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Deficiency of the first mannosylation step in the N-glycosylation pathway causes congenital disorder of glycosylation type Ik

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Defects of N-linked glycosylation represent diseases with multiple organ involvements that are classified as congenital disorders of glycosylation (CDG). In recent years, several CDG types have been attributed to defects of dolichol-linked oligosaccharide assembly in the endoplasmic reticulum. The profiling of [^{3}H]mannose-labeled lipid-linked oligosaccharides was instrumental in identifying most of these glycosylation disorders. However, this method is poorly suited for the identification of short lipid-linked oligosaccharide biosynthesis defects. To adequately resolve deficiencies affecting the first steps of lipid-linked oligosaccharide formation, we have used a non-radioactive procedure employing the fluorescence detection of 2-aminobenzamide-coupled oligosaccharides after HPLC separation. By applying this method, we have detected the accumulation of dolichylpyrophosphate-GlcNAc$_2$ in a previously untyped CDG patient. The accumulation pattern suggested a deficiency of the *ALG1* β1,4 mannosyltransferase, which adds the first mannose residue to lipid-linked oligosaccharides. This was supported by the finding that this CDG patient was compound heterozygous for three mutations in the *ALG1* gene, leading to the amino acid substitutions S150R and D429E on one allele and S258L on the other. The detrimental effect of these mutations on *ALG1* protein function was demonstrated in a complementation assay using *alg1 Saccharomyces cerevisiae* yeast mutants. The *ALG1* mannosyltransferase defect described here represents a novel type of CDG, which should be referred to as CDG-Ik.

INTRODUCTION

Inborn errors of glycosylation are a rapidly expanding family of genetic diseases encompassing various clinical entities. Deficiencies of N-linked glycosylation, also referred to as congenital disorders of glycosylation (CDG), represent multisystemic diseases with central and peripheral nervous involvements often associated with endocrine and coagulation disorders (1–3). Defects of *O*-mannosylation have recently been associated with Walker–Warburg syndrome (4) and different forms of muscular dystrophies like Muscle–Eye–Brain disease (5), Fukuyama congenital muscular dystrophy (6) and MDC1D (7). Dermatological (8) and bone disorders like hereditary multiple exostoses (9) are caused by alterations of glycosaminoglycan chain formation.

The broad symptomatology of glycosylation disorders and the tremendous structural diversity of glycoconjugates render the identification of glycosylation defects a difficult task. A simple test consisting of the isoelectric focusing separation of serum transferrin (10), a glycoprotein normally bearing two N-glycan chains, has greatly facilitated the detection of N-linked glycosylation defects. While this assay reliably identifies underglycosylation related to lowered sialylation, it lacks the resolution needed to pinpoint specific enzymatic defects. In combination with western blot analysis of serum transferrin, the isoelectric focusing test only allows discrimination between

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defects of oligosaccharide assembly and transfer, defined as CDG-I (11) and defects of N-linked glycan processing grouped as CDG-II.

Analysis of [^{3}H]mannose-labeled lipid-linked oligosaccharides (LLO) has enabled the characterization of several types of CDG-I caused by alterations of dolichylpyrophosphate (*DolPP*)-linked $GlcNAc_2Man_9Glc_3$ assembly at the membrane of the endoplasmic reticulum (ER) (12,13). However, a significant group of CDG-I patients, diagnosed by serum transferrin analysis, do not present any accumulation of incomplete oligosaccharides when using the established LLO profiling method. In fact, this method lacks the sensitivity required to detect accumulation of short LLOs such as those lacking mannose or those including only few mannose units. To remedy this problem, we have adapted a method based on the fluorescence detection of total cellular LLOs derivatized with 2-aminobenzamide (2AB). Using this novel approach, we have screened a group of untyped CDG-I patients and identified a case characterized by the accumulation of *DolPP*-$GlcNAc_2$. Genetic analysis confirmed in this patient a deficiency of the *ALG1* β1,4 mannosyltransferase, which catalyzes the first mannosylation step in the assembly of N-glycans.

RESULTS

The male patient FR was born after an uncomplicated pregnancy and presented early on with minimal signs of psychomotor development. There were no dysmorphic features present. The patient was affected by multiple intractable seizures, generalized muscular hypotonia and blindness. By 6 months of age, sepsis and pneumonia required prolonged hospitalization. Before 1 year of age, liver dysfunction became prominent as well as coagulation problems related to low antithrombin-III (12% of normal values). MRI scan of the brain was normal. The combination of developmental symptoms and coagulation disorder suggested a possible case of CDG. Isoelectric focusing of serum transferrin showed a typical CDG-I pattern with decreased tetrasialo and with increased disialo and asialotransferrin (Fig. 1), thus confirming the diagnosis. Phosphomannomutase activity measured in the patient fibroblasts yielded an intermediate value of 2.2 mU/mg protein (normal range 5.3 ± 1.7 mU/mg protein), which led to the sequencing of the candidate *PMM2* gene. The patient was found to be heterozygous for a point mutation causing the amino acid substitution E197A on the maternal allele. The *PMM2* E197A substitution has been found in combination with two genuine mutations in three other confirmed CDG-Ia patients. Hence, it is probably a polymorphism (unpublished data). It was concluded that it is unrelated to the disease in this patient.

To determine whether a defect of oligosaccharide assembly was the source of the glycosylation disorder, we analyzed the LLO profile in the patient fibroblasts after [^{3}H]mannose labeling using a procedure established previously (14–16). This analysis failed to reveal any accumulation of incomplete LLO structure (Fig. 2A–C). The level of [^{3}H]mannose incorporation was very low, indicating a limited LLO pool in the patient's cells. The detection of newly formed N-linked oligosaccharides (NLO) after 60 min labeling with [^{3}H]mannose showed the same profile as that found in cells from healthy controls (Fig. 2D–F), with peaks corresponding to

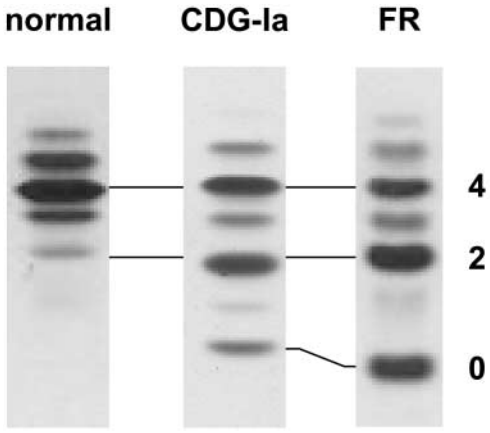

Figure 1. Isoelectric focusing of serum transferrin. Samples from a healthy control serum (normal), from a CDG-Ia control and from patient FR are shown. The number of negative charges is given at the right. The two glycan chains of normal transferrin contain mainly four sialic acids, whereas bands corresponding to disialo- and asialo-transferrin are visible in the FR sample.

$GlcNAc_2Man_8$, $GlcNAc_2Man_9$ and $GlcNAc_2Man_9Glc_1$. This result indicated that the fully assembled $GlcNAc_2Man_9Glc_3$ oligosaccharide was produced in the patient's cells, although in limited supply, and was successfully transferred onto nascent glycoproteins. $GlcNAc_2Man_9$ and $GlcNAc_2Man_9Glc_1$ arise from the trimming by glucosidases-I and -II, while $GlcNAc_2Man_9Glc_1$ can also arise from re-glucosylation during the process of protein folding (17). The $GlcNAc_2Man_8$ peak represents the oligosaccharide core trimmed by the ER α-mannosidase (18).

To support the hypothesis that the conversion of mannose-1-phosphate to GDP-mannose or to dolichylphosphate-mannose may be altered, the GDP-mannose pyrophosphorylase *GMPPA*, *GMPPB* genes and the dolichylphosphate-mannose synthase *DPM1*, *DPM2*, *DPM3* genes were screened by denaturing-HPLC (19). No mutation was found in any of these genes, thus ruling out a shortage of mannose substrates as a cause of the glycosylation disorder. This conclusion was supported by flow cytometry analysis where normal levels of the glycosylphosphatidylinositol (GPI)-anchored protein CD59, which also requires dolichylphosphate-mannose for the synthesis of the GPI-anchor, were found on the patient fibroblasts (data not shown).

To enable the detection of short LLOs that have escaped the established [^{3}H]mannose labeling procedure, we have adapted the recent method of Gao and Lehrman (20) to allow the efficient resolution of structures from *DolPP*-GlcNAc up to *DolPP*-$GlcNAc_2Man_9Glc_3$. Total LLOs were isolated from fibroblasts and hydrolyzed to liberate the glycan moiety. After a reductive amination with the fluorophore 2AB at their reducing termini, oligosaccharides were separated on a GlycoSep-N HPLC column, permitting the clear resolution of all oligosaccharide species found in LLOs. In the HPLC profile of patient FR, one can identify a peak comigrating with the external standard GlcNAc(β1,4)GlcNAc at 1.73 glucose units as compared with the elution positions of standard glucose oligomers (Fig. 3), whereas this peak is not detected in samples derived from control cells. The identity of this peak with GlcNAc(β1,4)GlcNAc was further confirmed by running

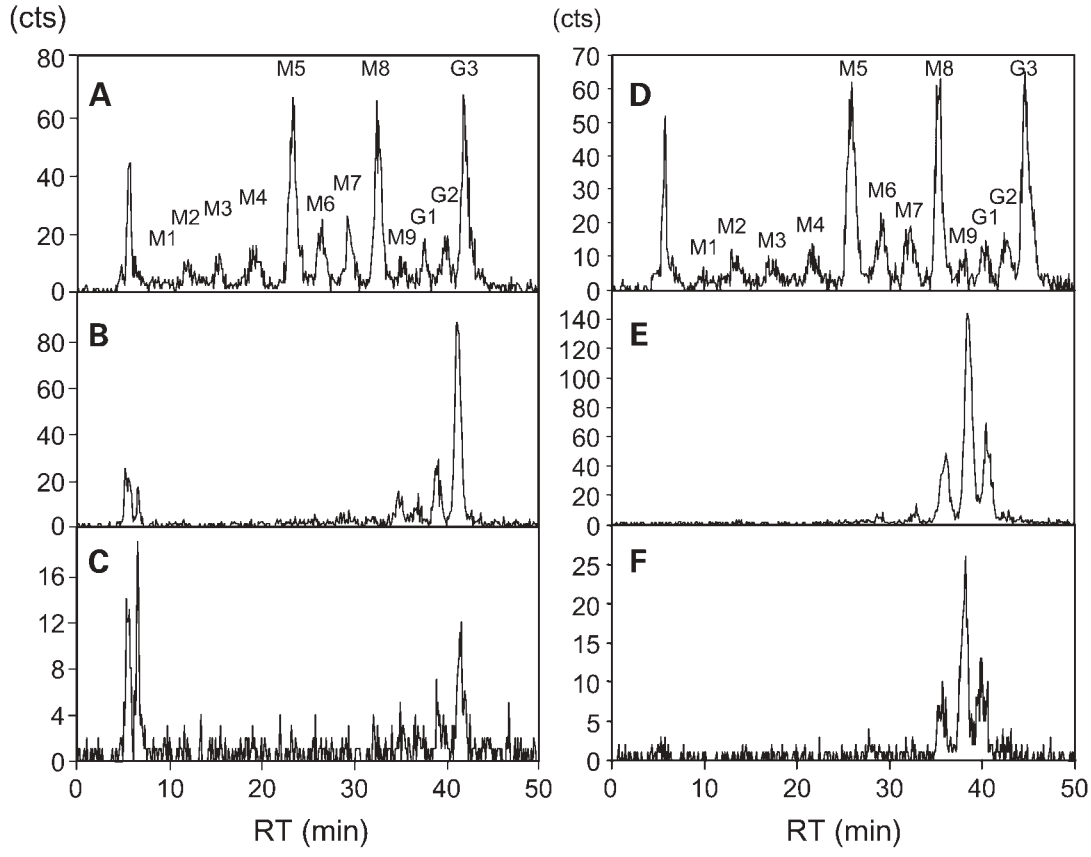

Figure 2. [^{3}H]Mannose-labeled lipid- and N-linked oligosaccharide profiles. HPLC separation of lipid-linked oligosaccharides from yeasts used as standard (**A**, **D**), of control human fibroblasts (**B**) and of patient FR fibroblasts (**C**) after metabolic labeling with [^{3}H]mannose for 60 min. Oligosaccharides were cleaved from dolichylpyrophosphate by mild acid hydrolysis and separated by HPLC. The identity of the oligosaccharide peaks ranging from $GlcNAc_2Man_1$ (M1) to $GlcNAc_2Man_9Glc_3$ (G3) is marked at the top of (A, D). [^{3}H]Mannose-labeled N-linked oligosaccharides from control cells (**E**) and from patient FR cells (**F**) were separated by HPLC after release from the protein by N-glycosidase F digestion. NLOs with peaks at M8, M9 and G1 are detected in control and patient fibroblasts.

collected fractions comprising the peak of interest onto a second dimension of reverse-phase HPLC (data not shown). This finding suggested an accumulation of *DolPP*-$GlcNAc_2$ to be at the origin of the glycosylation disorder in the patient FR. Also, in the GlycoSep-N HPLC profile of control fibroblasts, peaks corresponding to $GlcNAc_2Man_9Glc_{1\text{-}3}$ are visible. These peaks are also present in the patient HPLC profile, although with reduced intensity, thus confirming the limited supply of mature LLOs. The nature of the major peak, following the elution of chitobiose, is not known. However, after re-purification of the 2AB-labeled samples, the size of this peak relative to the chitobiose-peak was clearly reduced, indicative for non-carbohydrate, labeled material present in both fibroblast preparations (data not shown).

LLOs are assembled by the stepwise transfer of monosaccharides onto *DolPP*. The accumulation of *DolPP*-$GlcNAc_2$ implied a possible defect at the level of the addition of the first mannose residue catalyzed by the *ALG1* β1,4 mannosyltransferase enzyme. The human *ALG1* gene has been characterized recently (21). It encodes a protein of 464 amino acids displaying 36% similarity to the yeast Alg1 enzyme (22). cDNAs encoding homologous proteins were found in all eukaryotic genomes searched, such as in *Caenorhabditis elegans* and in *Drosophila melanogaster*. The sequence alignment of the putative *ALG1* proteins showed conserved domains, possibly regions representing the active site of the enzyme (Fig. 4). The *ALG1* cDNA was amplified by reverse transcription-PCR from control and from the patient FR fibroblasts. Sequencing of the DNA fragments revealed three heterozygous point mutations in the *ALG1* cDNA of patient FR (Fig. 4). These mutations, 450C>G, 773C>T and 1287T>A, lead to the amino acid substitutions S150R, S285L and D429E, respectively. These mutations were not found in control cDNAs sequenced in our laboratory, nor in 49 *ALG1* expressed sequence tags retrieved from GenBank (data not shown). The 450C>G, 773C>T and 1287T>A mutations detected in the patient FR are located on exons 4, 7 and 13 of the *ALG1* gene, respectively. Sequencing of these exons in DNA samples isolated from the parents of the patient FR indicated that the allele with S150R and D429E was inherited from the mother, whereas the S258L mutation stemmed from the father. The S258L mutation is located in a conserved domain of the *ALG1* protein. By contrast, the two maternal mutations do not correspond to positions conserved in the *ALG1* protein of the four species examined (Fig. 4).

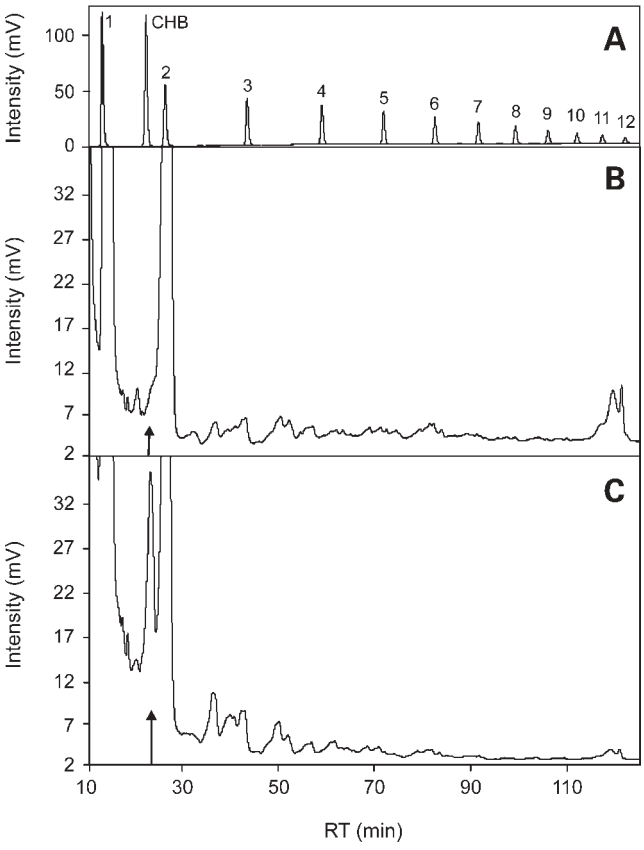

Figure 3. 2-Aminobenzamide-labeled oligosaccharide profiles on GlycoSep-N HPLC. (**A**) The separation of standard glucose oligomers with peaks corresponding to Glc_1 up to Glc_{12}, i.e. 1–12 glucose units. The external standard chitobiose (CHB), i.e. GlcNAc(β1,4)GlcNAc, elutes between Glc_1 and Glc_2 at 1.73 glucose units. The lipid-linked oligosaccharide profiles extracted from control (**B**) and patient FR (**C**) show in the FR sample a peak corresponding to the elution position of chitobiose, which is not visible in the control profile as indicated by the arrow.

To verify that the amino acid changes identified did impair *ALG1* protein function, the *ALG1* alleles of the patient FR and a normal human *ALG1* cDNA were introduced, under control of the strong glyceraldehyde phosphate dehydrogenase promoter (23), into *S. cerevisiae* yeasts carrying the *alg1-1* allele. This mutant allele does not support growth at elevated temperature due to reduced *ALG1* activity (24). As shown in Figure 5, growth at elevated temperature of the cell was restored by expressing the wild-type human *ALG1* cDNA. By contrast, the expression of the *ALG1* cDNAs isolated in the patient FR did not enable *alg1-1* yeasts to grow to the same extent as when transformed with the normal human *ALG1* cDNA. To examine the pathological impact of each of the two maternal mutations, we have transfected *alg1-1* yeasts with human *ALG1* cDNAs bearing the single mutation 450C>G [S150R] or the mutation 1287T>A [D429E]. The growth of *alg1-1* yeasts expressing the human *ALG1*[D429E] was similar to that of yeasts transfected with the wild-type human *ALG1* cDNA, indicating that this mutation likely represents a normal polymorphism. By comparison, the *ALG1* cDNA containing the 450C>G mutation failed to restore growth of *alg1-1* yeasts, which supports the pathological impact of the maternal S150R substitution on *ALG1* function (Fig. 5). Taken together, this analysis confirmed the direct relationship between the *ALG1* mutations and the glycosylation disorder detected in the patient FR. Thus, the *ALG1* defect reported here represents a novel type of CDG, which should be referred to as CDG-Ik following the nomenclature rules established previously (11).

DISCUSSION

A new genetic disorder affecting the first mannose transfer of dolichol-linked oligosaccharide biosynthesis was identified in this study. The defects in this disorder are caused by mutations in the *ALG1* β1,4 mannosyltransferase gene. The *ALG1* protein catalyzes the transfer of the first mannose residue onto *DolPP*-$GlcNAc_2$ using GDP-mannose as donor substrate. This reaction takes place at the cytosolic side of the ER membrane, where dolichol-linked oligosaccharides are assembled to *DolPP*-$GlcNAc_2Man_5$. The latter is then translocated ('flipped') into the lumen of the ER, in a protein-assisted process which requires Rft1 protein (25). On the lumenal side, the LLO assembly continues using dolichylphosphate-based donor substrates. The presence of the three terminal glucoses on LLOs is required for recognition by the oligosaccharyltransferase complex (26), although intermediate oligosaccharide structures can be transferred to nascent glycoproteins when the mature LLO is under limited supply. Usually under these conditions underglycosylation of proteins is observed as less sugar-chains are transferred. Such a transfer of incomplete oligosaccharides to proteins has been documented *in vivo* for example in yeast *alg* glycosylation mutants (27) as well as in CDG patients (28–30). Even though in the case of $GlcNAc_2$ transfer to protein has also been demonstrated *in vitro* (31) and *in vivo* in yeast (32), this occurs very inefficiently as it is a poor substrate for the oligosaccharyltransferase and, most likely, also for the flippase. Consequently, defects in $GlcNAc_2Man_5$ LLO assembly are severe and mostly lethal in yeast. The same severe phenotype can be expected in humans for complete blocks of LLO biosynthesis up to *DolPP*-$GlcNAc_2Man_5$. Even if transfer to protein would occur in patient cells, these truncated glycans are not expected to function properly in the glycan dependent quality control pathway (17,33). Also structures smaller than $GlcNAc_2Man_3$ would not support formation of complex type glycans. Therefore, the identification of glycosylation defects along the LLO cytosolic assembly line presupposes that the mutations encountered would only partially impair the activity of the corresponding glycosyltransferase enzymes. Yet, the resulting clinical manifestations can be quite severe, as observed in the patient reported in the present study.

Unlike the dolichylphosphate-mannose and -glucose dependent ER glycosyltransferases acting on luminally oriented LLOs, which are highly hydrophobic proteins with multiple transmembrane domains, the *ALG1* sequence predicts a type-II transmembrane topology reminiscent of Golgi-localized glycosyltransferases. Alignment with homologous proteins in several eukaryotic species shows strong sequence conservation in the C-terminal half of *ALG1* proteins, suggesting the localization of the catalytic domain in this part of the protein. This is supported by significant homology with several prokaryotic

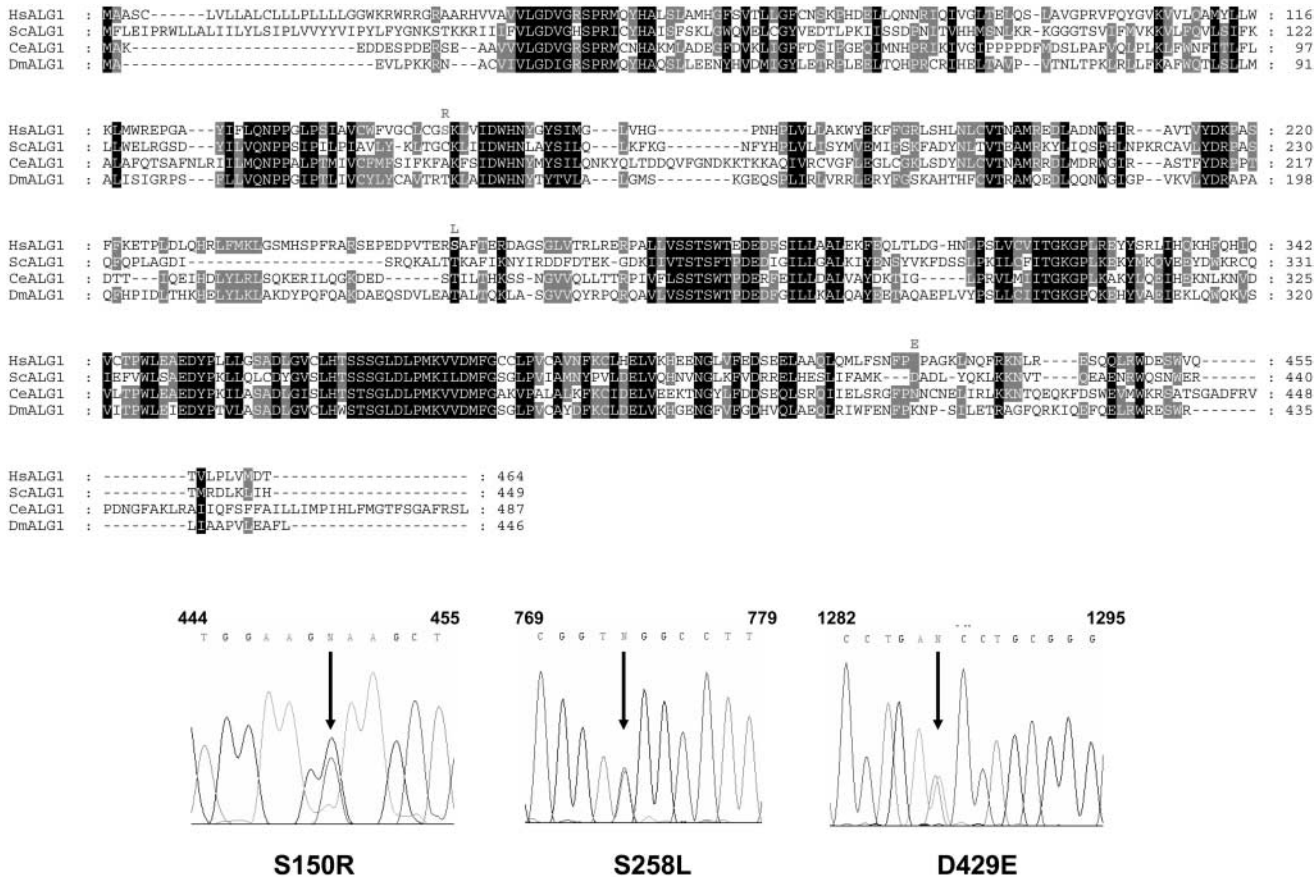

Figure 4. *ALG1* protein sequence comparison. Amino acid sequences of *ALG1* proteins from *Homo sapiens* (HsALG1), *S. cerevisiae* (ScALG1), *C. elegans* (CeALG1) and *D. melanogaster* (DmALG1) were aligned using the ClustalW program. Positions conserved in the four species are shaded in black, conserved in three species are shaded in gray. The amino acid changes S150R, S258L and D429E in patient FR are indicated above the human *ALG1* sequence. The electropherograms representing the corresponding mutations detected in the *ALG1* cDNA from patient FR are shown below the alignment. The maternal mutations S150R, D429E and the paternal S258L mutation are marked with arrows.

glycosyltransferase proteins in eubacteria (*Pseudomonas*, *Listeria*) and archae (*Methanosarcina*, *Methanococcus*). The three mutations identified in the patient FR were not at positions strictly conserved among *ALG1* protein homologs. This is consistent with a leaky phenotype as the observed residual activity in the patient fibroblasts enabled the formation of complete N-glycan chains on glycoproteins.

The *ALG1* deficiency represents the third type of CDG characterized by a defect of a cytosol-oriented ER-glycosyltransferase besides the *ALG2* mannosyltransferase (34) and *ALG7* N-acetylglucosamine-1-phosphotransferase (35) deficiencies, which have been assigned as CDG-Ii and -Ij, respectively. In these cases too, mutations lead to partial inactivation of the enzymes, resulting in low cellular pools of LLOs but to the transfer of complete oligosaccharides onto nascent glycoproteins.

For the *ALG1* patient studied here, the analysis of LLOs metabolically labeled with [^{3}H]mannose showed normal profiles, although with low incorporation yields, as observed in the cases of *ALG2* (34) and *ALG7* (35) deficiency described elsewhere. These findings are readily explained considering the enzymatic defects leading to the accumulation of LLO species containing no or at most two tritiated mannoses. Several CDG-I patients remain untyped because the analysis of LLO profiles obtained from their fibroblasts only shows low [^{3}H]mannose incorporation and a peak corresponding to the complete *DolPP*-$GlcNAc_2Man_9Glc_3$ structure. Thus, the efficient detection of accumulating short LLO structures requires the establishment of alternative methods. Gao and Lehrman (20) have recently presented a procedure allowing the quantitative detection of total LLOs from cell cultures and animal tissues without metabolic labeling. However, to permit separation and detection of all LLO structures in a single run, we separated 2AB-derivatized oligosaccharides using a GlycoSep-N HPLC column. As shown in the present study, this method allows the quantitative detection of short LLO species without the use of radioactive isotopes, which was critical for the diagnosis of the *ALG1* mannosyltransferase deficiency. The availability of this alternative LLO analysis procedure should enable the identification of further CDG-I types uncharacterizable using the radioactive method. Besides the medical importance of establishing a precise diagnostic, the characterization of CDG-I cases associated with the accumulation of short LLOs may help identification of still undiscovered glycosyltransferase genes along the ER-glycosylation pathway. This includes the UDP-GlcNAc:*DolPP*-GlcNAc β1,4 N-acetylglucosaminyltransferase

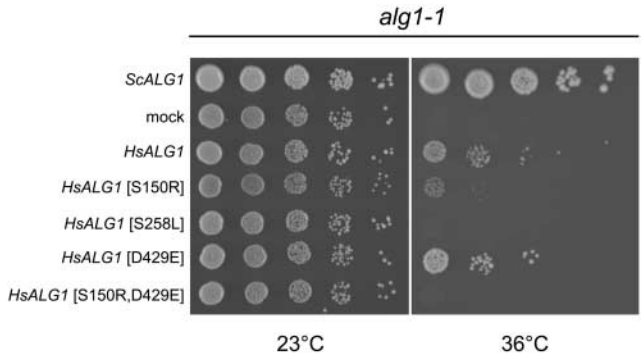

Figure 5. Complementation of *alg1-1* yeasts with human *ALG1* cDNAs. Transformants were spotted in 10-fold dilutions on YPD plates and incubated at 23 or 36°C for 90 h. Transformation was performed with the vector alone (mock), the pMJ-*ALG1* vector expressing the *S. cerevisiae ALG1* gene (*ScALG1*) and with plasmids expressing normal human *ALG1* cDNA (*HsALG1*), the mutated cDNAs from patient FR (*HsALG1*[S150R, D429E], *HsALG1*[S258L]) and *ALG1* cDNAs containing the isolated S150R and D429E mutations.

and the GDP-mannose:*DolPP*-$GlcNAc_2Man_2$ α1,6 mannosyltransferase genes.

MATERIALS AND METHODS

Glycan extraction

Patient primary fibroblasts were isolated from a skin biopsy and grown in Dulbecco's modified Eagle's medium (DMEM/F12, Gibco) with 4.5 g/l glucose and 10% fetal calf serum. Fibroblasts (5×10^7) were cultured to 90% of confluence and metabolically labeled with 150 µCi [^{3}H]mannose (54.0 Ci/mmol, Amersham Bioscience) as described previously (30). Short LLOs were extracted twice from the cell pellets with 3 ml of chloroform–methanol 3 : 2 (v/v). Long LLOs were then further extracted twice with 3 ml of chloroform–methanol–water 10 : 10 : 3 (v/v/v). N-linked oligosaccharides (NLOs) were recovered from the solid cell pellet after LLO extraction by N-glycosidase F digestion (30).

HPLC analysis of [^{3}H]mannose-labeled oligosaccharides

[^{3}H]Mannose-labeled oligosaccharides were separated on a 250 × 4.6 mm LC-NH_2 aminopropyl column (Supelco), equipped with an LC-NH_2 guard column, as described previously (36).

Hydrolysis and cleanup of total cellular LLOs

Total cellular LLOs were extracted from 5×10^7 fibroblasts as described above but without metabolic labeling. Dried LLOs were hydrolyzed with 2 ml of 0.1 M HCl in 50% isopropyl alcohol at 50°C for 60 min to release pyrophosphate-linked oligosaccharides (20). Hydrolysates were neutralized by adding 1 ml of 0.2 M NaOH and residual salt and lipids were removed by loading the samples onto C_{18} SepPak columns (Waters) directly connected to 3 ml ENVI-CARB solid phase extraction tubes (Supelco). These combined columns were conditioned with 5 ml of methanol, followed by 5 ml of acetonitrile and 5 ml H_2O–acetonitrile (3 : 1, v/v) then equilibrated with 9 ml of 2% acetonitrile/0.1 M ammonium acetate in H_2O. After loading of the samples, the columns were washed with 9 ml of the same solution. For elution of the oligosaccharides, the C_{18} SepPak cartridge was removed and glycans were eluted from the ENVI-CARB tube with 6 ml of H_2O–acetonitrile (3 : 1, v/v).

2-Aminobenzamide labeling of oligosaccharides and HPLC separation

The dried samples were labeled with 2AB according to Bigge *et al.* (37). The glycan cleanup was performed using the paper disk method as described in Merry *et al.* (38). The separation of 2AB-labeled N-glycans was performed by HPLC using a GlycoSep-N column (Glyko Inc.) according to Royle *et al.* (39) but modified to a three solvent system suitable for low pressure gradient mixing. Solvent A was 10 mM formic acid adjusted to pH 4.4 with ammonia solution in 80% acetonitrile. Solvent B was 30 mM formic acid adjusted to pH 4.4 with ammonia solution in 40% acetonitrile. Solvent C was 0.5% formic acid. The column temperature was 30°C. Gradient conditions were a linear gradient of 100% A to 100% B over 160 min at a flow rate of 0.4 ml/min, followed by 2 min 100% B to 100% C, increasing the flow rate to 1 ml/min. The column was washed for 5 min with 100% C, returning to 100% A over 2 min and running for 6 min at 100% A at a flow rate of 1 ml/min, then returning the flow rate to 0.4 ml/min for 5 min. Samples were injected in water.

Reverse transcription–PCR

RNA was extracted from 2×10^7 fibroblasts using Tri-reagent (Sigma) following the instructions of the manufacturer. cDNA was synthesized from 5 µg of total RNA using the specific *ALG1* reverse primer 5′-AACGCAGGATGAGGAGTTCT-3′, with 5% DMSO and 1 unit of reverse transcriptase ImPromII (Promega). The synthesis was performed at 42°C for 120 min. The protein coding region was amplified by PCR using 3 µl of RT product and the primers 5′-ATGGCGGCCTCATGCTTGGT-3′ and 5′-CCAAGCCTCCAGAGAAGA-3′. The cycling conditions were 30 cycles at 94°C for 45 s, 55°C for 30 s and 72°C for 2 min. Primers and unincorporated nucleotides were eliminated using Qiaquick columns (Qiagen) and the PCR products were directly sequenced (Microsynth, Balgach, Switzerland).

Genomic DNA PCR

Genomic DNA from patient FR and from his parents was isolated from 10^7 fibroblasts and from 5 ml of blood, respectively. *ALG1* exons 4, 7 and 13 were amplified with the primers 5′-CCATCACCAGCTGTTGTTAG-3′, 5′-CAGCATTCGGCCTGATTCAC-3′, 5′-TGGCCTGGTGCTGCTGATGT-3′, 5′-AGCTGCCAGCAGGATGGAGA-3′ and 5′-GTGGCTGCTTGGCCAGCTTA-3′, 5′-CGAAGAGCACTTGGAGATG-3′, respectively, for 30 cycles at 94°C for 45 s, 54°C for 30 s and 72°C for 1.5 min. The PCR products were directly sequenced (Microsynth, Balgach, Switzerland) after removal of the primers and unincorporated nucleotides. The other genes were screened essentially as described before (19).

Plasmid construction

The human *ALG1* cDNAs from healthy control, the S150R/D429E allele and the S258L allele from patient fibroblasts were amplified with the primers 5′-ACTGCTGCGGAGGATCCAAGATGGC-3′ and 5′-CCAAGCCTCCAGAGAAGA-3′, which contain a *Bam*HI or a *Hind*III restriction site (underlined). The fragments were subcloned into the *Bam*HI and *Hind*III sites of pBluescript-II SK$^+$ (Stratagene). From there, the human *ALG1* cDNAs from patient FR and from control fibroblasts were subcloned as *Bam*HI–*Xho*I fragments into p426GDP (40). To separate the S150R and D429E mutations, 467 bp *Eco*RI–*Pae*I or 58 bp *Kpn*2I–*Bpu*1102I fragments of the patient's S150R/D429E cDNA were replaced by the corresponding fragments from normal human *ALG1* cDNA. The resulting plasmids are multicopy yeast vectors with the *ALG1* cDNAs under control of the *TDH3* promoter. The plasmid pMJ-*ALG1*, a single-copy plasmid with the yeast *ALG1* gene under control of its own promotor, was created from pRS316-NES17 (41) by digestion with *Eco*RI followed by self-ligation.

Yeast strains and media

S. cerevisiae strains used in this study were derivatives of K57-6C (*MAT*a *alg1-1 ura3–52 mal gal2 can(r)*) (ATCC 208304). Standard yeast media and genetic techniques were used (42). Yeast cells were transformed using the LiOAc/PEG method and the transformants were selected on solid medium lacking uracil. Strain K57-6C and its transformants were propagated at 23°C.

Complementation of ALG1 mutants

Strain K57-6C and its transformants were grown in liquid medium lacking uracil but supplemented with 1 M sorbitol. For the spot assay, 5 µl of serial 10-fold dilutions of K57-6C transformants were spotted on full medium (YPD), starting at 5×10^5 cells. Plates were incubated at a given temperature for 90 h.

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