Deletion of New Covalently Linked Cell Wall Glycoproteins Alters the Electrophoretic Mobility of Phosphorylated Wall Components of Saccharomyces cerevisiae

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The incorporation of radioactive orthophosphate into the cell walls of Saccharomyces cerevisiae was studied. 32P-labeled cell walls were extensively extracted with hot sodium dodecyl sulfate (SDS). Of the remaining insoluble radioactivity more than 90% could be released by laminarinase. This radioactive material stayed in the stacking gel during SDS-polyacrylamide gel electrophoresis but entered the separating gel upon treatment with N-glycosidase F, indicating that phosphate was linked directly or indirectly to N-mannosylated glycoproteins. The phosphate was bound to covalently linked cell wall proteins as mannose-6-phosphate, the prime type of linkage shown previously for soluble mannoproteins (L. Ballou, L. M. Hernandez, E. Alvarado, and C. E. Ballou, Proc. Natl. Acad. Sci. USA 87:3368–3372, 1990). From the phosphate-labeled glycoprotein fraction released by laminarinase, three cell wall mannoproteins, Ccw12p, Ccw13p, and Ccw14p, were isolated and identified by N-terminal sequencing. For Ccw13p (encoded by DAN1 [also called TIR3]) and Ccw12p the association with the cell wall has not been described before; Ccw14p is identical with cell wall protein Icw (I. Moukadiri, J. Armero, A. Abad, R. Sentandreu, and J. Zueco, J. Bacteriol. 179:2154–2162, 1997). In cww12, cww13, or cww14 single or double mutants neither the amount of radioactive phosphate incorporated into cell wall proteins nor its position in the stacking gel was changed. However, the triple mutant brought about a shift of the 32P-labeled glycoprotein components from the stacking gel into the separating gel. The disruption of CCW12 results in a pronounced sensitivity of the cells to calcofluor white and Congo red. In addition, the cww12 mutant shows a decrease in mating efficiency and a defect in agglutination.

The walls of fungal cells can be considered vital extracellular organelles that have to withstand turgor pressures greater than 15 × 105 Pa (6). Baker’s yeast, Saccharomyces cerevisiae, invests about 20% of its total dry weight into building up this organelle, which consists of approximately equal parts of glucans and mannoproteins and less than 2% chitin (7). The protein moieties of the mannoproteins amount to about 10% of the wall, and more than 20 individual cell wall proteins have been identified so far (3, 4, 8, 17, 18, 21, 24, 25, 27, 33, 37, 42, 43, 48).

The extraordinary stability of the cell wall against tension due to high internal hydrostatic pressure can be explained, if it is assumed that there are phosphodiester bridges between the O-linked saccharides of mannoproteins and, for example, glucans of the cell wall. Such a type of linkage exists, for example, in the cell wall of Volvox, for which it was shown that O-linked chains may link extracellular matrix components by Ara-5-phospho-5-Ara bridges (44).

To identify such phosphodiester bridges, we studied the incorporation of radioactive phosphate into the cell wall of S. cerevisiae. During the course of this investigation three new covalently cell wall proteins (Ccw12p, Ccw13p, and Ccw14p) have been identified, whose electrophoretic behavior correlated with the most highly phosphorylated cell wall fraction. Ccw14p has been identified in the meantime also by Moukadiri et al. (26) as inner cell wall protein Icw. These cell wall proteins and their knockout phenotypes, as well as the structure of the phosphate-containing saccharides, are described in this paper.

**MATERIALS AND METHODS**

**Yeast strains.** The strains used in this study are shown in Table 1.

**Phosphate labeling of covalently linked cell wall proteins.** A total of 1.4 × 107 cells from a overnight culture of S. cerevisiae were pelleted and resuspended in 10 ml of a phosphate-free minimal medium (39). After the culture was shaken at 29°C for 2.5 h, 20 μl of 0.1 M K phosphate and 400 μCi of [32P]orthophosphate (specific activity, 3,000 Ci/mmol) were added, and the cells were incubated for another 3.5 h. Cells were spun down, an aliquot of the medium was counted, and the cells were broken by vortexing the suspension four times for 1 min with 0.5-mm-diameter glass beads in 300 μl of an extraction buffer (50 mM Tris-HCl [pH 7.5], 1 mM 2-mercaptoethanol, 1 mM phenylmethylsulfonyl fluoride, 1 mM benzamidine, 1 μg of antipain per ml, 5 μg of pepstatin per ml, 20 μg of leupeptin per ml). The extract was removed from the glass beads, and the latter was washed with 300 μl of the same buffer. The pooled extracts (600 μl) were centrifuged at 1,000 × g for 3 min. The supernatant (cytosol) was removed, and the pellet was extracted twice with 1 ml of sodium dodecyl sulfate (SDS)-Laemmli buffer (22) at 95°C. The pellet was then washed with 1 ml of 0.5 M NaCl and with 1 ml of H2O. Subsequently, the pellet was incubated in a total volume of 200 μl of a solution containing 50 mM Tris-HCl [pH 7.5], 50 mM MgCl2, DNase I (110 U), and RNase (50 μg) for 8 h at 30°C. The radioactivity staying...
in the pellet was considered to be associated with insoluble cell wall material. Most (90%) of this radioactivity was released when the pellet was treated for 4 h by electroblotting proteins onto nitrocellulose membranes, which were then incubated for 1 h in 10 mM Tris-HCl, pH 7.5, containing 0.1% Triton X-100 and 4% bovine serum albumin (BSA), followed by 1 h in the same buffer with 1% BSA and streptavidin-horseradish peroxidase conjugate (Sigma), at a dilution of 1:5,000. Blots were subsequently washed three times with the same buffer and developed with an ECL kit (Amersham, Little Chalfont, United Kingdom). Protein standards used for the estimation of molecular masses (in daltons) of proteins were as follows: myosin (205,000), β-galactosidase (116,000), phosphorylase b (97,400), BSA (67,000), ovalbumin (45,000), and carbonic anhydrase (29,000).

### Table 1. Yeast strains

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<th>Strain</th>
<th>Genotype</th>
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<tr>
<td>MEY1213</td>
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### NEW COMPONENTS OF THE YEAST CELL WALL

Disruption of genes coding for identified cell wall proteins. Standard procedures were used for all DNA manipulations (32). For all PCRs, genomic DNA isolated from strain SEY6210 (28) was used as a template. To construct strains MEY12A and MEY12B, the open reading frame (ORF) YLR110c was amplified by PCR with oligonucleotides 5'-TGGAGGTCTACCTTCTC-3' and 5'-CTCCGC GAGCTCAGG-3' and cloned into the Smal site of pGPD, resulting in plasmid pME12. The URA3 gene was isolated as a 1.1-kb HindIII fragment from the plasmid YEp24 (14) and cloned into PME12 (digested with Tn1111).

To construct the strain MEY13, the ORF YJR150c was amplified by PCR with oligonucleotides 5'-CTCTCGTAGAACCTCTCGT-3' and 5'-GGACCGGGAAATAGTTGGGACGAC-3' and cloned by blunt-end ligation into the Smal restriction site of pUC19, resulting in plasmid pME13. The TRP1 gene was cloned as a 1.3-kb BglII-SphI fragment from the plasmid pRS414 (38) into pME13 (digested with SphI). In the case of strains MEY14 and MEY234, N- and C-terminal fragments of YLR391w were amplified with oligonucleotides 5'-ATAAAGAATGGCGGGCCGACATACGCGAGACG-3' and 5'-CTATCCCGGGAGC CAAACGGTTGTTGCGTGAGTTGCGACC-3' and oligonucleotides 5'-CAAGCTTGGTGCTGTGAGCTTTGACC-3' and 5'-TGAGACGGCTGACGAGGAAAGCTACTCGGA-3', respectively. Both new PCR fragments of YLR391w with a 22-base overlap were fused in a second PCR, creating a new HindIII site and a new BamHI site. These sites were used subsequently for the insertion of the ura3-52 allele from the plasmid YEp24 and HIS3 (1.8-kb BamHI fragment from the plasmid JCW102, kindly supplied by J. Wan, San Diego, Calif.). Single disruptions were performed in strains SEY6210 and SEY6211. Yeast transformation was performed according to the method of Gietz et al. (10). Correct disruptions were analyzed by PCR.

To construct the cw12 cw13 double mutant, the direct disruption of CCW12 in the cw12 mutant (MEY12A) was unsuccessful. Therefore, MEY12A was crossed with MEY6211, and the obtained diploids were transformed with the plasmid cw13::TRP1 construct. The strain MEY1213 resulted from the sporulation of the diploid transformants. In order to construct MEY234 (cw12 cw13 cw14), MEY1213 was transformed with cw14::HIS3.

### Quantitation of mating efficiency.

Cells were grown to a density of 1 × 10^10 to 4 × 10^10 cells/ml. Equal numbers (10^10 cells) of strains of opposite mating types were mixed in 150 μl of YPD medium. The suspension was incubated for 6 h at 30°C, centrifuged, and resuspended in 100 μl of H2O. Serial 1:10 dilutions thereof were prepared. A total of 5 μl of each dilution was spotted on YPD medium, to which either 10 μg of calcicolin white per ml or 0.25 or 20 μg of Congo red per ml was added. The plates were incubated at 30°C.

### Agglutination assay.

Equal numbers (2 × 10^7 cells) of logarithmically growing cells of opposite mating types were mixed in 50 μl of YPD medium on microscope slides.

### Chromatography of phosphorylated cell wall components.

(i) TLC. Thin-layer chromatography (TLC) was performed on polyethyleneimine cellulose plates (Schleicher & Schuell) with 1 M ammonium formate, pH 3.4, as the solvent system (44).

(ii) Bio-Gel P 2 chromatography. Oligosaccharides were separated on a column (10 by 104 cm) equilibrated in 50 mM pyridine acetate, pH 5.2. Fractions of 1 ml were collected and analyzed for radioactivity or total carbohydrate by the phenol-sulfuric acid method (5). Molecular mass standards were stachyose, rafinose, and mannose.

### High-performance anion exchange chromatography (HPAEC).

To determine the sugar composition, samples were hydrolyzed with 4 M trifluoroacetic acid (TFA) at 100°C for 4 h and separated on a CarboPac PA1 column (4 by 25 mm) with 16.5 mM NaOH as an eluent at a flow rate of 1 ml/min. For the analysis of sugar-phosphates the same column was used by applying an isocratic elution of 150 mM Na acetate in 54 mM NaOH for 20 min, followed by an increase to 200 mM Na acetate in 39 mM NaOH within 10 min and at a flow rate of 1 ml/min; for detection a PAD (Gold) detector was used. With a mannose-6-phosphate standard the column was qualitatively and quantitatively calibrated.

### Preparation and characterization of phosphorylated cell wall oligosaccharides.

Commerically obtained baker’s yeast (weight, 150 g) was suspended in 150 ml of 10 mM Tris-HCl (pH 7.4) containing 1 mM phenylmethylsulfonyl fluoride and broken with a Bio-Spec bead beater (150 g of 0.5-mm-diameter glass beads) four times for 30 s. The disruption of cells was monitored by microscopy. The homogenate was centrifuged for 10 min at 5,000 × g, and the cell wall pellet was washed three times with a homogenization buffer, five times with 1 M NaCl, and five times with water. Cell walls were extracted twice with hot 50 mM Tris-HCl containing 2% SDS, 1% Triton X-100, and 1 M EDTA, and 40 mM sodium fluoride (pH 8) for 15 min at 100°C, followed by three washes with water (final yield was 60 g [wet weight]). The purified cell wall fraction was hydrolyzed in portions of...
15 g with 50 ml of 0.5 M TFA in boiling water for 2 h and then extensively
lyophilized to remove the acid (final yield was 840 mg).

(i) QAE-Sephadex A50 chromatography. The lyophilisate (400 mg) was dis-
solved in 15 ml of 2 mM Tris-base, applied to a column of 2.5 by 15 cm, and
culated at a flow rate of 1 ml/min with a step gradient of 2 mM Tris-base, 2 mM
Tris-base containing 100 mM NaCl, and 2 mM Tris-base containing 200 mM
NaCl (see Fig. 4). Fractions of 5 ml were collected, pooled, and dialyzed (2,000-
molecular-weight cutoff Spectroorp 6) against water.

(ii) Bio-Gel P2 chromatography. Quaternary aminoethyl (QAE) fractions 48
to 60 (see Fig. 4) were pooled and hydrolyzed with 2 M TFA for 2.5 h at 100°C,
dried under nitrogen, dissolved in 0.5 ml of water, and chromatographed on the
same column, and identical conditions were used for the radiolabeled material.

(iii) HPAEC. Pooled P2 fractions 54 to 57 and 58 to 62 were lyophilized and
purified further in several batches on a PA1 column with the sugar-phosphate
gradient. The sugar-phosphate peaks (compound I from the pool of fractions 54
to 57 and compound II from the pool of fractions 58 to 62) were desalted on
Dowex 50WX8 (H\(^+\)) and used for electrospray ionization tandem mass spec-
trometry (ESI-MS) and gas chromatography-mass spectrometry analysis.

(iv) ESI-MS. A Finnigan MAT TSQ 700 triple quadrupole mass spectrometer
equipped with a Finnigan electrospray ion source (Finnigan MAT Corp., San
Jose, Calif.) was used for ESI-MS. Native oligosaccharides were dissolved in
methanol containing 0.3% NH\(_4\), a concentration of approximately 10 pmol/μl,
infused at a flow rate of 1 μl/min into the electrospray chamber, and subjected
to negative-ion-mode ESI-MS. A voltage of 4.5 kV was applied to the electro-
spray needle. For collision-induced dissociation (CID) experiments, parent ions
were selectively transmitted by the first mass analyzer and directed into the
collision cell (argon was used as the collision gas) with the kinetic energy set
around 30 eV. The reduced and permethylated samples were dissolved in aci-
nitrile, saturated with NaCl (concentration, approximately 10 pmol/μl) and,
detected in the positive-ion mode with inverted voltages on the mass spectrom-
eter.

(c) Methylation analysis. For methylation analysis, oligosaccharides were per-
methylated according to the method of Hakomori (12), purified, hydrolyzed,
reduced, and peracetylated as described previously (29). The separation and
identification of partially methylated alditol acetates were performed on a Finni-
gan 1050 chromatograph (Finnigan MAT Corp.), equipped with a 30-m DB5
capillary column, connected to a Finnigan GCQ ion trap mass spectrometer.

RESULTS

Characterization of the phosphate-labeled glycans covalently linked to the cell wall. In order to address the
question whether glucan-phosphate or mannann-phosphate
linkages occur in the wall and in particular whether mild acid-
stable phosphodiester bridges of the type found in Volvox (44)
can be detected as a structural element, yeast cells were metab-
olically labeled with [\(^{33}\)P]orthophosphate. Isolated cell walls
were washed, and soluble, noncovalently linked glycoproteins
were removed by extraction with SDS under reducing condi-
tions. The residual wall was treated with mild acid to release
labile phosphodiester mannose of the Man-1-phospho-6-Man
type (31) and finally with DNase-RNase to remove radiola-
beled nucleic acid contaminants. The cell wall purified and
alyzed in this way contained 0.5 to 0.9% of the total \(^{33}\)P
incorporated (three experiments).

(i) TLC analysis. This purified radiolabeled cell wall was
partially hydrolyzed with 0.5 M TFA (2 h at 100°C); the total
radioactivity became soluble under this condition. Chromatog-
raphy of the \(^{33}\)P-labeled cell wall hydrolysate on polyethylenei-
mine cellulose thin-layer plates resulted in the detection of a
radioactive product that was hardly retained by the ion-ex-
change layer, as is typical for the mobility of sugar phosphodi-
ester compounds (Fig. 1). This chromatographic system has
previously been used to identify a phosphodiester of arabinose
of this same material on a Dionex HPAEC instrument showed
that the hexose phosphate has the mobility of mannose-6-
phosphate (data not shown; see below).

(ii) Bio-Gel P2 analysis. Analysis of the 0.5 M TFA hydro-
lysate on a Bio-Gel P2 column revealed that the material elutes
in the void volume (Fig. 2A), indicating that it is larger than 1.8
kDa. The isolated, excluded fraction was treated with stronger
acid and rerechromatographed on the same column. As shown in
Fig. 2B and C the radiolabeled material shown in Fig. 2A was
converted to \(^{33}\)P-labeled compounds of smaller size. Fractions
59 to 62, eluting between a di- and tetrasccharide reference,
as well as fractions 56 to 58 and fractions 53 to 55 (Fig. 2B)
were pooled and analyzed by TLC. All three fractions migrated
in the phosphodiester region, in accordance with the expected
behavior of the ion-exchange layer, which does not separate by
size. After further acid hydrolysis these compounds could be
converted to radioactive material, running like a hexose mono-
ophosphate (data not shown).

Structural analysis of the cell wall-bound sugar-phosphate.

(i) Isolation of phosphorylated oligosaccharides. To identify and
characterize the nature of the cell wall-bound sugar-phos-
phate described above, nonradioactive bulk cell wall material
was prepared. The procedure followed to obtain SDS-ex-
tected purified cell walls was identical to that described above.
A large-scale purification of the 0.5 M TFA-released cell wall fraction
was carried out as described in Materials and Methods
(Fig. 3). Determination of the carbohydrate composition of this
material after complete hydrolysis (4 M TFA at 100°C for
4 h) yielded 57% mannose, 41% glucose, and 2% mannose-6-
phosphate. Before the 0.5 M TFA hydrolysate was applied to
Bio-Gel P2, it was first fractionated on a QAE-Sephadex col-
umn to remove neutral material, according to the procedure of
Varki and Kornfeld (45) (Fig. 4). Three fractions were ob-
tained: a neutral, nonretarded one (fractions 12 to 28); frac-
tions 48 to 60, eluted with 100 mM NaCl; and fractions 81 to
105, eluted with 200 mM NaCl. Both charged pools after com-

complete hydrolysis had a similar carbohydrate composition, consisting of 96% mannose, 3.5% mannose-6-phosphate, and hardly any glucose. Only the pool of fractions 48 to 60 was further analyzed; due to the almost identical overall composition, it is assumed that the compounds in the two charged pools differ only by the charge density, i.e., the number of charges per molecule. The Bio-Gel P2 profile obtained after 2 M TFA hydrolysis of the pool of fractions 48 to 60 is depicted in Fig. 2D. Fractions 54 to 57 and 58 to 62 were pooled, and the phosphorylated compounds were purified to homogeneity by HPAEC. Both fractions contained phosphorylated saccharides and in addition still-neutral manno-oligosaccharides eluting in the flowthrough fraction. High-pressure liquid chromatography profiles of the phosphorylated compounds designated I and II are shown in Fig. 5A and B. The retention times of both peaks were shorter than that of mannose-6-phosphate, which was expected for a phosphodiester due to a reduced charge.

FIG. 2. Bio-Gel P2 profiles. Shown are the analysis of radiolabeled 0.5 M TFA extract (A), the void volume fraction shown in panel A further treated with 2 M TFA for 2 h (B) or 3 h (C), and the profile of the nonradioactive cell wall hydrolysate (D). QAE fractions 48 to 60 (Fig. 4) were pooled, dialyzed, and hydrolyzed with 2 M TFA for 2.5 h and applied to Bio-Gel P2. Fractions 54 to 57 (peak I) and 58 to 62 (peak II) were further purified by HPAEC (Fig. 5). The large carbohydrate peak, fractions 63 to 70, represents the position of monosaccharides.

FIG. 3. Flow sheet showing the isolation of phosphorylated saccharides from cell walls.

FIG. 4. QAE-Sephadex chromatography of 0.5 M TFA hydrolysate. The cell wall fraction released by 0.5 M TFA was loaded and eluted as described in Materials and Methods. Aliquots were analyzed for total carbohydrate by the phenol-sulfuric acid method. The arrows indicate the addition of 100 mM and 200 mM NaCl.
The arrow indicates the elution of the mannose-6-phosphate standard applied to a PA1 column for final purification with the sugar-phosphate gradient. To 57 (peak I) and 58 to 62 (peak II) from the Bio-Gel columns (Fig. 2D) were applied to a PA1 column for final purification with the sugar-phosphate gradient. The arrow indicates the elution of the mannose-6-phosphate standard.

Electrospray mass spectrometry of the native compound I with the phosphate-labeled material, 33P-labeled, insoluble cell wall material of the strain SEY6210 was treated with a β-glucanase. A total of 90% of the 33P-labeled material was released by laminaranase. Electrophoresis of this material revealed that the radioactivity remained in the stacking gel (Fig. 7B and C, WT lanes). Digestion with PNGase F resulted in the shift of the 33P-labeled material from the stacking gel to the separating gel (Fig. 7C), suggesting that 33P is associated with mannanose-6-phosphate.

The combination of these complementary sets of data suggests the structures P-6-Man-1→2-Man-1→6-Man, for the trisaccharide (compound I), and P-6-Man-1→6-Man, for the disaccharide (compound II). Assuming an α-configuration of the mannosyl residue, which is observed exclusively in mannoproteins isolated from yeast, the structures described are identical to the ones described for phosphorylated manno-oligosaccharides, which were isolated, however, from soluble glycoproteins.

Isolation, purification, and identification of new cell wall proteins. To find out which protein components are associated with the phosphate-labeled material, 33P-labeled, insoluble cell wall material of the strain SEY6210 was treated with a β-glucanase. A total of 90% of the 33P-labeled material was released by laminaranase. Electrophoresis of this material revealed that the radioactivity remained in the stacking gel (Fig. 7B and C, WT lanes). Digestion with PNGase F resulted in the shift of the 33P-labeled material from the stacking gel to the separating gel (Fig. 7C), suggesting that 33P is associated with mannoproteins.

The results obtained motivated the analysis of proteins contained in the stacking portion of the gel. Mrsa et al. (27) described a method for labeling S. cerevisiae cell wall proteins by biotinylation. By using this method, 20 cell wall proteins were labeled, and 11 of them were identified (4, 27). When proteins extracted from the wall by laminaranase were analyzed previously, the material remaining in the stacking gel was not included. Therefore, the biotinylation procedure was applied to analyze also that part of the gel which contains the phosphate. As shown in Fig. 7A, in addition to the proteins in the separating gel, the stacking gel also contained biotinylated material.

To identify these proteins, they were extracted from the stacking gel and purified on a Superose 12 column as described in Materials and Methods. N-terminal sequencing of the ma-
FIG. 6. ESI-MS spectra of compounds I and II. Negative-ion ESI-MS spectra of compound I (A) and compound II (B). (C) The detected deprotonated molecular ion suggests the presence of a monophosphorylated trisaccharide. The daughter ion spectrum of this molecular ion obtained after CID. The fragmentation pattern is explained in the scheme between panels B and C. The indicated secondary fragment ions are all due to the elimination of water. Additional fragment ions at m/z 553, 523, 403, and 463 are generated by the loss of one to four CH(OH) units from the reducing hexose, excluding a substitution at positions 2 to 4 of this residue. The intense fragment ion at m/z 301 can be assigned to the terminal phosphorylated hexose linked to an inner ring fragment incorporating two hydroxylated carbon units from the middle hexose residue.
The material obtained revealed one major protein sequence (Table 2) corresponding to the ORF assigned the Yeast Protein Database code YLR110c. Consistent with the previous designation of identified cell wall proteins (27), we named this gene CCW12 (because it encodes a covalently linked cell wall protein). CCW12 was found to be identical to the α0.6 gene, which was identified in a screen for genes in which transcription is switched off by α-factor (34). The corresponding protein, however, had not been identified so far. To test whether Ccw12p is the major protein component detected in the stacking gel, a ccw12 mutant was constructed. In the ccw12 mutant there is no obvious decrease in the amount of the biotin- or 33P-labeled material in the stacking gel (Fig. 7A and B).

To identify further protein components, preparative amounts of cell wall proteins of a ccw12 null mutant were extracted with laminarinase and isolated from the stacking gel as before. This revealed another protein sequence (YJR150c), and the gene was named CCW13 (Table 2). This gene was found to be allelic to the DNA1 gene, which was identified in a screen for genes induced during the anaerobic growth of yeast cells (35). The Dan1 protein had not been identified so far.

The 33P incorporation into the covalently bound cell wall material was checked in the ccw13 and the ccw12 ccw13 null mutants. In a ccw13 mutant no effect on the amount or on the running behavior of the biotinylated or radiolabeled cell wall proteins was found (data not shown). The same was true for the ccw12 ccw13 double mutant, for which the radioactivity was still concentrated in the stacking gel (Fig. 7A and B).

Therefore, we decided to test whether the Ccw14p protein, which we purified in a different context from a mnn9 mutant, might affect the running behavior of the 33P-labeled material. In the zymolyase extract of cell walls of the mnn9 mutant a double band could be seen on Coomassie blue-stained gels, with one band hardly migrating into the separating gel and the other with a molecular mass of about 150 kDa (data not shown). N-terminal sequencing of both bands revealed the same protein, here named Ccw14p (Table 2). The amino acid sequence showed that the protein was identical to the recently described inner cell wall protein (Icwp) (26). The disruption of CCW14 had no effect on the phosphate-labeled material in the stacking gel (data not shown). Only in the ccw12 ccw13 ccw14 triple knockout strain did the radioactivity incorporated into the SDS-extracted cell wall decrease slightly (data not shown) and the radioactively labeled material shifted from the stacking gel into the separating gel (Fig. 7B). In addition, no cell surface biotinylated material could be detected in the stacking gel anymore (Fig. 7A).

### Characterization of the newly identified cell wall proteins.

(i) Analysis of the sequences of Ccw12p, Ccw13p, and Ccw14p.

Ccw12p is a small, acidic protein of 133 amino acids and has all the properties characteristic of covalently linked cell wall proteins was found (data not shown). The same was true for the ccw12 ccw13 double mutant, for which the radioactivity was still concentrated in the stacking gel (Fig. 7A and B).

Table 2: N-terminal sequences of newly identified cell wall proteins

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<td>YLR110c</td>
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<td>Dan1p</td>
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</table>

<sup>a</sup> The experimentally determined sequence obtained (shown first) and the peptide derived from the gene sequence thought to be coding for the experimentally derived peptide (shown in parentheses) are shown for each protein.
It contains a typical signal sequence for directing the protein to the secretory pathway (amino acids 1 to 18), a large number of hydroxy amino acids (nearly 40% of the total amino acids), and a C-terminal sequence required for the potential attachment of a glycosylphosphatidylinositol (GPI) anchor. N-terminal sequencing of the protein predicted a mature protein of 93 amino acids and revealed that all serine and threonine residues between amino acid 19 and amino acid 51 were modified, indicating an exhaustive O-glycosylation of the protein. Besides, Ccw12p contains three potential N-glycosylation sites. The pronounced difference in the size of the calculated protein compared to the actual measured one suggests a very high degree of glycosylation. In the C-terminal part of the protein the amino acid motif TTEAPKNGTSTAAP is repeated twice. A similar motif is also present in the cell wall protein Sed1 (13, 36), where it is repeated four times with slight variations within the N-terminal part of the protein. Furthermore, the N-terminal part of Ccw12p (amino acid 28 to amino acid 73) is 72% identical to the region from amino acid 1229 to amino acid 1275 of the flocculation protein Flol1p (47). The same region has similar homology to three hypothetical FLO1 homologues (YKR102w, YHR211w, and YAL063c). It should also be mentioned that the S. cerevisiae genome contains another homologue of the Ccw12p gene (YD9302.09c/YD9302.10c), which is 83% identical to Ccw12p but contains a stop codon instead of the Q at position 67. The existence of this stop codon in our yeast strain has been confirmed by sequencing the PCR-amplified fragment (data not shown).

The second identified protein, Ccw13p, also conforms to the general properties of covalently linked cell wall proteins. It contains 298 amino acids (263 in the mature form) and a signal sequence (amino acids 1 to 19), about 40% of its total amino acids are hydroxy amino acids clustered in the C-terminal half of the gene, and finally, it has a putative C-terminal GPI-anchoring signal. Ccw13p, which is 93% identical to Ccw12p, contains all sequence elements typical for covalently linked cell wall proteins, including the serine-rich region in the C-terminal half of the protein and the putative GPI-anchoring signal.

(ii) Phenotypic characterization of ccw12, ccw13, and ccw14 null mutants. To assess possible functions of the three cell wall proteins, deletion mutants were constructed as described in Materials and Methods (Table 1). The ccw12, ccw13, and ccw14 single mutants showed no significant morphological phenotypes. The ccw13 and ccw14 mutants grew as well as the wild type, but the ccw12 mutant showed an increased generation time of about 40% compared to the wild type. In order to test whether Ccw12p, Ccw13p or Ccw14p are involved in stabilizing the cell wall, the effects of calcofluor white and Congo red, compounds known to interfere with cell wall biogenesis (18), on the growth of ccw12, ccw13, and ccw14 mutants were analyzed. As shown in Fig. 8, the ccw12 mutant is at least 100 times more sensitive to both dyes than the wild type. In the case of the ccw14 mutant, an increase in cell wall lability, as already reported by Moukadiri et al. (26), has been confirmed (data not shown). The mutation in the Ccw13 gene had no influence on the cell wall sensitivity towards the two agents (data not shown).

The ability of all three ccw disruptants to mate has also been tested. ccw mutants were mated with the wild-type SEY6211 (MATα) strain and tested for the growth of diploids. No mating defect was found for ccw13 and ccw14 mutants (data not shown). The ccw12 mutant, however, showed an apparent decrease in the mating efficiency (Fig. 9). To check whether the ccw12 mutant was also affected in agglutination, a standard agglutination assay was performed. Fig. 10 shows that the agglutination was indeed impaired, if one or both partners lack the Ccw12p protein. The different phenotype characteristics of cell wall protein mutants are summarized in Table 3.

DISCUSSION

Various components of the yeast cell wall are covalently linked to one another, as recently demonstrated and summa-
TABLE 3. Phenotypes of different cell wall protein mutantsa

<table>
<thead>
<tr>
<th>Strain</th>
<th>Growth</th>
<th>Sensitivity:</th>
<th>Mating</th>
<th>Agglutination</th>
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<tr>
<td></td>
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<td>Calcofluor</td>
<td>Congo</td>
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<td>red</td>
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<td>+</td>
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<tr>
<td>ccw12</td>
<td>Slow</td>
<td>+</td>
<td>++</td>
<td>–</td>
</tr>
<tr>
<td>ccw13</td>
<td>Normal</td>
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<td>–</td>
<td>+</td>
</tr>
<tr>
<td>ccw14</td>
<td>Normal</td>
<td>+</td>
<td>++</td>
<td>n.d.</td>
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a Different phenotypes of wild-type SEY6211 (WT) and the mutant strains MEY12A (ccw12), MEY 13 (ccw13), and MEY14 (ccw14) are summarized. n.d., not determined.

The possibility of a high-molecular-weight phosphorylated complex is suggested by the observation that all the 33P radioactivity solubilized by β-glucanase is retained in the stacking portion of an SDS gel (Fig. 7B). When biotinylated walls were prepared as described previously (27) it was indeed possible to demonstrate quite a significant amount of covalently bound protein material in the stacking gel after SDS electrophoresis (Fig. 7A). The corresponding proteins were purified and after partial N-terminal sequencing identified as Ccw12p, Ccw13p, and Ccw14p (Table 2). The corresponding genes had partly been identified previously in a different context (34, 35, 46); only for CCW14 has the protein been studied and shown to represent a cell wall component called Icpw, inner cell wall protein (26). The protein material in the stacking gel disappeared when CCW14 together with the other two genes was disrupted (Fig. 7A). Similarly, the amount of 33P incorporated into cell wall mannoproteins of this mutant was also slightly reduced, and the radioactivity was shifted into the separating gel. The fact that the 33P radioactivity was still associated with cell wall proteins of the triple mutant indicates, however, that further proteins besides Ccw14p get phosphorylated and that the running behavior of these proteins differs in the triple mutant from that of the wild type. This indicates some interaction or covalent connection of these various cell wall proteins. The question, however, of which cell wall protein(s) the phosphate is linked to has to remain unanswered, unfortunately.

It has been suggested that the covalently bound cell wall proteins are linked to the complex described by Köllár et al. (19) via a transmannosidase reaction, transferring the protein moiety together with part of its GPI anchor to the β-1,6-glucan (16, 23, 25). Since this transfer has been postulated to occur within the oligomannose portion of the GPI anchor, the newly attached mannoprotein should contain a fairly acid-stable phosphodiester linkage between ethanolamine and mannose (19). It has long been known that mild alkaline conditions, typically used for β-elimination reactions, cause drastic size changes in cell wall mannoprotein fractions (28); (ii) certain knockout mutants of PMT genes, which are responsible for protein O-mannosylation, lead to an osmolar phenotype, although a significant decrease in the total mannose content of the cell wall was not observed (9). Sugar chains O-linked to proteins could affect the secretory process of these cell wall proteins, or the sugar chains, although short, could contribute directly to cell wall rigidity. Either way these observations indicate that not only polysaccharide components, but cell wall proteins as well, should be considered important for cell wall rigidity. This could either be caused by O-mannosylated cell wall proteins as structural elements, or it could be related to the function of these proteins as extracellular enzymes; they could contribute to rigidity through the reaction they catalyze, for example, a transglycosylation.

Considering that protein-bound short O-linked sugar chains could be directly involved in building a rigid cell wall, the question of course arises of how this may be achieved. One possibility is the existence of a relatively acid-stable phosphate link between these chains and other cell wall polymers, a type of linkage existing in bacterial teichoic acids or in the arabino-protein of the Volvox extracellular matrix (11, 44). To test this hypothesis, it was investigated whether 33P gets incorporated into the insoluble yeast cell wall material remaining after the removal of soluble wall components by SDS. Indeed a significant amount of radioactivity was found in the insoluble fraction. About 90% of this radioactivity could be solubilized by laminarinase. Since its mobility on SDS gels was affected by PNGase F, it seemed obvious that 33P has been incorporated into mannoproteins covalently linked to cell walls. The postulated acid-stable phosphodiester, however, could not be detected. The structures finally determined, P-6-Man-1,2-Man-1,6-Man and P-6-Man-1,6-Man, correspond to linkages which have previously been identified as part of N-linked glycan chains on several soluble yeast glycoproteins, for example, on mannoproteins extractable with a citrate buffer and on carboprotease (1, 15). Biosynthetically these phosphomannoesters arise via a Man-1-P transfer from GDP-Man, yielding Man-1-P-6-Man-R and a subsequent release of the terminal mannose (2, 31). The Man-1-P-link is extremely acid labile (31) and would not have been preserved in the wall material studied here.

Since the first part of the paper gave a negative result—that the postulated stable phosphodiester does not exist—we tried in the second part to at least characterize the wall-bound phosphate. Surprisingly, phosphate incorporation into covalently bound cell wall proteins seems to be restricted to a few proteins or complex cell wall components containing mannoproteins. The possibility of a high-molecular-weight phosphorylated complex is suggested by the observation that all the 33P radioactivity solubilized by β-glucanase is retained in the stacking portion of an SDS gel (Fig. 7B). When biotinylated walls were prepared as described previously (27) it was indeed possible to demonstrate quite a significant amount of covalently bound protein material in the stacking gel after SDS electrophoresis (Fig. 7A). The corresponding proteins were purified and after partial N-terminal sequencing identified as Ccw12p, Ccw13p, and Ccw14p (Table 2). The corresponding genes had partly been identified previously in a different context (34, 35, 46); only for CCW14 has the protein been studied and shown to represent a cell wall component called Icpw, inner cell wall protein (26). The protein material in the stacking gel disappeared when CCW14 together with the other two genes was disrupted (Fig. 7A). Similarly, the amount of 33P incorporated into cell wall mannoproteins of this mutant was also slightly reduced, and the radioactivity was shifted into the separating gel. The fact that the 33P radioactivity was still associated with cell wall proteins of the triple mutant indicates, however, that further proteins besides Ccw14p get phosphorylated and that the running behavior of these proteins differs in the triple mutant from that of the wild type. This indicates some interaction or covalent connection of these various cell wall proteins. The question, however, of which cell wall protein(s) the phosphate is linked to has to remain unanswered, unfortunately.

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The disruption of the three genes coding for the cell wall proteins described herein revealed some apparent phenotypes.
of the corresponding mutants. The ccw12 mutant was particularly interesting, since a marked decrease in the mating ability of this strain was detected. Although it seemed unlikely that the mating defect was caused by a decrease in agglutination (24), the agglutination ability of the mutant was tested and found to be decreased (Fig. 10). However, when the presence of agglutinins in the ccw12 mutant was investigated, no change in the amount of α- or ω-agglutinins in the cell walls of the corresponding mating types could be seen, either on immunoblots of laminaranase cell wall extracts or by fluorescence microscopy of cells labeled with fluorescein isothiocyanate conjugates of α- or ω-agglutinin antibodies (data not shown). Thus, it has to be speculated that the inability of the mutant to agglutinate is due to an inaccessibility of agglutinins at the cell surface or to some other change in the structure of the cell wall. Analysis of other biotin-labeled cell wall proteins released by laminaranase showed that the lack of Ccw12p, as well as the lack of the other two proteins studied in this work, did not influence the presence and amount of any other protein in the cell wall.

Besides the described mating defect, the ccw12 mutant showed a significantly weakened cell wall, as indicated by the increased sensitivity to calcifluor white and Congo red. A similar effect has been reported previously (26) and is confirmed here for the Ccw14p (also called Icw1p) knockout. A similar effect has been reported previously (26) and is confirmed here for the Ccw14p (also called Icw1p) knockout. A marked decrease in the mating ability and cell wall.

The mutation of the third cell wall protein identified here, Ccw13p, did not yield a phenotype for the properties tested. It has to be mentioned that the gene coding for this protein, called DAN1, is repressed under aerobic growth conditions (35), a property reported also for another cell wall protein, Tir1p (40). Therefore, it can be assumed that Ccw13p plays a particular role restricted to anaerobic growth and that only a basal, constitutive level of Ccw13p was found in the cells studied here. Although it is presently not understood which cell wall functions may be specific in anaerobically grown yeasts, one may speculate that a whole set of cell wall proteins may be specifically produced during fermentative growth.

Thus, a number of open questions remain, including the central one of this paper, about the role of protein O-linked manno-oligosaccharides for cell wall stability. Cell wall structural and biosynthesis have to be explored further, which will yield interesting and most likely even surprising results.

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