Structures of the glycosylphosphatidylinositol membrane anchors from *Aspergillus fumigatus* membrane proteins

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Received on May 30, 2002; revised on September 3, 2002; accepted on September 3, 2002

Glycosylphosphatidylinositol (GPI)-anchored proteins have been identified in all eukaryotes. In fungi, structural and biosynthetic studies of GPIs have been restricted to the yeast *Saccharomyces cerevisiae*. In this article, four GPI-anchored proteins were purified from a membrane preparation of the human filamentous fungal pathogen *Aspergillus fumigatus*. Using new methodology applied to western blot protein bands, the GPI structures were characterized by ES-MS, fluorescence labeling, HPLC, and specific enzymatic digestions. The phosphatidylinositol moiety of the *A. fumigatus* GPI membrane anchors was shown to be an inositol-phosphoceramide containing mainly phytosphingosine and monohydroxylated C24:0 fatty acid. In contrast to *A. fumigatus*, even for *Gel1p*, a homolog of *Gas1p* in *S. cerevisiae*, ethanolamine-phosphoceramide containing mainly diacylglycerol. The *A. fumigatus* GPI glycan moiety is mainly a linear pentamannose structure linked to a glucosamine residue: Man₁₋₃Man₁₋₂Man₁₋₂Man₁₋₂Man₁₋₆Man₁₋₄GlcN. The *A. fumigatus* GPI glycan moiety is mainly a linear pentamannose structure linked to a glucosamine residue: Man₁₋₃Man₁₋₂Man₁₋₂Man₁₋₂Man₁₋₂Man₁₋₂Man₁₋₆Man₁₋₄GlcN.

Key words: *Aspergillus*/*glycoprotein/glycosylphosphatidylinositol*

Introduction

Numerous membrane glycoproteins of eukaryotic cells are anchored in the lipid bilayer by a glycosylphosphatidylinositol (GPI) membrane anchor. GPI-anchored proteins include receptors, enzymes, and protective cell surface coats. In fungi, GPI-anchored proteins are also involved in cell wall organization and biosynthesis. Indeed, gene disruption of numerous putative GPI-anchored proteins induces reduced growth, an altered cell wall, and a hyper-sensitivity to dyes interfering with cell wall polysaccharides (e.g., calcofluor white and congo red) (Rodriguez-Pena et al., 2000). Sequence analysis and gene fusion strategies with a reporter gene have suggested that more than half of the putative GPI proteins of *Saccharomyces cerevisiae* are covalently linked to the cell wall and are released by β-glucanase treatment (Caro et al., 1997; Hamada et al., 1998). Chemical evidence, at least for α-agglutinin and Tip1, showed these proteins are covalently associated to the β1-6/1-3glucan complex, the main yeast cell wall component, through the glycan moiety of the GPI (Kollar et al., 1997; Kapteyn et al., 1996; Fujii et al., 1999). In *Candida albicans*, the cell wall proteins present a similar organization (Kapteyn et al., 2000). Other GPI proteins associated with the plasma membrane possess enzymatic activities, such as β-glucanase and β-glucanosyltransferase, able to modify cell wall polymers (Boone et al., 1990, 1991; Cid et al., 1995; Popolo and Vai, 1999). Genetic and biochemical analysis showed that the new family of GPI-anchored β1-3glucanosyl-transferase, encoded by GEL in *Aspergillus fumigatus* and by the orthologous genes Gas1p in *S. cerevisiae* and Phr1p and Phr2p in *C. albicans*, is involved in cell morphology (Hartland et al., 1996; Mouyna et al., 2000a,b). Recently, a proteomic approach to identify GPI-anchored proteins of *A. fumigatus* lead to the identification of gene orthologs (CRH1, CRH2, ECM33) of genes known to play a role in yeast cell wall maintenance (Bruneau et al., 2001).

All protein-linked GPI anchors have a conserved core structure of ethanolamine-P-Man₃GlcN-PI, and GPI biosynthetic pathways are also largely conserved between organisms. In fungi, structural and biosynthetic studies of GPI are mostly restricted to the model yeast *S. cerevisiae*. These GPI molecules have a glycan with mainly four mannose residues, Man₃₋₂Man₁₋₂Man₁₋₂Man₁₋₂Man₁₋₄GlcN₃₋₆myo-inositol-1-PO₄, although some contain an additional α1-2- or α1-3-linked reducing terminal mannose residue (Frankhauser et al., 1993). The lipid part differs from mammalian cells with the presence of cereamide or hydroxy-fatty acid-containing diacylglycerol (Conzelmann et al., 1992; Frankhauser et al., 1993).

To analyze the structure of the mature GPI anchors of a filamentous fungi, we purified several GPI proteins of *A. fumigatus*, a human pathogen, and analyzed the lipid and glycan moieties of their anchors.

Results

Purification of GPI-anchored proteins from *A. fumigatus* membrane

To analyze the GPI anchor structure, membrane proteins were solubilized in 50 mM Tris–HCl, 2 mM ethylene-diamine-tetra-acetic acid (EDTA), pH 8.8 in presence of protease inhibitors, 2% Triton X100, and 5 mM HgCl₂ to
inhibit the endogenous GPI–phospholipase C (PLC). Two chromatographic steps were used to partially purify GPI-anchored proteins. All GPI-anchored proteins bound to the Q-Sepharose column at pH 8.8 and were eluted with 140 mM NaCl. This step allowed intact GPI-anchored proteins to be separated from phosphatidylinositol (PI)-PLC-cleaved GPI-anchored proteins, which were eluted with 25 mM NaCl. The Etienne Merck Darmstadt-DiEthyl Amino-Ethyl (EMD-DEAE) step allowed the purification of five GPI proteins (Figure 1). At pH 7.5, two GPI proteins were eluted with 50 mM NaCl (fraction F1: p56 and p60), one was eluted with 90 mM NaCl (fraction F2: p110), and two more were eluted with 190 mM NaCl (fraction F3; p70 and p80).

Identification of GPI proteins

Immunodetection with anti-Gel1p antibody and tryptic mass fingerprint data identified p56 as Gel1p. Edman sequencing of a purified tryptic peptide from p60 provided the sequence SFSAPXLTETTGDVF, which matches with ECM33p of \textit{A. fumigatus} (Chabanne, personal communication). The p70 and p80 proteins gave similar tryptic mass fingerprints, and Edman sequencing of a purified tryptic peptide from both proteins provided the sequence TGYVNYD. This sequence matched with PhoAp, an acid phosphatase. In addition, p70 and p80 reacted positively with a specific antibody against PhoAp, indicating that p70 and p80 correspond to two forms of the same protein (Bernard et al., 2002). Edman sequencing of a purified tryptic peptide of p110 provided the sequence QDFDAAAGYI that was already obtained from a GPI-anchored protein of 114 kDa of \textit{A. fumigatus} that shares homology with fungal phospholipases (Bruneau et al., 2001).

Analysis of PIs

PI moieties from partially purified GPI proteins were isolated from western blots on polyvinylidene difluoride (PVDF) membrane after nitrous acid deamination and butanol extractions. After purification on a silica column, PIs were characterized by negative ion electrospray mass spectrometry (ES-MS) and electrospray tandem mass spectrometry (ES-MS-MS) (Figure 2). The same data were obtained from all GPI-anchored proteins. The ES-MS spectra revealed one principal [M-H]$^-$ pseudomolecular ion at m/z 924 and three minor ions at m/z 910, 938, and 952. The fragmentation of each PI compound produced only two daughter ions at m/z 241 [inositol-1,2-cyclic phosphate]$^-$ and m/z 259 [inositol-monophosphate]$^-$.

Analysis of the GPI anchor glycans

The amino-bonded phase high-performance liquid chromatography (HPLC) analyses of the 2-aminobenzamide (2-AB)-labeled GPI glycan moieties isolated from all five GPI-anchored proteins are shown in Figure 3. The proteins p56, p60, p70, and p80 all produced similar HPLC profiles with a single major peak, whereas p110 produced two peaks.

![Fig. 1. SDS–PAGE and immunoblot of GPI-anchored proteins from \textit{A. fumigatus} isolated after Q-Sepharose and EMD-DEAE chromatographic purification steps. (A) Coomassie blue–stained 10% SDS–PAGE; (B) immunoblot using the anti-CRD epitope detection with (+) or without (–) PI-PLC treatment of isolated fractions.](https://academic.oup.com/glycob/article-abstract/13/3/169/608934/170)

![Fig. 2. ES-MS analysis of PI released by nitrous deamination from p80 on PVDF membrane. (A) Negative ion ES-MS spectrum of PI; (B) daughter ion ES-MS-MS spectrum of the ion at m/z 924.](https://academic.oup.com/glycob/article-abstract/13/3/169/608934/170)
The peak fraction from the chromatogram of the p80 2-AB-labeled GPI glycan was analyzed by MS. MALDI-TOF analysis revealed a major ion at \(m/z\) 1115.3, corresponding to \([\text{Hex}_5-\text{AHM}-2-\text{AB} + \text{Na}]^+\) (data not shown), whereas ES-MS revealed a major ion at \(m/z\) 1093.4, corresponding to \([\text{Hex}_5-\text{AHM}-2-\text{AB} + \text{H}]^+\) (Figure 4A). The daughter ion ES-MS-MS spectrum of \(m/z\) 1093.4 is consistent with this assignment (Figure 4B). However, the daughter ion spectrum of native material cannot readily distinguish linear from branched glycan species; therefore, the sample was analyzed further following permethylation (Dell et al., 1993). The daughter ion ES-MS-MS spectrum of \(m/z\) 1409.6 is shown in Figure 4C. In this case, the absence of daughter ions 14, 28, or 32 Da smaller than those at \(m/z\) 987.5, 783.4, and 579.3 implies a purely linear glycan structure.

The primary structures of the 2-AB-labeled GPI glycans were further characterized by HPLC before and after enzymatic digestions with exo-\(\alpha\)-mannosidases (Figures 5 and 6). All structures were degraded with jackbean \(\alpha\)-mannosidase to produce anhydromannose (AHM)-2-AB, indicating the exclusive presence of \(\alpha\)-mannopyranose residues. Specific \(\alpha1-2\) and \(\alpha1-6\) mannosidases did not degrade the structure from p80 (Figure 5), but the \(\alpha1-2,3\) mannosidase partly degraded it to form species cochromatographing with authentic Man\(_4\)-AHM-2-AB (Man\(_1\)-2Man\(_1\)-2Man\(_1\)-6Man\(_1\)-4AHM-2-AB) and Man\(_3\)-AHM-2-AB (Man\(_1\)-6Man\(_1\)-4AHM-2-AB) standards. Similar results were obtained from 2-AB-labeled GPI glycans isolated from p56, p60, and p70 (data not shown). The two 2-AB-labeled GPI glycans (Man\(_4\)-AHM-2-AB and Man\(_3\)-AHM-2-AB) from p110 were resistant to the \(\alpha1-6\) mannosidase, but the \(\alpha1-2\) mannosidase degraded the Man\(_4\)-AHM-2-AB structure to yield Man\(_2\)-AHM-2-AB. The \(\alpha1-2,3\) mannosidase activity degraded both structures slowly to form Man\(_2\)-AHM-2-AB. Taken together with the MS data, these results are consistent with 2-AB-labeled glycan structures of Man\(_1\)-3Man\(_1\)-2Man\(_1\)-2Man\(_1\)-6Man\(_1\)-4AHM-2-AB and Man\(_1\)-2Man\(_1\)-2Man\(_1\)-6Man\(_1\)-4AHM-2-AB. These glycan structures are combined with the PI structure already described to yield suggested structures for the *A. fumigatus* GPI anchors (Figure 7).

**Discussion**

In yeast, many GPI-anchor proteins are known to be involved in cell wall structural organization and biosynthesis
In filamentous fungi, cell wall organization is less extensively studied (Fontaine et al., 2000). Recent studies on the human pathogenic fungus A. fumigatus suggest that at least nine GPI-anchored proteins are common to filamentous fungi and yeast (Bruneau et al., 2001). However, in contrast to S. cerevisiae, nothing is known about structure and biosynthesis of GPI-anchor in filamentous fungi. GPI proteins can be selectively hydrolyzed by PI-PLC or GPI-PLC and detected with an anti-cross-reacting determinant (CRD) antibody. We took advantage of this selective detection to isolate five GPI-anchored proteins from A. fumigatus membrane preparations. Mass fingerprinting and/or Edman sequencing of these five A. fumigatus proteins revealed that they are Gel1p (p56), Ecm33p (p60), two species of PhoAp (an acid phosphatase) (p70 and p80), and a phospholipase (p110) that have been previously identified in our proteomic study (Bruneau et al., 2001).

Gel1p is a member of a new family of GPI-anchored β1-3 glucanoyltransferases involved in cell wall β-glucan modeling (Mouyna et al., 2000a,b). Ecm33p is a homolog of a putative yeast GPI-anchored protein thought to be involved in cell wall biosynthesis because ΔECM33 mutants show hypersensitivity to zymolyase (endoβ1-3glucanase), hygromycin B, and K1 killer toxin and have an altered glucose/mannose ratio (monosaccharides mainly found in the cell wall) (Caro et al., 1997).

PhoAp, an acid phosphatase purified as two protein bands on sodium dodecyl sulfate–polyacrylamide gel electrophoresis (SDS–PAGE) at 70 and 80 kDa, was identified by sequence homology to PhoAp from Penicillium chrysogenum and Aspergillus niger (Haas et al., 1992; Ehrlich et al., 1994; Bernard et al., 2002). This protein, with 46% sequence identity to the A. niger homolog, is the major GPI-anchored...
protein in the *A. fumigatus* membrane preparation. To date, PhoAp is the only protein in *A. fumigatus* found to be associated with the cell wall β1-3 glucan as it is released with an endo-β1-3 glucanase digestion. In *Kluyveromyces marxianus* cell wall β1-3 glucanase digestion also released an acid phosphatase (Yoda et al., 2000). Covalent linkage of GPI-anchored proteins to cell wall polymer has been mainly described in yeast, where β1-6 glucan constitutes a bridge between protein and β1-3 glucan, the main cell wall polysaccharide (Kapteyn et al., 1996, 1999; Kollar et al., 1997). However, no chemical proof of the covalent cross-linking for GPI-anchored PhoAp to cell wall β1-3 glucan has been established to date.

Based on our chemical and enzymatic analysis, we can suggest that the main GPI anchor structure in *A. fumigatus* is as shown in Figure 7. For all four proteins analyzed, the lipid part is exclusively IPC, most likely containing a C18-phytosphingosine long-chain base amide-linked to a monohydroxylated C24:0 fatty acid, as judged by its mass and by analogy with the *S. cerevisiae* structure. Inositol-phosphocheramides are common in yeast GPI structures and have also been described in *Dictyostelium discoideum* (Stadler et al., 1989; Haynes et al., 1993), plants (Oxley and Bacic, 1999), and trypanosomatid parasites (McConville and Ferguson, 1993; Serrano et al., 1995; Ferguson et al., 1999). To date, IPCs have not been found in mammalian GPI structures. In fungi, IPCs are also found as free phospholipids and as mannosylated IPC containing 2-monohydroxylated long chain fatty acids (Lester and Dickson, 1993). However, their biosynthesis seems to be independent from that of GPI anchors (Reggiori and Conzelmann, 1998). The major glycan component of the *A. fumigatus* GPI anchors is Manα1-3Manα1-2Manα1-2Manα1-6Manα1-4GlcN (Manα4GlcN), which conforms to the minimal Manα1-2Manα1-6Manα1-4GlcN (Manα4GlcN) core GPI glycan structure common to all protein-linked (type 1) GPI structures (McConville and Ferguson, 1993) and is identical to one of the two Manα4GlcN glycoforms found in a minority of GPI structures in *S. cerevisiae* (Frankhauser et al., 1993).

Although on-blots GPI glycan labeling and off-blot release methods have been described previously (Zitzmann and Ferguson, 1999; Zitzmann et al., 2000), as have GPI PI-fraction analyzed by ES-MS and ES-MS-MS (Serrano et al., 1995; Rudd et al., 1997; Treumann et al., 1998; Almeida et al., 2000), this is the first report to describe a novel off-blot method for GPI PI-fraction isolation prior to ES-MS and ES-MS-MS analysis. Thus, the entire GPI structure analysis described in this article was performed on protein bands transferred to PVDF membrane. The approach was effective and sensitive. However, the aqueous Hydrofluoric acid (HF) dephosphorylation step, neccessary to release the 2-AB-labeled GPI glycan from the PVDF membrane-bound protein component, results in the loss of all ethanolamine phosphate substituents. Thus, the ethanolamine phosphate bridge to the protein C-terminus shown in Figure 7 is drawn by analogy with other known GPI anchor structures (Ferguson et al., 1999). Whether or not the *A. fumigatus* GPI anchor has additional ethanolamine phosphate substituents on the first and second mannose residues, which are common in higher-eukaryote GPI anchors, is unknown. The absence of additional ethanolamine phosphate groups in mature GPI anchors of *S. cerevisiae* (Frankhauser et al., 1993) has been questioned recently, and it appears that at least some mature yeast GPI anchors retain the additional ethanolamine phosphate groups that are added during GPI biosynthesis (Canivenc-Gansel et al., 1998; Flury et al., 2000).

We considered the possibility that the *A. fumigatus* GPI anchors might contain galactofuranose substituents because this sugar occurs linked to mannann chains with similarity to the GPI structure in *A. fumigatus* galactomannans (Latgé et al., 1994) and because it has been described in the N- and O-linked oligosaccharides of *Aspergillus* glycoproteins (Buitrago et al., unpublished data; Takayanagi et al., 1994; Haido et al., 1998; Wallis et al., 2001). The acid-labile galactofuranose residues are known to be labile to the full 48% aqueous HF dephosphorylation conditions used in this study (Turco et al., 1989). Therefore, a mild aqueous HF treatment (using 25% aqueous HF for 24 h, data not shown) that retains a substantial proportion of galactofuranose residues was also investigated. However, the amino-bonded phase HPLC profiles of 2-AB-labeled glycan prepared in this way were identical to those shown in Figure 3, suggesting that galactofuranose is not a component of *A. fumigatus* GPI anchors. This is also in agreement with the lack of immunoreactivity of the five GPI-anchored proteins with a galactofuranose-specific mono-clonal antibodies (data not shown) (Stynen et al., 1992).

The data provided here on the mature GPI anchor structures of *A. fumigatus* provide a framework for probing the pathway of GPI biosynthesis in *A. fumigatus* that is presently unknown. From a structural point of view, it seems likely that the *A. fumigatus* GPI pathway will be similar to that of *S. cerevisiae* in that the GPI glycans contain a minimum of four αMan residues and the principal lipid is a ceramide instead of a glyceride.

Materials and methods

**Fungal culture and membrane preparation**

*A. fumigatus*, strain CBS 144-89, was grown in a 15-L fermenter in 2% glucose, 1% mycophosphate (Biokar...
Diagnósticos, Pantin, France) at 25°C for 24 h as described previously (Hartland et al., 1996). The mycelium was collected by filtration under vacuum, washed with water, and then disrupted in 200 mM Tris–HCl, 20 mM EDTA, pH 8.0, 1 mM phenylmethylsulfonyl fluoride buffer with 5 mg/ml bovine serum albumin (BSA) at 4°C by passing through a Dyno mill homogenizer (W. A. Bachofen AG, Basel, Switzerland) in presence of glass beads (0.5–0.75 mm diameter). Cell wall was removed by centrifugation at 10,000 × g for 10 min at 4°C. Total membranes were then collected by ultracentrifugation at 125,000 × g for 60 min at 4°C. The membrane pellet was resuspended in the disruption buffer without BSA with a Dounce homogenizer and then recentrifuged at 125,000 × g for 60 min at 4°C. The pellet was resuspended again in 20 mM Tris–HCl, 2 mM EDTA, pH 8.0, and stored at −80°C.

**Protein solubilization and purification**

Membrane preparations (30 ml at 20 mg protein/ml) were centrifuged at 50,000 × g for 40 min at 4°C. The membrane pellet was first resuspended with a Dounce homogenizer in 40 ml of 50 mM Tris–HCl, 2 mM EDTA, 20% glycerol, pH 8.8, with 5 mM HgCl2, two anti-protease pastilles (Complete anti-protease cocktail, Roche, Meylan, France) for 10 min on ice. The mixture was made 2% (v/v) with respect to Triton X100 and mixed in the homogenizer to solubilize membrane proteins for 10 min. Insoluble material was removed by centrifugation (50,000 × g for 40 min at 4°C). Soluble material was applied to a Q-Sepharose Fast Flow column (20 × 1.6 cm, Pharmacia, Orsay, France) equilibrated with the same buffer. Proteins were detected with the anti-CRD serum. The membrane pellet was resuspended in the disruption buffer with a Dounce homogenizer and then recentrifuged at 125,000 × g for 60 min at 4°C. The membrane was resuspended again in 20 mM Tris–HCl, 2 mM EDTA, pH 8.0, and stored at −80°C.

**SDS–PAGE and western blot**

Protein samples were analyzed by SDS–PAGE (Laemmli, 1970) using a 10% separating acrylamide gels. Protein bands were visualized by staining with Coomassie blue. Gel l and PhoAp (acid phosphatase) were detected on western blot using specific mouse or rabbit antibodies (Mouyna et al., 2000a; Bernard et al., 2002). GPI proteins were detected with an antiserum directed against soluble form of variant surface glycoproteins of *Trypanosoma brucei* that recognize the CRD epitope formed by the action of (G)PI-PLC on GPI proteins (Zamze et al., 1988). Protein samples (40 µl) were incubated with 10 µl 200 mM imidazole/acetic acid, pH 7.4, 5 mM dithiothreitol, and with or without 0.2% (v/v) PI-PLC from *Bacillus thuringiensis* (200–300 U/ml, Glyko) for 2 h at 30°C. GPI proteins were subsequently visualized by western blot with the anti-CRD serum.

**Isolation of PIs from GPI proteins**

Protein samples (1–2 nmol) were separated by large-scale SDS–PAGE, and proteins were transferred onto PVDF membrane and visualized with Ponceau Red staining. GPI proteins were cut out with a razor blade. PVDF membrane strips were washed in Eppendorf tubes with methanol and water. The samples were deaminated by submerging the blot strips in 200 µl of 300 mM sodium acetate, pH 4.0, and an equal volume of freshly prepared 1 M NaNO2 for 2–3 h at 37°C. The strips were washed three times with water, then PIs were extracted three times with 0.5 ml water-saturated butanol-1-ol for 20 min with vortex agitation and for 10 min in an ultrasonic bath. The butanol phases were concentrated under vacuum, and the PIs were repartitioned between 200 µl each butanol-1-ol and water. The butanol phase was re-extracted twice with 200 µl butanol-saturated water and dried. The PI extracts were purified by adsorption chromatography on a 100–200 µl silica column (Kieselgel 60, 70–230 mesh, Merck, Fontenay-sous-Bois, France): PI extracts were dissolved in chloroform: methanol (4:1, v/v) and applied to the small silica column equilibrated in the same solvent. After extensive washing, the PIs were eluted with 10 column volumes of chloroform: methanol (1:4 v/v). The eluate was dried and redissolved in chloroform:methanol (2:3 v/v) immediately prior to ES-MS analysis.

**Isolation of the GPI glycan moiety**

Protein samples (around 0.5 nmol) were separated by SDS–PAGE, transferred onto a PVDF membrane, and visualized with Ponceau Red. After cutting out the protein bands of interest, the labeling and release of GPI glycans was performed as previously described (Zitzmann and Ferguson, 1999; Zitzmann et al., 2000). Briefly, samples were deaminated and the free reducing end 2,5-AHM residue thus formed was labeled by reductive amination with 2-AB (Sigma-Aldrich, St. Louis, MO). The 2-AB-labeled GPI glycans were analyzed on an amino-bonded phase column (3 cm × 2.1 mm, Kromasil, Theale, UK) and detected with a Gilson (model 121) fluorescence detector. Oligosaccharides were separated using the following conditions: flow 0.2 ml/min; buffer A, 95% acetonitrile; buffer B, 15 mM ammonium acetate in 5% acetonitrile. Gradient: 0–5 min, isocratic (100% buffer A); 5–25 min, linear gradient (100% A, 0% B to 70% A, 30% B); 25–70 min, linear gradient (70% A, 30% B to 30% A, 70% B). 2-AB-labeled GPI glycans isolated from several *T. brucei* variant surface glycoproteins were used as standards.

**HPLC of 2-AB-labeled GPI glycans**

2-AB-labeled GPI glycans were analyzed on an amino-bonded phase column (3 cm × 2.1 mm, Kromasil, Hitchrom, Theale, UK) and detected with a Gilson (model 121) fluorescence detector. Oligosaccharides were separated using the following conditions: flow 0.2 ml/min; buffer A, 95% acetonitrile; buffer B, 15 mM ammonium acetate in 5% acetonitrile. Gradient: 0–5 min, isocratic (100% buffer A); 5–25 min, linear gradient (100% A, 0% B to 70% A, 30% B); 25–70 min, linear gradient (70% A, 30% B to 30% A, 70% B). 2-AB-labeled GPI glycans isolated from several *T. brucei* variant surface glycoproteins were used as standards.
Enzymatic digestion of 2-AB-labeled GPI glycans

Enzymatic digestions were done with exo-α-mannosidase activities. Samples were dried and resuspended in 10 µl of 100 mM ammonium acetate buffer at the optimum pH of each respective enzyme: non-specific α-mannosidase from jackbeans (0.5 mU, optimum pH 5.5, Calbiochem, Nottingham, UK), α2-6-mannosidase from Aspergillus saitoi (2 µU, optimum pH 4.0, Glyko), α1,2,3-mannosidase from Xanthomonas manihotis (10 U, optimum pH 6.0 with 5 mM CaCl2, New England Biolabs, Hitchin, UK), or α1-6-mannosidase from Xanthomonas manihotis (10 U, optimum pH 5.0, New England Biolabs). Reactions (37°C, overnight) were stopped by addition of 60 µl of ethanol, dried under vacuum, dissolved in 6 µl of water, and analyzed by HPLC on the amino-bonded phase column, as already described.

Permethylation of 2-AB-labeled GPI glycans

Samples were dried, redissolved in 50 µl dimethylsulfoxide, and treated with 50 µl of a 120 mg/ml slurry of NaOH in dimethylsulfoxide (20 min). Two aliquots (10 µl) of methyl iodide were added at 10-min intervals. The reaction was quenched by the addition of 15 µl acetic acid, 0.25 ml chloroform, and 1 ml water. The lower chloroform phase was washed four times with 1 ml water, dried, and redissolved in 80% acetonitrile, 0.5 mM sodium acetate.

ES-MS

PI samples were introduced into the electrospray source of a Micromass Quattro triple-quadrupole mass spectrometer at 6 µl/min in chloroform:methanol (2:3, v/v). Negative ion ES-MS spectra were recorded with a capillary voltage of 3.0 kV and a cone voltage of 50 V. Negative daughter ion ES-MS-MS spectra of [M-H] pseudomolecular ions of PIs were recorded with argon as the collision gas (2.5 × 10⁻³ Torr) and 60 V collision energy.

Native 2-AB-labeled GPI glycans were introduced into the nano-electrospray source of a Micromass Q-ToF mass spectrometer via a nanoinjection in 50% acetonitrile, 1% formic acid. Positive ion ES-MS and ES-MS-MS spectra were recorded with a tip voltage of 950 V and cone voltage of 40 V. The collision energy for ES-MS-MS was 40 V.

Permethylated 2-AB-labeled GPI glycans were introduced into the nano-electrospray source of a Micromass Q-ToF mass spectrometer via a nanoinjection in 80% acetonitrile, 0.5 mM sodium acetate. Positive ion ES-MS and ES-MS-MS spectra were recorded with a tip voltage of 950 V and cone voltage of 40 V. The collision energy for ES-MS-MS was 80 V.

Peptide analysis

Coomassie blue–stained GPI protein bands, isolated by SDS–PAGE, were excised from the gel. In-gel digests were done with bovine trypsin. Samples were desalted, and peptide masses were analyzed by MALDI-TOF MS (Shevchenko et al., 1996). In addition, internal peptides obtained by reverse-phase HPLC after tryptic digestion were sequenced on an Edman microsequencer (Applied Biosystem 470 gas-phase sequencer) following the procedure described in Beauvais et al. (1997). Analyses were performed by J. D’Alayer (Laboratoire de microsequencage, Institut Pasteur, Paris). MALDI-TOF and Edman sequencing data were matched against the NCBIinr and the Genome Therapeutics Corporation Pathogenome databases using the MS-Fit and MS-Edman programs (assembled into the Protein Prospector package, Baker, and Clauer), respectively. These protein identifications were performed by J. M. Brunéau (Aventis-Hoechst Marion Roussel, Romainville, France).

Acknowledgments

M.A.J.F. and A.H.M. are supported by a Wellcome Trust Programme (054491). D.L. is supported by a Wellcome Trust JIF grant (060269).

Abbreviations

2-AB, 2-aminobenzamide; AHM, anhydromannose; BSA, bovine serum albumin; CRD, cross-reacting determinant; EDTA, ethylenediamine tetra-acetic acid; ES-MS, electrospray mass spectrometry; ES-MS-MS, electrospray tandem mass spectrometry; GPI, glycosyolphosphatidyl inositol; HPLC, high-performance liquid chromatography; IPC, inositol-phosphoceramide; MALDI-TOF, matrix-assisted laser desorption ionization time-of-flight; PI, phosphatidylinositol; PLC, phospholipase C; PVDF, polyvinylidene difluoride; SDS–PAGE, sodium dodecyl sulfate–polyacrylamide gel electrophoresis.

References


