Two Pathways of Sphingolipid Biosynthesis Are Separated in the Yeast Pichia pastoris

Philipp Ternes*, Tobias Wobbe*, Marnie Schwarz*, Sandra Albrecht*, Kirstin Feussner‡, Isabelle Riezman‡, James M. Cregg‡‡, Ernst Heinz§, Howard Riezman§, Ivo Feussner‡, and Dirk Warnecke§

From the ‡Department of Plant Biochemistry, Albrecht von Haller Institute for Plant Sciences, Georg August University, Göttingen, Germany, the §Biozentrum Klein Flottbek, University of Hamburg, Hamburg, Germany, the ¶Department of Molecular Microbiology and Genetics, Georg August University, Göttingen, Germany, the ‡‡Department of Biochemistry, University of Geneva, Geneva, Switzerland, and the ‡‡Keck Graduate Institute of Applied Life Sciences, Claremont, CA, U.S.A.

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* These authors contributed equally to this work

1 Corresponding author. Present address: Department of Physical Biochemistry, Max Planck Institute for Biophysical Chemistry, Am Fassberg 11, 37077 Göttingen, Germany. Tel.: +49-201 2918; Fax: +49-551-201 2905; E-mail: philipp.ternes@mpibpc.mpg.de

2 Present address: Department of Plant Cell Biology, Albrecht von Haller Institute for Plant Sciences, Georg August University, Göttingen, Germany

3 Present address: Department of Biochemistry, University of Cambridge, Cambridge, UK

4 Corresponding author: Biozentrum Klein Flottbek, University of Hamburg, Ohnhorstristr. 18, 22609 Hamburg, Germany. Tel.: +49-40-42816 335; Fax: +49-40-42816 254; E-mail: warnecke@botanik.uni-hamburg.de.

While the yeast Saccharomyces cerevisiae has only one sphingolipid class with a headgroup based on phosphoinositol, the yeast Pichia pastoris as well as many other fungi have a second class, glucosylceramide, which has a glucose headgroup. These two sphingolipid classes are in addition distinguished by a characteristic structure of their ceramide backbones. Here, we investigate the mechanisms controlling substrate entry into the glucosylceramide branch of the pathway. By a combination of enzymatic in vitro studies and lipid analysis of genetically engineered yeast strains, we show that the ceramide synthase Bar1p occupies a key branching point in sphingolipid biosynthesis in P. pastoris. By preferring dihydroxy sphingoid bases and C_{16}/C_{18} acyl-coenzyme A as substrates, Bar1p produces a structurally well-defined group of ceramide species, which is the exclusive precursor for glucosylceramide biosynthesis. Correlating with the absence of glucosylceramide in this yeast, a gene encoding Bar1p is missing in S. cerevisiae. We could not successfully investigate the second ceramide synthase in P. pastoris, which is orthologous to S. cerevisiae Lag1p/Lac1p. By analyzing the ceramide and glucosylceramide species in a collection of P. pastoris knockout strains in which individual genes encoding enzymes involved in glucosylceramide biosynthesis were systematically deleted, we show that the ceramide species produced by Bar1p have to be modified by two additional enzymes, sphingolipid Δ4 desaturase and fatty acid α-hydroxylase, before the final addition of the glucose headgroup by the glucosylceramide synthase. Together, this set of four enzymes specifically defines the pathway leading to glucosylceramide biosynthesis.
In eukaryotic cells, sphingolipids are essential constituents of the plasma membrane as well as of intracellular membranes (1). In addition, intermediates of their biosynthesis and breakdown are important signaling molecules (2, 3). Two classes of complex sphingolipids can be distinguished based on the nature of their polar headgroups: phosphosphingolipids and glycosphingolipids. Phosphosphingolipids carry hydrophilic headgroups connected to the ceramide (Cer) backbone via a phosphodiester bond, whereas glycosphingolipids carry sugar residues directly linked to the ceramide backbone via a glycosidic bond. The typical phosphosphingolipid in mammalian cells is sphingomyelin with a phosphocholine headgroup, while the phosphosphingolipids of plants and fungi have headgroups based on phosphoinositol. The simplest compound of the latter class is inositol phosphorylceramide (IPC), but often sugar residues and additional phosphoinositol units are added to form glycosylated IPC (GIPCs). Glycosylceramides, in contrast, are found in all eukaryotic kingdoms. They can be either based on glucosylceramide (GlcCer) or galactosylceramide (GalCer), with GlcCer predominating in plants and fungi (4–6). Particularly in animals, both GlcCer and GalCer may carry extended, branched and highly variable glycan headgroups (7).

Important insights into sphingolipid metabolism and functions came from studies on the yeast \textit{Saccharomyces cerevisiae} (8). However, this yeast is an exception among eukaryotic organisms because it contains only one class of complex sphingolipids, namely (G)IPCs, but often sugar residues and additional phosphoinositol units are added to form glycosylated IPC (GIPCs). Glycosylceramides, in contrast, are found in all eukaryotic kingdoms. They can be either based on glucosylceramide (GlcCer) or galactosylceramide (GalCer), with GlcCer predominating in plants and fungi (4–6). Particularly in animals, both GlcCer and GalCer may carry extended, branched and highly variable glycan headgroups (7).

As illustrated in Fig. 1, GlcCer and (G)IPCs in fungi differ not only by the nature of their polar headgroups – glucose or (glycosyl)phosphoinositol – but also by the structure of their Cer backbones (4, 9). These include characteristic differences found in both the sphingoid base (LCB) and the amide-linked acyl group. The final structure of the LCbs found in GlcCer is defined by the enzymes introducing Δ4- and Δ8-double bonds as well as a C9-methyl group into Cer (12–14), whereas in (G)IPCs, the LCB typically carries a hydroxy group at the C4 position (15, 16). The characteristic feature distinguishing the fatty acids in GlcCer and (G)IPCs is their α-hydroxylation by the fatty acid α-hydroxylase Scs7p (15). A characteristic feature distinguishing the fatty acids in GlcCer and (G)IPCs is their chain length. While GlcCer typically has a C16 or C18 long-chain fatty acid, (G)IPCs are characterized by a very long-chain fatty acid with 24 or 26 carbons. Elongation of long-chain to very long-chain fatty acids is performed at the level of acyl-coenzyme A (CoA) by the fatty acid elongase complex.

Despite the fact that all enzymes responsible for the biosynthesis of GlcCer and IPC including their specific backbone structures are known and the corresponding genes have been cloned, it is still an open question how these enzymes integrate into specific pathways leading to just two structurally well-defined end products, GlcCer and IPC. In this study, we investigate the hypothesis that the separation between these two pathways is initiated by the activity of Cer synthases, which link an LCB and a CoA-activated fatty acid. The phylogenetic tree in Fig. 2 shows that many eukaryotic organisms have several Cer synthases, suggesting that individual isoforms may have evolved functional specializations. This has been investigated more closely in animal cells, where Cer synthases differ regarding their preferred acyl-CoAs chain length as well as in their physiological functions (17, 18).

To investigate how substrate entry into the pathway for GlcCer biosynthesis is controlled, we combined \textit{in vitro} investigations of the \textit{P. pastoris} Cer synthase Bar1p with lipid analysis of a collection of \textit{P. pastoris} strains in which the enzymes involved in GlcCer biosynthesis were systematically deleted (Fig. 1 and Table 1). It turned out that efficient GlcCer biosynthesis requires the introduction of specific functional
EXPERIMENTAL PROCEDURES

Yeast Strains—The construction of an S. cerevisiae strain expressing P. pastoris Bar1p under the control of the constitutive GPD1 promoter, of the P. pastoris knockout strains shown in Fig. 1, and of the P. pastoris strains overexpressing GlcCer synthase (GCS) is described in the Supplemental Methods. Genotypes and references for these strains are listed in Table 1.

Yeast Culture and Lipid Extraction for the Analysis of Cer and GlcCer—S. cerevisiae strains WBY616-LAG1 and WBY616-BAR1 as well as P. pastoris strains with GS115 background were grown in liquid YPD medium (1% yeast extract; 2% peptone; 2% glucose; all w/v). P. pastoris cells overexpressing GCS (strains gcsΔGCS, delta4ΔGCS, and ssc7ΔGCS) were switched to MM medium (1.34% yeast nitrogen base; 0.4 µg/ml biotin; 0.5% methanol; all w/v) 24 hours before harvesting to induce the AOX1 promoter. In the case of P. pastoris, cells from 100 ml of culture were harvested by centrifugation, washed with water, weighed to determine the fresh weight, resuspended, and heated in a boiling water bath for 15–20 min to inactivate lipid-metabolizing enzymes. In the case of S. cerevisiae, growth of a 100 ml culture was stopped by adding 5 g of trichloroacetic acid and heating in a boiling water bath for 10 min. The cells were harvested by centrifugation and washed twice with phosphate-buffered saline (137 mM NaCl; 2.7 mM KCl; 101 mM Na₂HPO₄; 17.6 mM KH₂PO₄) before heating in a boiling water bath for 10 min. The boiled cells were sedimented by centrifugation and resuspended in 8 ml (P. pastoris) or 9 ml (S. cerevisiae) of chloroform/methanol, 1:2 (v/v). To allow quantification of Cer and GlcCer, 15 nmol of Cer containing either a C₁₇ fatty acid (S. cerevisiae) or a C₁₅ fatty acid (P. pastoris) and 15 nmol of GlcCer containing a C₁₂ fatty acid (P. pastoris only) were added as internal standards. After shaking at 4°C for 4–5 hours, the cells were sedimented and the supernatant was exchanged for chloroform/methanol, 2:1 (v/v) and the shaking was continued over night. The supernatants from both extractions were combined and filtered through cotton to remove cell debris (P. pastoris only). A phase separation was induced by adding 8 ml (P. pastoris) or 9 ml (S. cerevisiae) of chloroform and 6 ml (P. pastoris) or 6.75 ml (S. cerevisiae) of 0.45% NaCl (w/v), vortexing, and centrifuging (19). The lower phase was transferred to a glass tube, the upper phase was extracted a second time with 16 ml (P. pastoris) or 18 ml (S. cerevisiae) chloroform, and the solvent was evaporated under a stream of nitrogen.

Mild Alkaline Hydrolysis of Lipid Extracts—To remove glycerolipids, the dried lipid extracts were dissolved in 2 ml of 0.2 M NaOH in methanol and heated to 40°C for 90 min. Phase separation was induced by adding 4 ml of chloroform and 1.5 ml of 0.45% NaCl (w/v), vortexing, and centrifuging (19). The lower phase was transferred to a glass tube, the upper phase was extracted a second time with 4 ml chloroform, and the solvent was evaporated under a stream of nitrogen.

Fractionation of the Lipid Extract—Before first use, a 100 mg/1 ml Strata SI-1 silica cartridge (Phenomenex, Torrance, CA, U.S.A.) was flushed with 4 ml of chloroform, 4 ml of acetone/2-propanol, 9:1 (v/v), and 2 ml of methanol, and then equilibrated with 1 ml of chloroform. The dried lipid extract was dissolved in 1 ml of chloroform and loaded onto the cartridge. The lipids were eluted as three separate fractions with 2 ml of chloroform, 4 ml of acetone/2-propanol, 9:1 (v/v), and 2 ml of methanol. The acetone/2-propanol fraction was evaporated under a stream of nitrogen, dissolved in chloroform/methanol, 5:1 (v/v) and stored at 4°C until analysis by UPLC/MS. This fraction was shown by thin-layer chromatography (TLC) to contain both Cer and GlcCer.

Analysis of Cer and GlcCer by UPLC/MS—The molecular species of Cer and GlcCer present in the acetone/2-propanol fraction were separated on an ACQUITY UPLC™ system coupled to an LCT Premier™ electrospray ionization time-of-flight mass spectrometer (ESI-TOF-MS) analyzer
Chromatography was performed on an ACQUITY UPLC™ BEH SHIELD RP18 column (1 × 100 mm; particle size, 1.7 µm; Waters) at a temperature of 50°C and a flow rate of 0.2 ml/min. The Cer and GlcCer species were eluted under the following conditions: 80% solvent B for 0.5 min, followed by a gradient from 80 to 100% solvent B in 6.5 min, and finally 100% solvent B for 4 min. The column was re-equilibrated at 80% solvent B for 4 min. Solvent A was water/methanol/acetonitrile, 90 : 5 : 5 (v/v/v), solvent B was acetonitrile. 0.1% formic acid was added to both solvents to facilitate ionization.

Mass spectra in the range from 500 to 1000 Da with a mass resolution of > 104 were acquired by ESI-TOF-MS in positive ionization mode using ‘W’ optics and Dynamic Range Enhancement with a scan time of 0.5 s and an interscan delay of 0.1 s. The capillary and cone voltages were maintained at 2700 V and 30 V, and the desolvation and source temperatures at 250°C and 80°C, respectively. Nitrogen was used as cone (30 l/h) and desolvation gas (600 l/h). For exact mass measurement of > 5 ppm root mean squared, all analyses were monitored using leucine enkephaline (m/z = 556.2771; Sigma-Aldrich) and its double 13C isotopomer (m/z = 558.2828) as lock spray reference compound at a concentration of 0.5 µg/ml in acetonitrile/water, 1 : 1 (v/v) at a flow rate of 30 µl/min (515 HPLC pump, Waters). Data were recorded in centroid format and analyzed using MassLynx software (Waters).

Identity of Cer and GlcCer Species—The retention times of Cer species produced in the in vitro Cer synthase assay with single substrates (Supplemental Table S1) were used as references for the identification of Cer species in the lipid extracts from P. pastoris and S. cerevisiae. It was found that elongation of the fatty acid by two carbon atoms increases the retention time by ≈ 1.0 min. Concerning the functional groups on LCB and fatty acid, introduction of one double bond into the LCB decreases the retention time by ≈ 0.4 min, of an α-hydroxy group at the fatty acid by ≈ 0.6 min, and of a C4-hydroxy group at the LCB by ≈ 1.1 min. Thus, Cer species with a trihydroxy LCB and a non-hydroxylated fatty acid elute before isobaric species with a dihydroxy LCB and an α-hydroxylated fatty acid. This was supported by the lack of isomers with the longer retention times (representing the α-hydroxylated species) in the P. pastoris strain scs7A. This pattern was found to be consistent throughout the whole spectrum of Cer and GlcCer species. GlcCer species in P. pastoris consistently elute ≈ 1.5 min before the corresponding Cer species.

Yeast Culture and Lipid Extraction for the Analysis of IPC, MIPC and M(IP)_2C—P. pastoris cells were grown in liquid YPD medium, harvested by centrifugation, and stored at -20°C until lipid extraction. The cells were resuspended in 5 % (w/v) of ice-cold trichloroacetic acid, incubated on ice for 30 min, and washed twice with ice-cold water. 0.5–0.6 g fresh weight of cells was resuspended in 6 ml of ethanol/water/diethyl ether/pyridine/2 M ammonium hydroxide, 15 : 15 : 5 : 1:0.038 (v/v/v/v) (20). 5 nmol of Cer containing a C15 fatty acid and 5 nmol of GlcCer containing a C12 fatty acid were added as internal standards. Glass beads were added until slightly below the meniscus, and the samples were heated at 60°C for 30 min. During this time, each sample was vortexed twice for 3 min. The cells were sedimented by centrifugation and extracted a second time using the same procedure. The supernatants from both extractions were combined, mixed, split into two equal aliquots, and evaporated under a stream of nitrogen. To remove glycerolipids, one aliquot of each sample was dissolved in 2 ml of methanol/water/n-butanol/33 % (w/w) methylamine in ethanol, 4 : 3 : 1 : 5 (v/v/v/v/v) and heated at 55°C for 60 min. The solvent was evaporated under a stream of nitrogen.

Both hydrolyzed and non-hydrolyzed samples were dissolved in 2 ml of water-saturated n-butanol. The samples were washed by adding 2 ml of water, vortexing for 3 min, and centrifuging for 30–60 min at 1000 g to achieve phase separation. The upper phase was transferred to a glass tube, the lower phase was extracted a second time with 2 ml of water-saturated n-butanol, and the solvent was evaporated under a stream of nitrogen.

Analysis of IPC, MIPC and M(IP)_2C by MS-MS—The molecular species of IPC, MIPC, and M(IP)_2C present in the hydrolyzed samples were analysed on a 320-MS triple quadrupole mass
spectrometer (Varian, Santa Clara, CA, U.S.A.) in negative ionization mode. Individual molecular species of IPC and M(IP)\(_2\)C were detected by multiple reaction monitoring using a transition of 241 corresponding to phosphoinositol while for MIPC species, a transition of 421 corresponding to mannosylated phosphoinositol was used. Since no standards for IPC, MIPC, and M(IP)\(_2\)C were available, we used GlcCer containing a C\(_{12}\) fatty acid as internal standard for comparing the samples against each other. Therefore, all mol% reported in the figures have to be regarded as apparent mol%.

**Quantitative Analysis of the LCB Composition**—LCBs were liberated from whole cells or from GlcCer purified from a lipid extract of *P. pastoris* GS115 by strong alkaline hydrolysis with Ba(OH)\(_2\), converted to their DNP derivatives, and analyzed by reverse-phase high-performance liquid chromatography (HPLC) (12, 13). See Supplemental Methods for details.

**Yeast Culture and Preparation of Microsomes for in Vitro Assays**—Cells of the *S. cerevisiae* strain WBY616-BAR1 grown in 200 ml of liquid YPD were harvested by centrifugation, resuspended in 2 ml of Lysis Buffer (20 mM HEPES/KOH, pH 7.4; 25 mM KCl; 2 mM MgCl\(_2\); 250 mM sorbitol) and 50 µl Proteinase Inhibitor Cocktail (Sigma-Aldrich) per gram of cells, and broken by bead-bashing at 4°C for 1½ hours. Cell debris was removed by centrifuging at 1000 g at 4°C for 10 min. The supernatant was loaded on a 60% (w/w) sucrose cushion and centrifuged at 100000 g for 1 hour. The microsomes were collected from the interphase, snap-frozen in liquid nitrogen and stored at −80°C.

**In Vitro Assay of Cer Synthase Activity**—The in vitro Cer synthase activity was performed essentially as described in (21) and (22) with 1.5 µM defatted bovine serum albumin, 1 µM LCB, and 5 µM acyl-CoA, and 6.6 µg of microsomal protein in a final volume of 120 µl made up with Lysis Buffer. In case that several LCB or acyl-CoAs were mixed, the concentrations were 1 µM for each LCB and 5 µM for each acyl-CoA. Preliminary experiments showed that these high total concentrations of acyl-CoAs had no negative effect. Radiolabeled substrates were diluted with the corresponding unlabeled compound to achieve the desired molarity. The reaction was pre-incubated by shaking at 30°C for 5 min and started by adding either LCB or acyl-CoA, depending on the conditions to be tested. After shaking at 30°C for the times indicated in Results and in legend of Fig. 5, the reaction was stopped by adding 450 µl chloroform/methanol, 1 : 2 (v/v). A phase separation was induced by adding 150 µl chloroform and 150 µl water, vortexing, and centrifuging (23). The upper phase was discarded and the lower phase washed once with methanol/water, 1 : 1 (v/v). The lower phase was transferred to a new tube, dried under a stream of nitrogen, and dissolved in chloroform/methanol, 5 : 1 (v/v).

In case that the reaction was performed with either \(^3\)H-labeled LCB or \(^14\)C-labeled acyl-CoA, the reaction products were separated by TLC in chloroform/methanol, 100 : 7 (v/v), detected using a Cyclon PhosphorImager (Packard Instruments; now PerkinElmer, Waltham, MA, U.S.A.) for \(^3\)H and an FLA-3000 phosphorimager (Fujifilm, Tokyo, Japan) for \(^14\)C, and analyzed with ImageJ (http://rsb.info.nih.gov/ij). Cer was identified by co-migration with an unlabeled standard (detected by iodine staining). In the case of unlabeled substrates, the Cer species formed in the reaction were analyzed by UPLC/MS as described above.

**RESULTS**

**Generating a Collection of *P. pastoris* Mutant Strains Impaired in the Biosynthesis of GlcCer**—To investigate the pathway leading to GlcCer biosynthesis, we determined the molecular species of Cer and GlcCer in *P. pastoris* wild type (WT) and in mutant strains each impaired in the activity of one enzyme involved in GlcCer biosynthesis. For this purpose, we deleted the genes encoding the putative Cer synthase Bar1p, the fatty acid α-hydroxylase Scs7p, the sphingolipid ∆4-desaturase, the sphingolipid ∆8-desaturase, the sphingolipid-C9-methyltransferase and the GCS by homologous recombination (Fig. 1 and Table 1). In addition, we created three different strains overexpressing recombinant GCS under control of the strong *AOX1* promoter.

First, we checked both knockout and overexpressing strains for the presence of GlcCer
(Fig. 3). As expected, the lipid extract from WT cells showed a single band of GlcCer on the TLC plate while GlcCer was undetectable in the gcsΔ strain, confirming previous results (24). Also, the deletion of the gene encoding the ceramide synthase Bar1p resulted in the loss of GlcCer. This supports our hypothesis that Bar1p is responsible for the biosynthesis of those Cer species which are used as precursors for GlcCer biosynthesis. A similar finding has been reported for a knockout of the Bar1p ortholog in K. lactis (25). Surprisingly, deletion of the α-hydroxylase Scs7p or of the Δ4-desaturase also resulted in a complete loss of GlcCer. In contrast, GlcCer could still be detected in P. pastoris strains in which the sphingolipid Δ8-desaturase or the C9-methyltransferase were deleted.

Similarly unexpected results were obtained with the P. pastoris strains overexpressing GCS. While in the complemented strain gcsΔGCS, the intensity of the ‘normal’ GlcCer is strongly increased, this band is missing in the strains scs7ΔGCS and delta4ΔGCS lacking the α-hydroxylase or the Δ4-desaturase, respectively. Instead, a strong additional band appears above the ‘normal’ band in all three strains overexpressing GCS. From the MS analysis shown below, it can be concluded that the ‘normal’ band contains GlcCer species with an α-hydroxylated C_{10}/C_{18} fatty acid, while the additional band contains untypical GlcCer species with either a non-hydroxylated C_{10}/C_{18} fatty acid or an α-hydroxylated C_{24}/C_{26} fatty acid.

P. pastoris Strains Lacking GlcCer Show No Obvious Phenotype—All P. pastoris knockout strains including those which completely lack GlcCer were viable, and no obvious growth defects were observed in full (YPD) medium. Growth of the bar1Δ strain was indistinguishable from WT on YPD plates (Supplemental Fig. S1A). In addition, cell wall morphology and bud formation (calcofluor white staining), organization of the actin cytoskeleton (phalloidin-rhodamine staining), and the staining pattern of fluorescent markers directed to the endoplasmic reticulum (ER), ER exit sites, and Golgi apparatus were investigated, but no differences between the bar1Δ strain and the WT were found (Supplemental Fig. S1B).

### Analysis of Cer and GlcCer Species in P. pastoris Wildtype and Mutant Strains

In order to investigate how the enzymes highlighted in Fig. 1 cooperate during GlcCer biosynthesis, the molecular species of Cer and GlcCer were analyzed in P. pastoris WT cells and in the collection of mutant strains. For this purpose, the lipid extracts were fractionated on a silica cartridge, and the fraction containing Cer and GlcCer was analyzed by UPLC/MS. Individual Cer and GlcCer species were detected based on their retention times and exact masses (mass accuracy < 0.01 Da) and quantified relative to internal standards. The complete list of Cer and GlcCer species is shown in Supplemental Table S1.

Individual selections from this data set are displayed in Figs. 4, 6, and 7, depending on the structural features to be discussed. Since the absolute amounts of Cer (and to a lesser extent GlcCer) showed a much higher sample to sample variation than the relative proportions of individual species, we decided to display the data using a relative rather than an absolute scale. In Figs. 4, 6, and 7, 100% corresponds to 70 ± 60 nmol/g fresh weight for Cer and 30 ± 2 nmol/g fresh weight for GlcCer (average and standard deviations of three independent WT samples). Because of these standard deviations, only the absolute amounts of GlcCer, but not of Cer can be reliably compared between different strains. In contrast, the relative proportions of both Cer and GlcCer species within each strain were very reproducible (error bars in Figs. 4, 6, and 7). Since the UPLC/MS method does not allow fragmentation of the Cer and GlcCer species, only the total number of carbon atoms could be determined. But since P. pastoris sphingolipids contained > 95% C_{18} LCBs (Supplemental Fig. S2), the number of acyl carbons in the Cer and GlcCer species could be easily deduced and is referred to in the following text.

A Group of Cer Species with a Dihydroxy LCB and C_{10}/C_{18} Fatty Acids is the Precursor of GlcCer—Cer species in the WT strain can be separated into two groups, one with a dihydroxy LCB and C_{10}/C_{18} fatty acids, the other with a trihydroxy LCB and C_{24}/C_{26} fatty acids (Fig. 4). GlcCer species exclusively contained a dihydroxy
LCB and C_{16}/C_{18} fatty acids, indicating that Cer species from only one group can enter the pathway leading to GlcCer biosynthesis.

To test whether the Cer synthase Bar1p produces the Cer species available for GlcCer biosynthesis, we checked which Cer and GlcCer species could be detected in the bar1Δ strain (Fig. 4, bar1Δ; see Supplemental Fig. S4 for minor species). Strikingly, the Cer species with a dihydroxy LCB and C_{16}/C_{18} fatty acids as well as the corresponding GlcCer species disappeared, while the Cer species with a trihydroxy LCB and C_{24}/C_{26} fatty acids were unaffected. Very likely, the latter group of Cer species is produced by the activity of the second Cer synthase encoded in the P. pastoris genome, Lag1p (Fig. 2). A tiny proportion of GlcCer with a dihydroxy LCB and a C_{24} fatty acid could be detected in the WT, which was increased to a small but significant extent in the bar1Δ strain (Supplemental Fig. S4). In the gcsΔ strain, in which the GCS was deleted, GlcCer was missing, but both groups of Cer species were present. Surprisingly, the proportion of Cer species with a dihydroxy LCB and C_{16}/C_{18} fatty acids is not significantly increased although less Cer is used for GlcCer biosynthesis.

Together, these data suggest that the Cer synthase Bar1p produces a distinct group of Cer species with a dihydroxy LCB and C_{16}/C_{18} fatty acids that serve as precursors for GlcCer biosynthesis.

Bar1p Shows Cer Synthase Activity in Vitro with a Preference for Dihydroxy LCBs and C_{16}/C_{18} acyl-CoAs—To confirm the specificity of Bar1p for dihydroxy LCB and C_{16}/C_{18} fatty acids, in vitro Cer synthase assays were carried out. As enzyme source, an S. cerevisiae strain was engineered to express P. pastoris Bar1p as its only Cer synthase under the control of the constitutive GPD1 promoter. In the resulting strain, the genes encoding the endogenous Cer synthases Lag1p and Lac1p were deleted but the alkaline ceramidases Ype1p and Ydc1p were intact. Using ^3H-labeled sphinganine or sphing-4-enine and unlabeled acyl-CoAs, the formation of ^3H-labeled Cer could be detected with acyl chain lengths ranging from 16 to 22 carbons with a maximum at 18 (Supplemental Fig. S3). Using ^14C-labeled C_{18} acyl-CoA, the formation of ^14C-labeled Cer could be detected with all three LCBs tested: sphinganine, sphing-4-enine, and 4-hydroxsphinganine (structures shown in Fig. 1B). Cer formation using sphinganine or sphing-4-enine as substrates was three times more efficient than with 4-hydroxsphinganine.

In order to more systematically investigate different combinations of LCBs and acyl-CoAs, we developed a non-radioactive version of this assay, in which the Cer species produced in the reaction were analyzed by UPLC/MS. This allowed arbitrary combinations of LCBs and acyl-CoAs to be used as substrates either individually or as a mixture. With single LCBs and acyl-CoAs as substrates, Bar1p showed a clear specificity for C_{16} and C_{18} compared to longer acyl-CoAs. α-Hydroxylated species were preferred over non-hydroxylated C_{18} acyl-CoA, and the dihydroxy LCBs sphinganine and sphing-4-enine were preferred over the trihydroxy LCB 4-hydroxsphinganine (Fig. 5A, upper panel).

When substrate selectivity was tested using mixtures of different LCBs and acyl-CoAs, the preference for certain LCBs and acyl-CoAs became more pronounced than with individual substrates. Bar1p preferred C_{18} over C_{16} acyl-CoA and the ∆4-desaturated LCB sphing-4-enine over the saturated sphinganine, while 4-hydroxsphinganine was heavily discriminated against. α-Hydroxylated was strongly preferred over non-hydroxylated C_{18} acyl-CoA (Fig. 5A, lower panel).

An S. cerevisiae Strain Expressing Bar1p Produces Cer Species with Dihydroxy LCBs and C_{16}/C_{18} Fatty Acids—The results above were confirmed by analysis of the Cer species produced in vivo by the same Bar1p-expressing S. cerevisiae strain that was used as enzyme source for the in vitro assays. In the control strain (expressing S. cerevisiae Lag1p), the most abundant Cer species was composed of a trihydroxy LCB and an α-hydroxy C_{26} fatty acid, as expected (26, 27, 29). In the strain expressing P. pastoris Bar1p, however, Cer species with a dihydroxy LCB and α-hydroxy C_{16}/C_{18} fatty acids were prevalent (Fig. 5B). This was despite the fact that this strain contained a WT allele encoding the sphingolipid C4-hydroxylase Sur2p, so trihydroxy LCBs should be plentiful. As
in the *in vitro* assay, Bar1p discriminates against trihydroxy LCBs.

Together with the *in vitro* assay, these data show that the preference of Bar1p for dihydroxy LCBs and C_{16}/C_{18} acyl-CoAs is directly responsible for the characteristic structural features of the Bar1p-dependent Cer pool shown in Fig. 4.

Efficient GlcCer Biosynthesis Requires Structural Features Specific to the Bar1p-Dependent Cer Pool—We next addressed the question to which extent the other structural features highlighted in Fig. 1 were required for GlcCer biosynthesis. First, we consider the fatty acid hydroxylation of the Cer and GlcCer species shown in Fig. 4 (see Supplemental Fig. S4 for minor species). In the WT strain, Cer species with both α-hydroxylated and non-hydroxylated fatty acids were present. In contrast, GlcCer contained exclusively α-hydroxylated fatty acids. In the *scs7*Δ strain, in which the fatty acid α-hydroxylase is deleted, Cer species with α-hydroxylated fatty acids were missing with a concomitant increase in non-hydroxylated species. Strikingly, GlcCer was completely missing, showing that non-hydroxylated Cer cannot be converted to GlcCer. Fatty acid α-hydroxylation is thus essential for efficient GlcCer biosynthesis from the Bar1p-dependent Cer pool, but not for the biosynthesis of the Bar1p-dependent Cer pool itself.

The role of the desaturation and methylation of the LCB becomes evident in Fig. 6 (see Supplemental Fig. S5 for minor species). In this figure, only dihydroxy LCBs are presented, because Δ4-desaturation (including the subsequent Δ8-desaturation and C9-methylation, see below) and C4-hydroxylation of the LCB are mutually exclusive. The displayed molecular species therefore belong to the Bar1p-dependent Cer pool and have C_{16}/C_{18} fatty acids. In the WT strain, Cer was mainly saturated or Δ4-monounsaturated. In contrast, GlcCer was either Δ4-mono- or Δ4,8-diunsaturated, and approximately two thirds of diunsaturated GlcCer were in addition C9-methylated. Methylated monounsaturated species were not detected in Cer or in GlcCer.

In the *gcs*Δ strain, in which no Cer is consumed for GlcCer biosynthesis (see above), a large proportion of Δ4,8-diunsaturated Cer with a C9-methyl group could be detected. This demonstrates that both Δ8-desaturation and C9-methylation can occur at the level of Cer, which is in agreement with previous results showing that Cer, but not GlcCer is a substrate for C9-methylation (14). Most likely, the proportion of Δ4,8-diunsaturated Cer species with a C9-methyl group was very low in the WT strain because these species were immediately consumed for GlcCer biosynthesis.

Since Δ4,8-diunsaturated Cer species with a C9-methyl branch seem to be the preferred substrates for GlcCer biosynthesis, we next asked whether GlcCer levels would be affected in the *c9*Δ strain, in which the C9-methyltransferase is deleted. While methylated Cer and GlcCer were missing in this strain, the proportions of the corresponding non-methylated species of both Cer and GlcCer were increased. This shows that LCB methylation is not essential for GlcCer biosynthesis, in confirmation of previous results (14).

Similar results were obtained with the *delta8*Δ strain, in which the Δ8-desaturase is deleted. Diunsaturated species of both Cer and GlcCer were replaced by equivalent proportions of monounsaturated species. Neither Cer nor GlcCer were C9-methylated in this strain because Δ8-desaturation is required for the reaction mechanism of the C9-methyltransferase (14). These results show that neither Δ8-desaturation nor C9-methylation are required for the biosynthesis of the Bar1p-dependent Cer pool or the subsequent formation of GlcCer.

In contrast, GlcCer was completely missing in the *delta4*Δ strain, in which the Δ4-desaturase is deleted. This confirms previous results (28). Neither mono- nor diunsaturated Cer could be detected in this strain, but the level of saturated Cer was enhanced in comparison to WT. This shows that Bar1p forms a corresponding Cer pool in the *delta4*Δ strain, but that these saturated Cer species cannot be converted to GlcCer. At the same time, this pattern shows that in *P. pastoris*, Δ4-desaturation is a prerequisite for Δ8-desaturation. The LCB modifications in the Bar1p-dependent Cer pool thus follow the sequence Δ4-desaturation → Δ8-desaturation → C9-methylation, as illustrated in Fig. 10.
In summary, Δ4-desaturation of the LCB and α-hydroxylation of the fatty acid are strictly required for entry of the Bar1p-dependent Cer pool into the pathway leading to GlcCer biosynthesis. Δ8-desaturation and C9-methylation are optional, but if present, Δ4,8-diunsaturated Cer species with a C9-methyl branch are the preferred substrates for GlcCer biosynthesis.

If Overexpressed, GCS Gains Access to the Cer Pool with a Trihydroxy LCB and C16/C26 Fatty Acids—Next, we wanted to see whether the loss of GlcCer in the strains gcsΔ, delta4Δ, and scs7Δ (in which the GCS, the Δ4-desaturase, and fatty acid α-hydroxylase are deleted, respectively) could be compensated for by overexpression of the GCS. For this purpose, these strains were transformed with a construct containing the P. pastoris GCS under the control of the strong, methanol-inducible AOX1 promoter. The expression of the glucosyltransferase was induced by the addition of methanol to the culture medium 24 hours before harvesting of the cells.

Fig. 7 (see Supplemental Fig. S6 for minor species) shows that overexpression of the GCS in the gcsΔ strain complemented the deletion, since compared to WT, the proportion of GlcCer was significantly higher in the resulting gcsΔGCS strain. Interestingly, the overexpressing strain contained GlcCer species with a trihydroxy LCB and C16/C26 fatty acids in addition to the regular species with a dihydroxy LCB and C16/C18 fatty acids. When GCS was overexpressed, both Cer pools could be used for GlcCer biosynthesis, but utilization of Cer species with trihydroxy LCBs was less efficient.

In the strain delta4ΔGCS, in which the GCS is overexpressed and the Δ4-desaturase is deleted, the proportion of Cer and GlcCer species with dihydroxy LCB and C16/C18 fatty acids was significantly lower than in the gcsΔGCS strain. In contrast, Cer species with trihydroxy LCB and C24/C26 fatty acids were present in similar proportions and were used in low efficiency for GlcCer biosynthesis. This shows that even when GCS is overexpressed, efficient GlcCer biosynthesis from the Bar1p-dependent Cer pool requires Δ4-desaturation.

In the strain scs7ΔGCS, in which the GCS is overexpressed in the absence of fatty acid α-hydroxylase activity, GlcCer was still detectable, but the levels of all GlcCer species were extremely low compared to the gcsΔGCS strain. This shows that efficient GlcCer biosynthesis from either Cer pool requires α-hydroxylated fatty acids.

Surprisingly, the levels of Cer species with a non-hydroxylated fatty acid are reduced in all three GCS-overexpressing strains compared to the WT (same figure) or the scs7Δ strain (Fig. 4). This cannot be directly explained by an increased consumption because only α-hydroxylated Cer species are being used for GlcCer biosynthesis. Although an increased demand for α-hydroxylated Cer species might potentially lead to an up-regulation of the fatty acid α-hydroxylase activity, such an explanation has to be taken with care because the absolute amounts of Cer vary considerably between samples (see above). Also, an influence of the carbon source (glucose or methanol) on the extent of α-hydroxylation cannot be excluded.

In summary, both Cer pools can be used for GlcCer biosynthesis if GCS is overexpressed, but α-hydroxylation of the fatty acid and a C4-modification of the LCB (either Δ4-desaturation or C4-hydroxylation) remain important requirements. Like Δ4-desaturation, C4-hydroxylation provides an electron-dense environment at the C4-position of the LCB.

Biosynthesis of IPC, MIPC, and M(IP)_2C Is Independent of GlcCer Biosynthesis—To investigate whether the biosynthesis of GlcCer and of the three phosphosphingolipids IPC, MIPC, and M(IP)_2C were interconnected, their levels were investigated in the WT and in the strains bar1Δ, gcsΔ, and scs7Δ. The Cer backbone of all three phosphosphingolipids mainly consisted of 4-hydroxyphinganine as LCB and α-hydroxylated C24/C26 fatty acids, except for the scs7Δ strain, in which the α-hydroxylated fatty acids were replaced by the equivalent non-hydroxylated ones (Fig. 8). A small but significant proportion of IPC species containing phinganine and both α-hydroxylated and non-hydroxylated fatty acids could also be detected in all strains except for bar1Δ. This shows that the Bar1p-dependent Cer pool is incorporated into IPC to a limited extent, but that these IPC species are not processed further into MIPC and M(IP)_2C, suggesting an
additional selection mechanism. The complete list of IPC, MIPC, and M(IP)₂C species is shown in Supplemental Table S2.

Fig. 8 shows that the levels of IPC, MIPC, and M(IP)₂C were not significantly reduced in the strains bar1Δ and gcsΔ, thus phosphosphingolipid biosynthesis proceeds in the absence of GlcCer or of the Bar1p-dependent Cer pool. In the gcsΔ strain, the levels of MIPC and M(IP)₂C are even increased relative to the WT. This could potentially explain why Cer levels remain constant in this strain although less Cer is consumed for GlcCer biosynthesis (Fig. 4). In scs7Δ, α-hydroxylated species of all three phosphosphingolipids were replaced by the equivalent non-hydroxylated species. This shows that while fatty acid α-hydroxylation is essential for GlcCer biosynthesis, it is dispensable for the biosynthesis of phosphosphingolipids. In conclusion, the biosynthesis of IPC, MIPC, and M(IP)₂C is independent of GlcCer biosynthesis and does not require α-hydroxylation of the fatty acid.

The Abundance of the (G)IPC-Specific Sphingolipid Pool Greatly Exceeds that of the Bar1p-Dependent Pool—A comparison of the relative proportions of GlcCer and (G)IPCs should be useful to elucidate the quantitative aspect of substrate flow into the two branches of sphingolipid biosynthesis. Unfortunately, the reported MS data are not suitable for a quantitative comparison of the GlcCer- and (G)IPC-specific sphingolipid pools. Therefore, we analyzed the total LCBs liberated from P. pastoris WT cells by HPLC and compared them with the LCBs found in purified GlcCer from the same cells (Fig. 9).

In this analysis, the dihydroxy LCBs d18:0 (1 mol%), d18:1 (2 mol%), d18:2 (see below), and d18:2-9m (3 mol%) represent the Bar1p-dependent Cer species and GlcCer. The exact proportion of d18:2 could not be determined since it had the same retention time as t18:0. But a comparison with purified GlcCer in the lower panel shows that the proportion of d18:2 should be similar to that of d18:1, thus ≈ 2 mol%. Together, the Bar1p-dependent branch of sphingolipid metabolism made up ≈ 10 mol% of the total sphingoid bases. The trihydroxy LCBs t18:0 (90 mol%) and t20:0 (4 mol%) represent the branch leading to (G)IPC biosynthesis and account for ≈ 90 mol%.

From our enzymatic investigation of Bar1p and from qualitative and quantitative analyses of sphingolipids and their quantitative relation to other lipids, we deduced a simplified model showing the flow of precursors via ceramide pools into different sphingolipid classes in P. pastoris (Fig. 10). A complete picture should also include degradative and recycling pathways because they likely influence both the quantity and the molecular species composition of the depicted lipid pools. In the present illustration, they had to be omitted because insufficient information is available for an accurate representation.

DISCUSSION

The yeast P. pastoris contains two structurally distinct Cer pools whose main distinguishing features are the hydroxylation of the LCB (dihydroxy or trihydroxy) and the chain length of the fatty acid (C₁₆/C₁₈ or C₂₄/C₂₆). These structural differences have decisive consequences for their conversion into the two downstream products, GlcCer and (G)IPCs. Our data define a set of four enzymes which are required for GlcCer biosynthesis: Cer synthase Bar1p, sphingolipid Δ4-desaturase, fatty acid α-hydroxylase, and GCS. Deletion of any of the corresponding genes results in the complete loss of GlcCer.

Two additional enzymes, ∆8-desaturase and C9-methyltransferase, are optional in the sense that GlcCer biosynthesis can proceed in P. pastoris strains in which the corresponding genes are deleted and the corresponding functional groups are thus missing in the Cer backbone. In the following, we will discuss three aspects of GlcCer biosynthesis (formation of ceramide by the Cer synthase Bar1p, introduction of backbone modifications, and final glucosylation of Cer by the GCS) as well as the functional significance of GlcCer and GIPC biosynthesis.

The Substrate Specificity of the Ceramide Synthase Bar1p Provides the Basis for the Formation of a GlcCer-Specific Ceramide Backbone—The molecular species of the Cer pool with a dihydroxy LCB and C₁₆/C₁₈ fatty acids are specifically used for GlcCer biosynthesis.
The substrate specificity of Barlp matches the structural properties of the Barlp-dependent Cer pool, i.e. a preference for dihydroxy LCBs and C_{16}/C_{18} fatty acids. The only difference is that Cer species with non-hydroxylated C_{16}/C_{18} fatty acids are slightly more abundant in vivo (Fig. 4) while α-hydroxylated C_{18} acyl-CoA is clearly preferred in the in vitro assay (Fig. 5). This apparent discrepancy may be due to the fact that exclusively Cer species with α-hydroxylated fatty acids are used for GlcCer biosynthesis so that Cer species with non-hydroxylated fatty acids accumulate. Indeed, the gcsΔ strain contains approximately equal levels of Cer species with the dihydroxy LCB linked to an α-hydroxylated or non-hydroxylated fatty acid. In addition, recent results show that α-hydroxylation very likely takes place at the level of Cer instead of free acyl-CoAs (H.R., unpublished observations). The preference of Barlp for α-hydroxylated acyl-CoA thus could imply that substrates from a putative recycling pathway might be favored over non-hydroxylated acyl-CoA biosynthesized de novo.

In S. cerevisiae, both Laglp and Laclp produce Cer with a C_{24}/C_{26} fatty acid (26, 27, 29). Unfortunately, we did not succeed in cloning the orthologous gene from P. pastoris, and the native in vitro Cer synthase activity in microsomes prepared from the P. pastoris barlpΔ strain was too low to carry out an enzymatic characterization of Laglp. But if P. pastoris Laglp also preferred trihydroxy over dihydroxy LCBs and C_{24}/C_{26} over shorter acyl-CoAs, the structural features defining the two Cer pools, hydroxylation of the LCB and chain length of the fatty acid, could be entirely explained by the substrate specificities of the two Cer synthases, Barlp and Laglp.

A Defined Sequence of Ceramide Backbone Modifications Precedes the Final Glucosylation Step—The LCB modifications characteristic for GlcCer of P. pastoris strictly follow the sequence Δ4-desaturation → Δ8-desaturation → C9-methylation (illustrated in Fig. 10). The dependency of Δ8-desaturation on Δ4-desaturation might be caused by a specificity of the Δ8-desaturase for Δ4-desaturated LCB or Cer species. In plants, Δ4 desaturation is not a prerequisite for Δ8-desaturation (28). Instead, one of the two Δ8-desaturases is specific for C4-hydroxylated LCBs or Cer species (30), demonstrating that desaturases can indeed discriminate between different LCBs.

C9-methylation depends on Δ8-desaturation because this SAM-dependent methyltransferase requires the presence of a double bond next to the methyl group to be introduced (14). This is confirmed by data showing that C9-methylated LCBs are not detectable in C. albicans and P. pastoris strains in which the Δ8-desaturase has been deleted (Ref. 31 and this study). While the presence of the C9-methyl group is not required for GlcCer biosynthesis, its absence has functional consequences in several fungal species. (31–33).

Here, it may be interesting to point out that the introduction of a methyl group into the middle of a saturated acyl group results in a substantial decrease of the phase transition temperature of the corresponding phospholipid comparable in its extent to the effect of a Z-double bond at this position (34).

The GCS Uses Different Cer Substrates Depending on its Expression Level—As discussed above, Cer species with a Δ4,8-diunsaturated, C9-methylated LCB and an α-hydroxylated fatty acid are the preferred substrates for GlcCer biosynthesis in WT cells, although only Δ4-desaturation and α-hydroxylation are strictly required. In contrast, the enzyme in addition uses Cer species with a trihydroxy LCB and C_{26}/C_{26} fatty acids in the P. pastoris strains overexpressing GCS. This Cer pool, which normally serves as substrate for IPC biosynthesis, is now to a limited extent used for GlcCer biosynthesis. This implies that after the specific generation of the two Cer pools by Barlp and (probably) Laglp, a second mechanism must exist to ensure the separation of the two branches shown in Fig. 10. This mechanism (but not the requirement for a C4-modification of the LCB and α-hydroxylation of the fatty acid) can be circumvented by overexpression of the GCS.

Only Small Proportions of the C_{16}-acyl-CoA and Sphinganine Pools Are Recruited for GlcCer Biosynthesis—In addition to the qualitative aspects discussed so far, the quantitative control of substrate entry into the two branches of the sphingolipid biosynthetic pathway is of similar importance (Fig. 10). Under steady state
conditions, the resulting sphingolipid classes are present in very different quantities: In *P. pastoris* WT cells, the GlcCer branch represents only \( \approx 10 \text{ mol}\% \) of the amount of (G)IPCs (determined by the ratio of GlcCer-specific LCBs to 4-hydroxysphinganine in Fig. 9). As illustrated in Fig. 10, this qualitatively and quantitatively very unequal flux may originate at one major branching point. At this step, Bar1p competes directly with several other enzymes for its two preferred substrates, sphinganine (d18:0) and 18:0-CoA, respectively. Bar1p, the fatty acid elongase, the \( \Delta 9 \)-fatty acid desaturase and several acyltransferases involved in glycerolipid and sterol biosynthesis compete for 18:0-CoA. According to the low proportion of GlcCer compared to (G)IPCs and the glycerolipids, one would infer a significantly higher consumption of 18:0-CoA by the elongases, the \( \Delta 9 \)-desaturase and the acyltransferases than by Bar1p. In addition, Bar1p has to compete with the C4-hydroxylase Sur2p for its second substrate, sphinganine. Also here, Bar1p can only recruit a minor fraction for the biosynthesis of the Cer species d18:0/18:0.

Our data on the specificity and selectivity of Bar1p can fully explain the qualitative separation of the two Cer pools into the two branches of sphingolipid biosynthesis. In contrast, the quantities of the end products might be controlled by the activity ratios of the competing enzymes just mentioned. So far, no kinetic data are available for these enzymes. Our data therefore represent steady state levels resulting from the integration of all individual enzyme activities involved in the pathway. In addition, both the quantity and the molecular species composition of (G)IPCs and GlcCer as well as of the two Cer pools might be influenced by degradative and recycling pathways (not included in Fig. 10). As an example, the apparent discrepancy between the extent of \( \alpha \)-hydroxylation of the Cer species produced by Bar1p *in vivo* (Fig. 4) and *in vitro* (Fig. 5) might be explained by preferential recycling of \( \alpha \)-hydroxylated fatty acids (see above). In the future, metabolic labeling experiments as well as knockout strains in which degradative or recycling enzymes are inactivated could help resolve these issues.

**Functional Significance of GlcCer and (G)IPC Biosynthesis**—A number of studies in fungi indicate that GlcCer and GIPCs fulfill different functions. These experiments have been performed with inhibitor-treated cells or with knockout mutants impaired in the activity of the enzymes involved in GlcCer or IPC biosynthesis, respectively.

In our study, all *P. pastoris* mutant strains impaired in GlcCer biosynthesis were viable and did not show any growth defects. This is consistent with previous reports showing that a bar1\( \Delta \) strain of *Kluyveromyces lactis* (*BAR1* is called *LAC1* in that study) and a delta4\( \Delta \) strain of *Schizosaccharomyces pombe* are viable (25, 35). These observations are in contrast to studies with dimorphic or filamentous fungi: Deletion of different genes involved in GlcCer biosynthesis in such fungi, e.g. *Candida albicans*, *Cryptococcus neoformans*, or *Fusarium graminearum*, resulted in viable mutants with widely varying phenotypes regarding growth, morphology or host colonization (24, 31–33, 36–38). Importantly, the proportions of GlcCer relative to (G)IPCs in *P. pastoris* are similar as in filamentous fungi (39). These phenotypes therefore suggest that while GlcCer may be dispensable under optimal laboratory conditions, it may become important in more complex growth modes, under non-optimal environmental conditions, or in order to carry out specialized functions.

On the other hand, deletion or pharmacological inhibition of the IPC synthase of *S. cerevisiae* is either lethal or results in severe growth defects, although the severity of the phenotype is partially attributable to the accumulation of Cer as the precursor of IPC biosynthesis (27, 40–45). We did not systematically investigate the enzymes involved in the biosynthesis of (G)IPCs in *P. pastoris*. Despite repeated efforts, it was not possible to delete the genes encoding the Cer synthase Lag1p and the C4-hydroxylase Sur2p. This may suggest that (G)IPCs are essential for viability in *P. pastoris* and that the C4-hydroxylation of the LCB is required for the Lag1p-dependent Cer pool to be used for (G)IPC biosynthesis. Interestingly, *sur2\( \Delta \) strains of *S. cerevisiae* are viable and C4-hydroxylation of the LCB is not required for
(G)IPC biosynthesis (15, 16), while an equivalent knockout in *A. nidulans* shows a severe growth defect (46). This suggests that the requirements for C4-hydroxylation of the LCB differ between fungal species.

**Conclusions**—Cer species finally found as backbones in GlcCer have to pass two filters imposing both qualitative and quantitative controls. At the first point, the Cer synthase Bar1p selectively uses sphinganine and 18:0-CoA in competition with other enzymes, which use the bulk of both substrates. The second control point in GlcCer synthesis is exerted by the GCS. This enzyme most likely does not accept the Cer species d18:0/18:0, the primary product of Bar1p, but requires Δ4-desaturation of the LCB and α-hydroxylation of the fatty acid.

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**FOOTNOTES**

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5 The abbreviations used are: Cer, ceramide; CoA, coenzyme A; ER, endoplasmic reticulum; ESI, electrospray ionization; FW, fresh weight; GalCer, galactosylceramide; GCS, glucosylceramide synthase; GIPC, glycosyl inositol phosphorylceramide; GlcCer, glucosylceramide; HPLC, high-performance liquid chromatography; IPC, inositol phosphorylceramide; LCB, long-chain (sphingoid) base; MS, mass spectrometry; TLC, thin-layer chromatography; TOF, time-of-flight; WT, wild type.

**REFERENCES**


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TABLES

TABLE 1

Yeast strains used in this study

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**FIGURE LEGENDS**

**Fig. 1.** **Fungi have two sphingolipid classes.** *A,* Predominant molecular species of GlcCer and IPC in *P. pastoris,* with the structural features distinguishing the two sphingolipid classes highlighted. In addition, the enzymes introducing these structural features as well as the corresponding gene names or, where applicable, the names of the knockout strains used in this study are given. *B,* Commercially available LCBs used in the *in vitro* enzyme assays shown in Fig. 5 and Supplemental Fig. S3. Lipid names are according to the recommendations of the International Lipid Classification and Nomenclature Committee (47). Sphinganine (commonly called dihydrosphingosine) is the initial LCB that serves as precursor for the biosynthesis of the other LCBs. Phospho-4-enine (sphingosine) is representative of the desaturated LCBs found in GlcCer while 4-hydroxysphinganine (phytosphingosine) is the typical LCB of (G)IPCs.

**Fig. 2.** **Most animals, plants and fungi have multiple Cer synthases which fall into distinct phylogenetic groups.** *S. cerevisiae* has two Cer synthases Lag1p and Lac1p, which share a high degree of sequence identity (73%). In contrast, most fungi have two Cer synthases with a much lower degree of sequence identity (∼30%), which fall into distinct phylogenetic groups. In the text, we refer to the enzymes orthologous to *S. cerevisiae* Lag1p/Lac1p as Lag1p (for longevity assurance gene; Ref. 50) and to the enzymes from the phylogenetic group that is missing in *S. cerevisiae* as Bar1p (for biocontrol agent resistance; Ref. 51). From the latter group, *Aspergillus nidulans* BarA and *Kluyveromyces lactis* Lac1p (the name is misleading because this enzyme is not an ortholog of *S. cerevisiae* Lac1p) were investigated previously (25, 51). It is evident that, with the exception of the six mammalian Cer synthases (52), there is no consensus regarding gene nomenclature. A systematic nomenclature for Cer synthases from all organisms is urgently needed. The phylogenetic tree was constructed using Tree Puzzle (53) from an alignment of full-length protein sequences generated with T-Coffee (54). Only genes which have been investigated experimentally are depicted. UniProt identifiers are: (1) P38703; (2) P28496; (3) Q6CVA7; (4) C4QWW1; (5) Q5BAG6; (6) C4R2K3; (7) Q6CP21; (8) Q5B548; (9) Q6NQ18; (10) Q9LDF2; (11) Q9LJK3; (12) Q7Z139; (13) Q9GYR9; (14) Q96G23; (15) Q8IU89; (16) Q9HA82; (17) Q8N5B7; (18) Q6ZMG9; (19) Q9W423; (20) Q9XWE9; (21) P27544

**Fig. 3.** **Presence or absence of GlcCer in mutants of *P. pastoris* with altered activities of enzymes involved in sphingolipid biosynthesis.** Lipids extracts from WT and mutant lines were separated by TLC in chloroform/methanol, 85:15. Glycolipids were visualised by spraying with α-naphthol/sulfuric acid and subsequent heating to 160°C. For interpretation of the results see text. The WT and the knockout mutants were grown in complete medium (YPD), whereas the GCS-overexpressing strains (right three lanes) were grown in minimal methanol medium to induce expression of the GCS. Overexpression of the GCS resulted in the appearance of an additional glycolipid band above the ‘normal’ GlcCer band, which turned out to be a mixture of steryl glucoside (SG) and atypical GlcCer species (see text and Fig. 7). Biosynthesis of SG is typical for *P. pastoris* cells grown in minimal medium. One representative of several experiments is shown.

**Fig. 4.** **Cer and GlcCer species can be classified into two groups which are distinguished by the chain length of the fatty acid and the hydroxylation of the LCB.** Molecular species of Cer and GlcCer from WT and the knockout strains *bar1Δ, gesΔ,* and *ses7Δ* are grouped by the number of acyl carbons (assuming a C18 LCB) as well as by the hydroxylation of the LCB (dihydroxy or trihydroxy) and the fatty acid (hydroxy or non-hydroxy). The quantities of Cer and GlcCer in the knockout strains are given as mol-% of the sum of all species relative to the WT so that a direct comparison between the strains is possible. Shown are averages and standard deviations of three independent experiments.

**Fig. 5.** **The substrate preference of Bar1p matches the properties of the Cer pool with a dihydroxy LCB and C16/C18 fatty acids.** *A,* The substrate preference of Bar1p for different LCBs and
acyl-CoAs was tested by a ceramide synthase assay with microsomes prepared from a lag1Δlac1ΔS. cerevisiae strain expressing FLAG-tagged P. pastoris Bar1p as its only ceramide synthase (incubation time, 5 min). Non-hydroxylated acyl-CoAs with different chain lengths are compared on the left, while the preference for α-hydroxylated versus non-hydroxylated C18 acyl-CoA is shown in the middle. Sphing-4-enine was used as LCB. On the right, the preference for the LCBs sphinganine, sphing-4-enine, and 4-hydroxy-sphinganine is shown in combination with non-hydroxylated C18 acyl-CoA. In the upper row, the substrate specificity was tested using both a single LCB and a single acyl-CoA per reaction (one reaction per combination), while in the lower row, substrate selectivity was tested by offering mixtures of the LCBs or acyl-CoAs to be compared against each other (one reaction per panel). Shown are averages and standard deviations from three independent reactions.

**Fig. 6.** Δ4 desaturation, but not Δ8 desaturation or C9 methylation is essential for the conversion of a Cer pool with a dihydroxy LCB and C16/C18 fatty acids into GlcCer. Molecular species of Cer and GlcCer from WT and from the knockout strains gcsΔ, c9Δ, delta8Δ, and delta4Δ are grouped by the desaturation of the LCB (d18:0, saturated; d18:1, monounsaturated; d18:2, diunsaturated; d18:1-9m, monounsaturated and C9-methylated; d18:2-9m, diunsaturated and C9-methylated) and by the hydroxylation of the fatty acid (hydroxy or non-hydroxy). Only Cer and GlcCer species with dihydroxy LCBS are shown because no species with desaturated trihydroxy LCBS could be detected. The acyl chain length of these species is almost exclusively 16 or 18 since nearly all Cer species with a C24/C26 fatty acid have a trihydroxy LCB (not included in this figure), and GlcCer species with a C24/C26 fatty acid occur only in trace amounts (Fig. 4). The quantities of Cer and GlcCer in the knockout strains are given as mol-% of the sum of all species relative to the WT so that a direct comparison between the strains is possible. Shown are averages and standard deviations of three independent experiments.

**Fig. 7.** Overexpression of GCS makes the Cer pool with a trihydroxy LCB and C24/C26 fatty acids accessible for GlcCer biosynthesis. Molecular species of Cer and GlcCer from WT and from the overexpressing strains gcsΔGCS, delta4ΔGCS, and scs7ΔGCS are grouped by the number of acyl carbons (assuming a C18 LCB) as well as by the hydroxylation of the LCB (dihydroxy or trihydroxy) and the fatty acid (hydroxy or non-hydroxy). The quantities of Cer and GlcCer in the overexpressing strains are given as mol-% of the sum of all species relative to the WT so that a direct comparison between the strains is possible. Shown are averages and standard deviations of three independent experiments.

**Fig. 8.** Analysis of IPC, MIPC, and M(IP)2C in the P. pastoris strains lacking GlcCer. Molecular species of IPC, MIPC, and M(IP)2C from WT and from the knockout strains bar1Δ, gcsΔ, and scs7Δ are grouped by the hydroxylation of their fatty acids. Only species containing a trihydroxy LCB are shown. The WT strain contains in addition ≈ 11% of IPC species with a dihydroxy LCB, in confirmation of a previous study (55). MIPC and M(IP)2C species with a dihydroxy LCB were not detectable. The quantities of IPC, MIPC, and M(IP)2C are given as mol-% of the sum of all species relative to the WT so that a direct comparison between the strains is possible. Shown are averages and standard deviations of
three independent experiments. An absolute quantification was not possible since no standards were available.

Fig. 9. **Analysis of LCBs from WT *P. pastoris***. LCBs were released from sphingolipids by strong alkaline hydrolysis, converted into dinitrophenyl derivatives and separated by HPLC. Upper panel: LCBs were released from Cer, GlcCer and (G)IPCs of whole *P. pastoris* cells. The total LCBs consisted of ≈ 90% of the trihydroxy LCBs t18:0 and t20:0. Dihydroxy LCBs from the Bar1-dependent Cer pool and from GlcCer made ≈ 10%. The left peak represents mainly t18:0 and a low proportion of d18:2, which cannot be separated by this method. Lower panel: LCBs were released from purified GlcCer from *P. pastoris*, consisting of the three dihydroxy LCBs d18:1, d18:2 and d18:2-9m. Shown is one representative experiment out of three.

Fig. 10. **Simplified model of sphingolipid biosynthesis in *P. pastoris* showing qualitative and quantitative routing of substrates into Cer, GlcCer and IPC.** Intermediates of the pathway are given with the predominant molecular species indicated underneath. The width of the arrows and the letters indicate the relative quantitative proportions of the end products of lipid biosynthesis in *P. pastoris* (not to scale). The compounds with a gray background were subjects of our analyses. The early steps of sphingolipid biosynthesis, the late steps of GIPC biosynthesis, and degradative and recycling pathways have been omitted. For simplicity, the model only shows species containing the dominating C$_{18}$ and C$_{24}$ fatty acids, but it should be considered that *P. pastoris* also synthesizes a smaller proportion of species containing C$_{16}$ and C$_{26}$ fatty acids.
Figure 2
Figure 3

WT
bar1Δ
scs7Δ
delta4Δ
delta8Δ
c9Δ
gcsΔ
gcsGCS
delta4GCS
scs7GCS

GlcCer
GlcCer + SG
Figure 4

[Graph showing the mol% of Cer or GlcCer species relative to WT (100%) for different mutants: WT, bar1Δ, gcsΔ, scsΔ. The graph includes bars for each number of acyl carbons (16, 18, 20, 22, 24, 26) with percentages for hydroxy and non-hydroxy species, as well as the corresponding LCB (trihydroxy, dihydroxy).]
Figure 5

A

- **Acyl chain length**
  - % of most abundant product
  - Bars for lengths 16, 18, 20, 22, 24, 26

- **C₁₈ acyl chain hydroxylation**
  - Bars for non-hydroxy, hydroxy, sphinganine, sphing-4-enine, 4-hydroxysphinganine

- **LCB**
  - Bars for single substrates (specificity)
  - Bars for combined substrates (selectivity)

B

- **Lag1p**
  - Mol-% of all Cer species
  - Bars for lengths 16, 18, 20, 22, 24, 26

- **Bar1p**
  - Mol-% of all Cer species
  - Bars for lengths 16, 18, 20, 22, 24, 26

- **LCB**
  - Bars for trihydroxy and dihydroxy

**Legend:**
- C₁₈ = C₁₈ acyl chain
- LCB = Long-chain base

Figure 5
Figure 6

The figure shows the mole percent of Ceramide and GlcCer species relative to wild type (WT) for different genetic backgrounds:

- **WT**
  - Ceramide: d18:0, d18:1, d18:2, d18:1-9m, d18:2-9m
  - GlcCer: d18:0, d18:1, d18:2, d18:1-9m, d18:2-9m

- **gcsΔ**
  - Ceramide: d18:0, d18:1, d18:2, d18:1-9m, d18:2-9m
  - GlcCer: d18:0, d18:1, d18:2, d18:1-9m, d18:2-9m

- **c9Δ**
  - Ceramide: d18:0, d18:1, d18:2, d18:1-9m, d18:2-9m
  - GlcCer: d18:0, d18:1, d18:2, d18:1-9m, d18:2-9m

- **delta8Δ**
  - Ceramide: d18:0, d18:1, d18:2, d18:1-9m, d18:2-9m
  - GlcCer: d18:0, d18:1, d18:2, d18:1-9m, d18:2-9m

- **delta4Δ**
  - Ceramide: d18:0, d18:1, d18:2, d18:1-9m, d18:2-9m
  - GlcCer: d18:0, d18:1, d18:2, d18:1-9m, d18:2-9m

The fatty acid composition is indicated as hydroxy or non-hydroxy.
Figure 7
mol-% of all species relative to WT (100%)
Figure 9
Figure 10

glycerolipids
sterol esters
18:1-CoA

acyltransferases
Δ9-desaturase

16:0-CoA
Elo1p
18:0-CoA
elongase
24:0-CoA

Bar1p
LCBs
d18:0
C4-hydroxylase
t18:0

Lag1p


ceramide
C9-methyltransferase
Δ8-desaturase
Δ4-desaturase
α-hydroxylase

d18:2-9m
18:0
18:2
18:0
18:1
18:0

GCS

GlcCer

d18:2-9m
d18:2
d18:1
18:0
18:0

present only with GCS overexpressed
IPC species normally present

4-hydroxyceramide

GlcCer

t18:0
t18:0
24:0
24:0

IPC synthase

IPC

t18:0
t18:0
24:0
24:0

GlcCer species normally present