiolabeling with [2-³H]myo-inositol

For further analysis, mutant strains were labeled with [2-³H]myo-inositol ([³H]Ins). Cells were grown in SDCUA medium, 2.5 OD₆₀₀ U of exponentially growing cells were resuspended in 0.25 ml SDCUA and were centrifuged 20 min at 37°C, and 5 μg [³H]Ins were added. Cells were then incubated for 20 min at 37°C, and diluted with 1 ml of prewarmed SDCUA, and further incubated for 70 min at 37°C. At the end, cells were washed with water. Lipids were extracted and desalted by butanol extraction as described (70). Lipid extracts were analyzed by ascending TLC using 0.2-mm-thick silica gel plates with the solvent system chloroform/methanol/ water (10:6:3). As standards, we used previously characterized [²H]Ins and [²H]mannosylabeled lipids from S. cerevisiae. (61, 70). Radioactiv- ity was detected by two-dimensional radioscanning (LB 2842; Berthold AG, Regensdorf, Switzerland) or else, TLC plates were sprayed with ENHANCE and exposed to film (X-OMAT; Eastman Kodak Co., Roch- ester, NY) at ~80°C.

Analysis of Abnormal

[²H]myo-inositol–labeled Lipids

Purification of radiolabeled glycolipids was achieved by preparative TLC in the same solvent system as above, radioactive glycolipids of interest were localized by two-dimensional radioscanning, and were scraped and eluted with the solvent. Before further analysis, an aliquot of purified gly- colipids was run on analytical TLC to check for purity. Soluble head groups were obtained from purified glycolipids through selective removal of acyl groups attached to the Ins using methanolic NH₃ followed by PI-PLC treatment in 20% l-propanol (60). Fatty acids and lipids were removed by butanol extraction. Head groups were added to hydrofluoric acid (HF) dephosphorylation and then to N-acetylation, and were desalted using mixed-bed ion exchange resin AG-501-X8 (Bio- Rad Laboratories, Hercules, CA) (60). N-acetylated, water-soluble head
group fragments were separated by horizontal silica gel 60 HPTLC in three consecutive runs in solvent A (1-propanol/acetic acid/water 9:6.5: vol/ vol) and solvent B (1-propanol/acetic acid/water 5:4:1, vol/vol) used in the order A, B, A as described (68). Previously described methods were used for mild base hydrolysis (18), jack bean a-mannosidase (JBAM) treatment (62), and GPI-PLD treatment (12) of lipid mixtures. Treated lipid mixtures were desalted by extraction with butanol before TLC.

**Measurement of Invertase Secretion**

To measure periplasmic invertase in intact cells, the cells were grown to mid-logarithmic phase in SDCA with the glucose content raised to 5% (SDCA) at 24°C with shaking. 10 OD600 U of cells were pelleted, resuspended in 20 ml SDCA, and preincubated for 60 min at 37°C. Cells were then pelleted, washed with water at 37°C, resuspended in 20 ml of SDCA with the glucose content reduced to 0.05% (SDS0.05CA), and incubated at 37°C. 200-μl aliquots were removed every 15 min during 1 h. These aliquots were adjusted to 10 mM Na2S, 10 mM NaF, and 10 μg/ml cycloheximide, and were kept on ice until they were washed three times with water and external invertase activity was measured (19). The OD600 of each aliquot was measured to allow calculation of the invertase activity per OD600 U of cells.

**Invertase Glycosylation**

Cells were grown to mid-logarithmic phase in SDCA at 24°C with shaking. 5-OD600 U aliquots were resuspended in 1 ml SDCA, and incubated for 60 min at 24°C or 37°C, respectively. Cells were then washed with water at 24°C or 37°C, and resuspended in SDCA, and incubated at 37°C. Cells were then pelleted, washed with water at 37°C, resuspended in 20 ml of SDCA with the glucose content reduced to 0.05% (SDS0.05CA), and incubated at 37°C. 200-μl aliquots were removed every 15 min during 1 h. These aliquots were adjusted to 10 mM Na2S, 10 mM NaF, and 10 μg/ml cycloheximide, and were kept on ice until they were washed three times with water and external invertase activity was measured (19). The OD600 of each aliquot was measured to allow calculation of the invertase activity per OD600 U of cells.

**Expression of α-agglutinin at the Cell Surface**

Cells were grown at 24°C to an OD600 of 1–2 in SDCA, and buffered to pH 5.0. Cells were resuspended in fresh SDCA, pH 5, and 0.16-ml aliquots (0.625 OD600/ml) of cells were either stimulated by a-factor (70 U/ml, final concentration), or control incubated for 3 h at 24°C or 37°C, respectively. Cells were then adjusted to 10 μg/ml cycloheximide, washed with 1 ml buffer A (10 mM Tris/HCl, pH 7.4, 100 mM MgCl2, 0.5% Tween 20, 1% Triton X-100, 1% BSA, 5% FCS, 10 μg/ml cycloheximide). Cells were resuspended in 90 μl buffer A, 10 μl rabbit anti-α-agglutinin antiserum was added, and incubation was continued for 30 min at 24°C. Cells were washed three times with 1 ml buffer A, and resuspended in 250 μl buffer A. 1 μl anti-rabbit-IgG/alkaline phosphatase conjugate was added, and cells were incubated for 45 min at 24°C. Cells were washed five times with buffer A, and alkaline-phosphatase activity was measured by incubation of cells with paranitrophenylphosphate during 10 min as described (79). No activity was observed when the second antibody was omitted.

**Maturation of Gas1p**

Maturation of Gas1p was followed by pulse-chase experiments using [35S]methionine and [35S]cysteine (Tran35/S label; ICN Biomedicals Inc., Irvine, CA), 1,027 Ci/mmol; 20 μCi/OD600 of cells) followed by immunoprecipitation using a polyclonal rabbit anti-Gas1p antiserum (17) and protein A-Sepharose as described (26). Western blotting was carried out with the same antiserum as described (26).

**Results**

**Elaboration of Conditions for Immunoselection**

Mutants with defects in the structural genes of α- and β-agglutinins previously have been obtained by selecting for cells unable to form aggregates when mixed with cells of the opposite mating type (34, 65). This approach was relatively unsuccessful for obtaining GPI-deficient mutants, possibly because this procedure selects for a complete absence of agglutinins from the surface, so that cells exhibiting constitutive levels of agglutinins are eliminated, and only cells with defects in the agglutinin structural genes are selected. Thus, a less restrictive immunoselection procedure using a highly specific polyclonal rabbit antibody against α-agglutinin was developed. As can be seen in Fig. 1, W303-1B MA Tα cells, when induced with a-factor, were strongly stained by the antiserum, whereas only vacuolar staining was visible in noninduced cells. In preliminary experiments, W303-1B MA Tα cells were first induced with a-factor at 37°C, and were then incubated with anti-α-agglutinin antibodies. Absorption of these cells onto anti-IgG-coated magnetic beads was very efficient, even if cells had not been induced to express α-agglutinin before. However, after extensive washing of the beads, only 4% of noninduced, but 85% of induced cells remained fixed to the beads. Thus, through three consecutive rounds of adsorption onto magnetic beads, followed each time by extensive washings, cells not expressing α-agglutinin at 37°C could theoretically become enriched up to 300-fold.

**Immunoselection of GPI Mutants**

Mutants were selected using the procedure outlined in Fig. 2. Strain W303-1B was mutagenized with ethyl methane-sulfonate, and surviving cells (21%) were allowed to recover in SDCA through six mitotic cell cycles at 24°C. 106 mutagenized cells were then induced to express α-agglutinin at 37°C, and the cells expressing more than constitutive levels of α-agglutinin were removed using three consecutive rounds of immunoselection. The negatively selected remaining cells (8.4%) were assumed to comprise all the dead cells generated by mutagenesis. On the basis of this assumption, we calculate that the immunoselection had removed 97% of living cells. The negatively selected cells were then plated on YPD plates for growth at 24°C. The
MATα cells
mutagenesis, recovery
induction of α-agglutinin with a mating factor at 37°C
immunoselection using anti-α-agglutinin antibodies
discard adherent cells
plate nonadherent cells (deficient in α-agglutinin expression)
screen for clones with ts phenotype for growth on agar (not growing at 37°C)
screen for ts clones that secrete acid phosphatase at 37°C
Screen for clones that do not incorporate [3H]myo-inositol into proteins
or that accumulate abnormal GPI lipids at 37°C

Figure 2. Protocol for selection of gpi mutants.

Plating efficiency was only 10%, suggesting that a major fraction of the selected cells indeed were dead cells left over from the mutagenesis. Of the growing clones, those that did not grow at 37°C were selected (20%), and these ts clones were further screened for acid phosphatase secretion at 37°C. 72% of ts clones secreted acid phosphatase normally, and these clones were labeled with [2-3H]Ins. Lipid extraction, TLC, and fluorography were used to screen for the presence of abnormal [2-3H]Ins-labeled lipids, whereas the incorporation of [2-3H]Ins into proteins was monitored by SDS-PAGE and fluorography. 10 mutant isolates accumulated a distinct, abnormal [2-3H]Ins-labeled lipid, and one mutant (gpi9) accumulated one major and several minor abnormal species (Fig. 3). In all 11 mutants, the amount of [2-3H]Ins-labeled proteins accumulated during a 90-min pulse was significantly reduced as compared with wild type. This reduction was observed in all mutants when cells were labeled at 37°C, and in many mutants even after labeling at 24°C (Fig. 4). On the other hand, all mutants incorporated [2-3H]Ins into phospholipids as efficiently as wild-type cells (50–80% of added radioactivity). In none of 400 other isolates was the incorporation of [2-3H]Ins into proteins abolished. Retesting of the growth phenotype showed that several of the 11 isolates that initially had scored as ts were in fact not temperature sensitive for growth (Table I). In most mutants, the accumulation of the abnormal lipid was enhanced when cells were labeled at 37°C, but in several mutants, the abnormal lipid could also be observed after labeling at 24°C (Fig. 3, Table I). The 11 mutant isolates were outcrossed three times to X2180, and all tetrads were labeled with [2-3H]Ins at 37°C. The accumulation of an abnormal lipid segregated 2:2 in all cases and the ts growth phenotype, if present, cosegregated with the abnormal lipid in all but one isolate (gpi7-1). Also, the accumulation of distinct abnormal lipids behaved as a stable trait, and the same lipids as in the original isolate were consistently observed in segregants. gpi7-4 and gpi8 stem from a single mutant isolate containing two independent GPI defects; during crossing of this isolate, two different spore phenotypes accumulating two different abnormal lipids were obtained. The two phenotypes were unlinked, and consistently segregated 2:2 through three further outcrosses. One mutant (isolate 839) could not be mated. For complementation analysis, all mutants accumulating the same abnormal lipid were crossed with each other and also with the isolate that accumulates a range of different abnormal lipids (gpi9, Fig. 3). Diploids were checked for the accumulation of abnormal lipids and, if ts strains were crossed, for growth at 37°C. The five isolates that accumulated lipid α were also crossed with sec53, sec59, dpml1, and pmr40, a series of ts mutants with known defects in mannose biosynthesis or mannose utilization. These mutants also accumulate lipid α. All five isolates, and all four known mutants accumulating lipid α complemented each other, except for one of our isolates that did not complement sec53. This isolate was not studied further. Our isolates accumulating lipid α were classified as

Figure 3. Accumulation of abnormal lipids in gpi mutants. Lipids from mutant cells labeled at 24°C or 37°C with [2-3H]Ins were run on TLC and revealed by fluorography for 6 d. The first lane on left represents an experiment where a threefold longer exposure had been performed allowing a better view of the minor CP of gpi9. As will be shown below, lipid α corresponds to GlcN-acylIns-P-lipid; β to Man3GlcN-acylIns-P-lipid; γ to Manα-GlcN-acylIns-P-lipid. O, origin.
lipid β from mutant 839 with Man3-GlcNAc-Ins (Fig. 5). Fragments of lipid γ from gpi7 and of CP1/CP2 from gpi8 comigrated with Man4-GlcNAc-Ins (Fig. 5). Thus, HF fragments of the major abnormal lipid of gpi7 and gpi8 are identical, but only the lipid of gpi8 comigrates with CP’s on TLC, whereas lipid γ of gpi7 is less polar. It therefore is possible that the lipid of gpi7 lacks the polar phosphoethanolamine substituent characteristic of CP’s. Lipid α of gpi9 produced a GlcNAc-Ins fragment, but this mutant contains several additional lipids the most polar of which comigrates with CP2 (Fig. 3).

The three GPI biosynthesis intermediates of yeast characterized so far contained an acyl chain on the Ins, rendering them resistant to PI-PLC (9, 55, 70). The [2-3H]Ins-labeled lipid extracts of all mutants were treated with PI-PLC and analyzed by TLC/fluorography. All abnormal mutant lipids were resistant to PI-PLC, whereas PI was completely hydrolyzed as expected (data not shown). Thus, by their comigration with well-characterized GPI intermediates on TLC, by the comigration of their HF fragments with GPI-derived HF fragments, and by their resistance to PI-PLC, the abnormal [2-3H]Ins-labeled mutant lipids behave as biosynthetic intermediates of the GPI pathway. To con-

**Characterization of Abnormal Lipids**

Structural analysis was performed on the abnormal lipids of mutants to see whether or not they represent biosynthetic intermediates of the GPI pathway. For this, [2-3H]Ins–labeled abnormal lipids were isolated from preparative TLC plates, and were fragmented using HF. Under the conditions used, HF specifically cleaves phosphoester bonds, and generates Man0- to Man4-GlcNAc-Ins (70). Mixtures of two of these standards and Ins were run in parallel on the same plate, and the positions of the respective standards were highlighted on the borders. The presence of Ins in M0–M4, Man0– to Man4-GlcNAc-Ins (70). Mixtures of two of these standards and Ins were run in parallel on the same plate, and the positions of the respective standards were highlighted on the borders. The presence of Ins in 839 and gpi7 is probably due to inadvertent hydrolysis by HF favored by heat production during neutralization at the end of the HF treatment.

**Figure 4.** Incorporation of [2-3H]Ins into proteins of *gpi* mutants. 3 × outcrossed mutant strains were grown to mid-log phase, and were labeled with [2-3H]Ins. Proteins were extracted, run in SDS-PAGE, and revealed by fluorography. Each lane contains the total extract of 2.5 OD600 U of cells labeled with 5 μCi of [2-3H]Ins. It should be noted that mature GPI-anchored proteins are extensively and heterogeneously glycosylated, which leads to crowding at the border of the lane and smearing out (33, 55). In parallel, the four strains from individual tetrads of the third outcross (see below) of each mutant were labeled with [2-3H]Ins to determine the efficiency of incorporation of [2-3H]Ins into mutant strains. Efficiency of incorporation was calculated by dividing the mean of cpm in the lipid extracts of the two mutants by the mean of cpm of the two wild-type strains derived from a single tetrad. Given as percentage of wild type, mutants incorporated with efficiencies of 104% (gpi4), 72% (gpi5), 81% (gpi6), 95% (gpi7-1), 123% (gpi7-2), 108% (gpi7-3), 120% (gpi7-4), 155% (gpi8), 124% (gpi9).

gpi4, gpi5, gpi6, and gpi9. Four isolates accumulating lipid γ did not complement each other, and were classified as gpi7. Labeling of diploid strains also allowed to conclude that lipid accumulation in gpi4, gpi5, gpi6, gpi7, gpi8, and gpi9 is a recessive trait.

The three GPI biosynthesis intermediates of yeast characterized so far contained an acyl chain on the Ins, rendering them resistant to PI-PLC (9, 55, 70). The [2-3H]Ins–labeled lipid extracts of all mutants were treated with PI-PLC and analyzed by TLC/fluorography. All abnormal mutant lipids were resistant to PI-PLC, whereas PI was completely hydrolyzed as expected (data not shown). Thus, by their comigration with well-characterized GPI intermediates on TLC, by the comigration of their HF fragments with GPI-derived HF fragments, and by their resistance to PI-PLC, the abnormal [2-3H]Ins-labeled mutant lipids behave as biosynthetic intermediates of the GPI pathway. To con-
firm that the abnormal lipid accumulating in \textit{gpi8} is identical with CP1/CP2 (Fig. 3), we performed additional chemical or enzymatic treatments. Thereby the abnormal lipid of \textit{gpi8} was compared with the well-characterized CP's contained in the [2-^3H]mannose-labeled lipid extract of \textit{pmi40}, a mutant which, at 37°C, incorporates high amounts of [2-^3H]mannose due to a temperature-dependent defect of mannose biosynthesis (57, 70). As reported previously, all lipid moieties of CP1 and CP2 are removed by mild base hydrolysis; they are cleaved by GPI-PLD and only three of the four mannoses of the isolated head groups are protected against JBAM (70). As shown in Fig. 6, treatment of CP1 and CP2 with JBAM increases their mobility to the extent that is expected for the removal of a single mannose residue. The abnormal lipid of \textit{gpi8} shows the same behavior as the authentic CP2 from \textit{pmi40} in all treatments. We thus conclude that \textit{gpi8} accumulates a complete GPI precursor. To confirm that lipid \( \gamma \) of \textit{gpi7} is an earlier intermediate of GPI biosynthesis, the double mutant \textit{gpi7-1 gpi8} was constructed. The double mutant only accumulated lipid \( \gamma \) (not shown). Thus, \textit{gpi7} is epistatic to \textit{gpi8}, a finding consistent with the idea that lipid \( \gamma \) is a precursor of CP2.

**Secretion of Invertase Is Independent of the Surface Expression of \( \alpha \)-agglutinin and Maturation of Gas1p**

While mutants deficient in the surface expression of \( \alpha \)-agglutinin but able to secrete acid phosphatase had been selected, the phenotype of these mutants with regard to secretion of soluble proteins and surface expression of \( \alpha \)-agglutinin had to be verified. Invertase was induced by glucose deprivation both after a 10-min and a 1-h preincubation at 37°C. The latter time was chosen to demonstrate invertase secretion in the time window during which \( \alpha \)-agglutinin normally appears at the cell surface (36). As can be seen in

![Figure 6. Characterization of the abnormal lipid accumulating in \textit{gpi8}. \textit{Gpi8} was labeled with [2-^3H]Ins, \textit{pmi40} with [2-^3H]-mannose (70), both labelings at 37°C. Desalted lipid extracts were subjected to mild base hydrolysis, GPI-PLD treatment, or JBAM treatment as indicated at the bottom (+). Control incubations without the hydrolytic agent were done in parallel (–). Treated lipids were desalted and analyzed by TLC/fluorography. DPM, dolicholphosphomannose.](image)

| Table 1. Summary Table |
|------------------------|
| Complementation class  | \( ^{\circ} \) C | gpi4-1 | gpi5-1 | gpi6-1 | gpi7-1 | gpi7-2 | gpi7-3 | gpi7-4 | gpi8-1 | gpi9-1 | W303 |
|------------------------|
| Growth                 | 24 | + | + | + | + | + | + | + | + | + | + | + | + |
|                        | 37 | + | + | + | + | + | + | + | + | + | + | + | + |
| Accumulation of abnormal lipid (Fig. 3) | 24 | + | + | + | + | + | + | + | + | + | + | + | + |
|                        | 37 | + | + | + | + | + | + | + | + | + | + | + | + |
| Growth on 1 mg/ml CFW (Table I) | 24 | + | + | + | + | + | + | + | + | + | + | + | + | + |
|                        | 37 | + | + | + | + | + | + | + | + | + | + | + | + | + |
| Secretion of invertase (Fig. 7) | 37 | + | + | + | + | + | + | + | + | + | + | + | + | + |
| Induction of \( \alpha \)-agglutinin on cell surface at 37°C (Fig. 8) | 37 | + | + | + | + | + | + | + | + | + | + | + | + | + |
| Accumulation of immature Gas1p (Fig. 9) | 37 | + | + | + | + | + | + | + | + | + | + | + | + | + |
| Slowed export of Gas1p out of ER (Fig. 10) | 37 | + | + | + | + | + | + | + | + | + | + | + | + | + |
| Hypersensitivity to vanadate | 37 | n.t.* | n.t. | n.t. | n.t. | + | + | + | + | + | + | n.t. | + |
| Sensitivity to hygromycin B (50 \( \mu \)g/ml) | 37 | n.t.* | n.t. | n.t. | + | + | + | + | + | + | + | + | + | + |
| Growth on Ca\( ^{++} \) (50 mM) | 37 | n.t.* | n.t. | n.t. | + | + | + | + | + | + | + | + | + | + |
| Status of N-glycans of invertase (Fig. 11) | 37 | n.t.* | n.t. | n.t. | + | + | + | + | + | + | + | + | + | + |
| Incorporation of [2-^3H]Ins into proteines | 37 | n.t.* | n.t. | n.t. | + | + | + | + | + | + | + | + | + | + |
| Size of HF fragment of abnormal GPI lipid | 37 | M0 | M0 | M0 | M2 | M4 | M4 | M4 | M4 | M4 | CP1 | **M0 | CP2 |
|                        | 37 | de. | s.r. | s.r. | s.r. | s.r. | s.r. | s.r. | s.r. | s.r. | s.r. | s.r. | s.r. | s.r. |

* Not tested;
\(^{1}\), normal;
\(^{1}\), dependent;
\(^{1}\), reduced;
\(^{1}\), slightly reduced;
** accumulates several intermediates from GlcN-acylPI up to CP2.

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Figure 7. Secretion of invertase by gpi mutants. 3 × outcrossed strains were grown to mid-log phase at 24°C, were preincubated in SD, CUA for 1 h at 37°C, and invertase secretion was induced by transferring cells into SD, 0.05 CUA. After further incubation at 37°C for 0, 15, 30, 45, or 60 min, periplasmic invertase activity was determined.

Fig. 7, invertase was secreted into the periplasmic space by all mutants except for gpi6, which secreted normally immediately upon shift to 37°C (not shown), but was unable to secrete invertase after 1 h of preincubation at 37°C. Incidentally, normal secretion of invertase also documents that a given mutant has no defects in transcription (4, 5), translation, and translocation of secretory proteins. α-Agglutinin expression was measured by an ELISA test, whereby the conditions and the duration of induction with a factor were the same as in the initial mutant selection procedure (Fig. 8). A conceptual difficulty of this assay lies in the fact that α-agglutinin expression was tested after three outcrosses to X2180, a strain which has a relatively high, constitutive level of expression, and which induces α-agglutinin only 1.3-fold (79). Thus, the different mutants are not isogenic and cannot be compared among each other, but each mutant has to be considered independently. In doing so, one can see that in all but three mutants, the induction of α-agglutinin expression on the cell surface at 37°C is significantly lower than at 24°C. Exceptions are gpi7-1, gpi7-4, and gpi8. These mutants can be assumed to have filtered through the original immunoselection, because gpi7-4 and gpi8 were present in the same clone, and gpi7-1 was combined with another, unrelated mutation causing a ts growth phenotype (see above). Thus, it is conceivable that the combination of mutations in these original isolates resulted in a low expression of α-agglutinin at 37°C.

To test further whether GPI anchor addition was compromised, the biosynthesis of Gaslp was studied in the mutants blocked at later stages of GPI biosynthesis. On SDS-PAGE, the ER form of Gaslp has an apparent molecular mass of 105 kD; upon entry into the Golgi apparatus, the elongation of N- and O-glycans increases the size to 125 kD (17, 74). Gaslp is retained in the ER as long as the GPI anchor is not attached to it (26, 53). Protein extracts from mutants precultured at 24° or 37°C were analyzed by Western blotting with anti-Gaslp antibody. As can be seen in Fig. 9, as compared to wild-type cells, the relative amount of the ER precursor form of Gaslp was increased in several mutants already when they were grown at 24°C, and this tendency was enhanced in cells grown at 37°C. This suggested that the maturation of Gaslp was delayed in these mutants. To further document this idea, the transit of Gaslp from the ER to the Golgi apparatus was studied by pulse-chase experiments in gpi7-1, gpi8, and 839, three strains which secrete invertase normally (Fig. 7). As shown in Fig. 10, maturation of the pulse-labeled 105-kD ER form of Gaslp into the mature 125-kD form during chase at 37°C was severely delayed in gpi8 and 839, and somewhat delayed in gpi7-1, but eventually still occurred. The delay can account for the accumulation of immature Gaslp observed by Western blotting (Fig. 9); the fact that maturation of Gaslp is eventually still possible is in keeping with the fact that these strains still can grow at 37°C.

N-Glycosylation of Most gpi Mutants Is Normal

Mutants deficient in the biosynthesis of the dolichol-linked oligosaccharide precursors for N-glycosylation (alg2, alg3) are not deficient in the biosynthesis of GPI anchors (8), nor do they accumulate any abnormal [2-3H]Ins-labeled lipids (data not shown). Nevertheless, we wanted to rule
Figure 9. Gpi7 and gpi8 contain increased amounts of immature Gaslp. 3 × outcrossed strains were grown to mid-log phase at 24°C, and were then further incubated for 1 h at 24°C or 37°C. Proteins were extracted, separated in SDS-PAGE, and blotted. Western blotting was carried out with rabbit anti-Gaslp followed by sheep anti-rabbit-IgG/peroxidase, and bands were revealed by chemiluminescence.

out that the accumulation of abnormal GPI intermediates in gpi mutants was an indirect consequence of more general perturbations of the ER and the secretion pathway. Since perturbations of this kind very often compromise the N-glycosylation and/or the elongation of N-glycans, we chose to monitor the N-glycosylation of invertase. The electrophoretic mobility of secretory invertase in native gels is a good indicator of the status of N-glycans on this glycoprotein (1, 2). Native gel electrophoresis showed that invertase of gpi9 is underglycosylated to the same extent as the invertase retained in the ER of sec18 cells, that invertase of gpi4 and gpi6 is partially underglycosylated, and that the other gpi mutants glycosylated invertase normally (Fig. 11). This suggests that gpi4, gpi6, and gpi9 contain a pleiotropic mutation affecting the GPI biosynthesis pathway, as well as N-glycosylation. It should be noted that these mutants accumulate the same GPI intermediate (GlcN-acylPI) as pmi40, sec53, sec59, and dpm1, all mutants deficient in the biosynthesis or activation of mannose (9, 55, 70). The accumulation of the abnormal lipid of gpi4, gpi5, gpi6, and gpi9 mutants persists even if mannose is added to the culture medium (not shown). Thus, gpi4, gpi6, and gpi9 may be further genes required for the activation of mannose.

Gpi Mutants Are Hypersensitive to Calcofluor White and Hygromycin B

Sequence analysis of several cell wall proteins reveals the presence of COOH-terminal hydrophobic sequences that may direct the attachment of a GPI anchor (72), and for certain proteins, the GPI anchor represents a necessary and sufficient signal allowing them to get targeted and integrated into the cell wall (69, 80). These findings led us to probe the intactness of the cell walls of gpi mutants with calcofluor white (CFW) (64). As shown in Table II, wild-type cells are not inhibited by 1.5 mg/ml of CFW, whereas all mutants that are not ts for growth in the absence of CFW are inhibited by the dye at 37°C. On the other hand, five mutants (gpi4, gpi7-1, gpi7-4, gpi8, and gpi9) are not able to grow in high concentrations of CFW already at 24°C, indicating that their defect can be made apparent already at 24°C.

An increased fragility of the cell wall at 37°C was also indicated by the fact that several mutants did not grow in the...
Table II. Calcofluor White Sensitivity of Yeast GPI Mutants

| Strain  | CFW concentration (mg/ml) | 0       | 0.5      | 1       | 1.5      |
|---------|---------------------------|---------|----------|---------|----------|
| W303    | 24°C                      | ++      | ++       | ++      | ++       |
|         | 37°C                      | ++      | ++       | ++      | ++       |
| gpi4-1  | 24°C                      | ++      | ++       | ++      | +        |
|         | 37°C                      | --      | --       | --      | --       |
| gpi5-1  | 24°C                      | ++      | ++       | ++      | ++       |
|         | 37°C                      | +       | +        | -       | _        |
| gpi6-1  | 24°C                      | ++      | ++       | ++      | ++       |
|         | 37°C                      | --      | --       | --      | --       |
| 839     | 24°C                      | ++      | +        | +       | +        |
|         | 37°C                      | ++      | +        | --      | --       |
| gpi7-1  | 24°C                      | ++      | +        | ++      | ++       |
|         | 37°C                      | +       | +        | -       | _        |
| gpi7-2  | 24°C                      | ++      | +        | +       | +        |
|         | 37°C                      | +       | +        | -       | _        |
| gpi7-3  | 24°C                      | ++      | +        | +       | +        |
|         | 37°C                      | +       | +        | +       | +        |
| gpi7-4  | 24°C                      | ++      | ++       | ++      | ++       |
|         | 37°C                      | +       | +        | +       | +        |
| gpi8-1  | 24°C                      | ++      | +        | +       | +        |
|         | 37°C                      | +       | +        | +       | +        |
| gpi9-1  | 24°C                      | ++      | +        | +       | +        |
|         | 37°C                      | --      | --       | --      | --       |

**Discussion**

We have developed a new approach for the selection of GPI-anchoring mutants in yeast. The procedure selects cells that do not express a GPI protein at the cell surface, and follows the same strategy as was used to isolate mammalian GPI-anchoring mutants (28). Since GPI anchoring has been claimed to be a vital process for yeast cells, it was necessary to select for temperature-sensitive mutants. α-Agglutinin, although minor among the numerous GPI-anchored proteins, represents an ideally suited target antigen for immunoselection. It can be induced after a temperature shift, and it becomes detectable on the outside of the cell wall, whereas other GPI proteins such as Gas1p remain anchored in the plasma membrane, and cannot be detected by antibodies on intact cells. Since the negative immunoselection enriched not only for gpi mutants but, a priori, also selected for mutants in signal transduction via the α-factor receptor, transcription, translation, translocation, secretion, and cell-wall integration of α-agglutinin, it was necessary to perform additional screens. By eliminating mutants unable to induce and secrete acid phosphatase at 37°C, mutants deficient in transcription, translation, translocation, and secretion are removed, and theoretically one is left with mutants deficient in GPI anchoring, α-factor receptor signaling, and cell-wall integration. Among those, our screen detected gpi mutants at a frequency of 1:70, and we have not tested whether the other mutants really are deficient in signaling or cell-wall integration. It is somewhat difficult to estimate the efficiency of our selection procedure. When screening for colonies that fail to incorporate [2-3H]Ins into proteins, Leidich et al. (33) isolated five mutants from 25,000 colonies tested, but it remains uncertain if any of our mutants would have scored in their screen, since none of our mutants seems to be deficient in [2-3H]Ins incorporation into proteins to the same extent as the mutants isolated by Leidich et al. (33). On the other hand, it is quite conceivable that our screening procedure selected for leaky mutants, since a mutant that rapidly dies at 37°C would probably not have scored as a secretor in the 2-d plate assay for secretion of acid phosphatase. Yet, we believe that GPI anchoring is affected in all of our mutants, since all but the gpi9 mutant accumulate a well-defined GPI lipid intermediate, suggesting that one specific step of the pathway has become rate-limiting in each mutant. Such defects are compatible with the fact that all of the mutants are recessive, and that among the mutants that have a growth defect at 37°C, the ts growth phenotype cosegregates with the accumulation of an abnormal lipid. By testing a large panel of known mutants, we also could exclude that the accumulation of specific GPI lipids occurred as an indirect consequence of some other perturbation of the secretory pathway; neither secretion mutants (sec1 to sec 23) (16, 52, 61) nor ER or Golgi-retention mutants (erd1, pmr1, anp1, van1) (6, 22, 66), nor mutants in N-glycosylation (alg2, alg3) (27), nor mutants in O-glycosylation (mnn1, mnn2, mnn3, mnn5, mnn9, mnt1) (1, 23), nor in protein synthesis (prt1-1) accumulated any abnormal [2-3H]Ins-labeled lipids (Sipos, G., and M. Benghezal, unpublished data). In fact, the only glycosylation mutants that accumulate abnormal GPI intermediates are some mutants with defects in mannose metabolism (sec53, sec59, dpm1, dpm40) and some of our mutants which accumulate GlcN-aclylPI. It is noteworthy that none of the 800 isolates tested exhibited any defect in the biosynthesis of PI, inositolphosphoceramides, mannosylinositol phosphoceramide, or inositolphospho-mannosylinositolphosphoceramide (61, 71), a finding that argues the other perturbation of the secretory pathway; neither secretion mutants (sec1 to sec 23) (16, 52, 61) nor ER or Golgi-retention mutants (erd1, pmr1, anp1, van1) (6, 22, 66), nor mutants in N-glycosylation (alg2, alg3) (27), nor mutants in O-glycosylation (mnn1, mnn2, mnn3, mnn5, mnn9, mnt1) (1, 23), nor in protein synthesis (prt1-1) accumulated any abnormal [2-3H]Ins-labeled lipids (Sipos, G., and M. Benghezal, unpublished data). In fact, the only glycosylation mutants that accumulate abnormal GPI intermediates are some mutants with defects in mannose metabolism (sec53, sec59, dpm1, dpm40) and some of our mutants which accumulate GlcN-aclylPI. It is noteworthy that none of the 800 isolates tested exhibited any defect in the biosynthesis of PI, inositolphosphoceramides, mannosylinositol phosphoceramide, or inositolphospho-mannosylinositolphosphoceramide (61, 71), a finding that argues that our selection procedure enriched for GPI mutants, or else selected against defects in the biosynthesis of these phosphoinositides.

What are the steps which are blocked in the various mutants? Several mutants (gpi4-gpi6, gpi9) accumulate a GlcN-aclylinositol-lipid intermediate, and therefore might have a defect in the α1,4-mannosyltransferase adding the first mannose of the GPI core structure or in the generation of dolicholphosphomannose required for this trans-
ferase (42, 55). Although both elongation of N-glycans and GPI biosynthesis are compromised in some of these mutants, the defect may well concern biosynthesis and transport of dolicholphosphomannose, rather than biosynthesis of GDP-mannose, since dolicholphosphomannose seems to be required for both of these processes. In fact, *dmp1*, a ts mutant in dolicholphosphomannose-synthase, has been shown to make (55) and to secrete (Benghezal, M., unpublished results) a severely underglycosylated invertase. This suggests that Och1p (50, 51) or subsequent elongating Golgi mannosyltransferases depend on the presence of some dolicholphosphomannose-derived core mannoses. Hence, the presence of some invertase with slightly or drastically increased mobility in *gpi4*, *gpi6*, and *gpi9* at 37°C (Fig. 11) might be indicative of some difficulty in making dolicholphosphomannose. Isolate 839 and *gpi7* might be deficient in the α1,2-mannosyltransferase adding the third mannosyl and the phosophoethanolamine group of the GPI core structure, respectively. 839 and *gpi7* might be in genes homologous to the mammalian PIG-B and PIG-F (29, 31). *Gpi8* might be deficient in the hypothetical transamidase that attaches CP’s to GPI proteins or in a flippase that transfers CP’s from the cytosolic to the luminal side of the ER (76, 77). At the moment, direct assays to measure these activities in microsomes have yet to be developed. Recently, *gaa1*, a ts mutant with a phenotype similar to *gpi8*, has been described (20). We find that *GPI8* and *GAA1* are different genes since *gpi8* and *gaa1* mutants are complementing each other and are synthetic lethal when combined in a single haploid strain. Also, transfection of the *GAA1* gene on a multicopy vector does not cure the defects of *gpi8* cells (not shown). Although not all mutants are ts for growth, cloning of the various *gpi* genes should be aided by the fact that all mutants are defective for growth on CFW at 37°C.

Some mutants accumulate severely reduced amounts of [2-3H]lns-labeled proteins, but don’t accumulate large amounts of abnormal lipids, whereas others accumulate large amounts of abnormal lipids, but are less severely affected in the incorporation of [2-3H]lns into proteins. Mutants of both types can even be found among the various alleles of a single complementation class, *gpi7*. To explain this paradox, several possibilities might be considered: (a) It should be kept in mind that our pulse-labeling protocol in trying to obtain additional mutations affecting the interaction of enzymes of the multienzyme complex forming an assembly line in which substrates are transferred from one enzyme to the next without having to diffuse freely in the membrane. In this case, a mutation that renders a given enzyme of the assembly line rate limiting might lead to a significant reduction of GPI biosynthesis without causing the accumulation of an abnormal lipid, as long as the GPI intermediates proximal to the blocked enzyme cannot leave the assembly line. On the other hand, mutations affecting the interaction of enzymes of the multienzyme complex might disrupt the complex and lead to the accumulation of abnormal lipids that now have to reach the following enzyme by diffusion. (f) Mutations might also render enzymes insensitive to some negative feedback control, which might coordinate the amount of GPI biosynthesis with the rate of GPI protein synthesis.

The increased sensitivity of *gpi* mutants to CFW and hygromycin B suggests that GPI-anchored proteins are required for the integrity of the yeast cell wall. The requirement of GPI anchoring for cell-wall integrity has also been documented recently by the group of Frans Klis. Deletion of *GAL1* results in CFW hypersensitivity (63) and *cwh6*, a CFW-hypersensitive mutant, has a defect in the yeast homologue of PIG-A, a gene required for the first step of GPI biosynthesis, namely the addition of GlcNAc onto PI (78).

It appears that our mutant isolation screen is by no means exhaustive, since many mutants were only obtained once. In addition, several intermediates of the GPI pathway such as GlcNAc-PI, GlcN-PI, and GlcN-acetylglucosaminyl-PI-lipid would not have been detected since they are expected to comigrate on TLC with PI and inositolphosphoceramides. We currently use slight modifications of this screening protocol in trying to obtain additional *gpi* mutants.

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