

Review

Congenital disorders involving defective N-glycosylation of proteins

H. Schachter

Department of Structural Biology and Biochemistry, The Research Institute, The Hospital for Sick Children, 555 University Avenue, Toronto, Ontario M5G 1X8 (Canada), Fax +1 416 813 5022, e-mail: harry@sickkids.on.ca
Department of Biochemistry, University of Toronto, Toronto Ontario M5G 1X8 (Canada)

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Abstract. This review deals with several of the main autosomal recessive congenital disorders involving defective N-glycosylation of proteins (the addition of glycans linked to the polypeptide chain by a β -linkage between the anomeric carbon of N-acetylglucosamine and the amido group of L-asparagine). These congenital disorders of glycosylation (CDG, previously known as carbohydrate-deficient glycoprotein syndromes) are a group of multisystemic diseases often involving severe psychomotor retardation. Six distinct variants of CDG in group I (types Ia–If) have been described to date and the defects have been localized to deficiencies in the assembly of the dolichylpyrophosphate-linked oligosaccharide N-glycan precursor and its transfer to asparagine residues on the nascent polypeptides. Two variants of CDG group

II (types IIa and IIb) have been identified as defects in the processing of protein-bound N-glycans. Hereditary erythroblastic multinuclearity with a positive acidified-serum lysis test (HEMPAS; congenital dyserythropoietic anemia type II) presents as a relatively mild dyserythropoietic anemia. The genetic defect in most cases of HEMPAS is not known, but α -3/6-mannosidase II is involved in at least some patients. Leukocyte adhesion deficiency type II (LAD II) is a rare disorder characterized by recurrent infections, persistent leukocytosis and severe mental and growth retardation. LAD II is due to lack of availability of GDP-fucose. The study of these diseases and of relevant animal models has provided strong evidence that N-glycans are essential for normal mammalian development.

Key words. Glycosylation; N-glycans; congenital disease; congenital disorders of glycosylation; congenital dyserythropoietic anemia; leukocyte adhesion deficiency; mannose metabolism; fucose metabolism.

Introduction

A glycoconjugate is a covalent complex between carbohydrate and non-carbohydrate moieties. The non-carbohydrate moiety may be a protein, peptide, amino acid, lipid or some other aglycone. This review will deal with congenital diseases involving defects in the glycosylation of proteins. Glycans can be conjugated to amino acids either by N-glycosyl or O-glycosyl linkages [1]. The only N-glycan in animals involves a beta-linkage between the anomeric carbon of N-acetylglucosamine (GlcNAc) and the amido group of L-asparagine (Asn) although other

N-glycan linkages have been found in bacterial glycoproteins. Several O-glycan linkages are present in animals. The alpha-linkage between the anomeric carbon of N-acetylgalactosamine (GalNAc) and the hydroxyl group of either serine (Ser) or threonine (Thr) was first described in mucins but is also commonly found in non-mucinous glycoproteins. Other common O-glycan linkages in animals are the beta-linkage between xylose (Xyl) and the hydroxyl group of Ser (characteristic of proteoglycans) and the beta-linkage between galactose (Gal) and the hydroxyl group of hydroxylysine (characteristic of the collagens). Proteoglycans are a subclass of glycoproteins

in which the carbohydrate moieties are polysaccharides that contain amino sugars (glycosaminoglycans).

Carbohydrate macromolecules usually consist of various building blocks (monosaccharides such as mannose, galactose, GalNAc, etc.) that can be linked together in several different ways (the anomeric carbon of one sugar can be attached in alpha- or beta-linkage to one of several carbons of the linking sugar). This allows the structure to become branched. Whereas the other major biological macromolecules (proteins, nucleic acids) are linear and are synthesized by a linear template mechanism, large carbohydrates must be made on an assembly line (the endoplasmic reticulum-Golgi apparatus) along which various enzymes add and remove sugars. The sugar sequences and branching patterns are controlled not by copying a template but by the substrate specificities of these enzymes (mainly glycosyltransferases and glycosidases).

The diversity of linkages and branching patterns between monomer building blocks confers on carbohydrates the ability to carry an enormous amount of information in very compact structures [2]. The cell surface is covered with protein- and lipid-bound carbohydrate structures that vary significantly between cell types and at different stages of mammalian development. There is considerable evidence that these carbohydrates play important roles in the interaction of a cell with its cellular and fluid environment [3–5]. The essential role of glycoproteins and proteoglycans in development has been demonstrated by studies on mice with null mutations in various glycosyltransferases and glycosidases [6–14], on mutant *Drosophila melanogaster* [15] and *Caenorhabditis elegans* [16–19], and on human congenital diseases with defects in the glycosylation of proteins [20, 21].

This review will deal with several of the main autosomal recessive congenital disorders involving defects in the synthesis of Asn-linked glycans (tables 1, 2), congenital disorders of glycosylation (CDG), congenital dyserythropoietic anemia type II, and leukocyte adhesion deficiency type II. Other defects in glycosylation are listed in tables 1 and 3. Since at least 0.5–1% of the transcribed human genome is devoted to the production of proteins involved in the synthesis, degradation, and function of glycoconjugates [11], many other such congenital diseases may exist.

Congenital Disorders of Glycosylation

CDG (previously known as carbohydrate-deficient glycoprotein syndromes) are a group of congenital multisystemic diseases characterized by defective N-glycosylation. The discovery of these diseases was based on the observation by Jaeken et al. [22] of decreased serum thyroxine-binding globulin and increased arylsulfatase A activity in two patients with familial psychomotor retardation. In 1984, Jaeken et al. [23] reported sialic acid deficiency in

serum and cerebrospinal fluid transferrin from identical twin sisters with demyelinating disease, demonstrating for the first time that this new syndrome was due to defective protein glycosylation. There were about 280 patients with this disease worldwide as of October 1998 [24].

In 1999, at a meeting held in Belgium, a new classification and nomenclature for CDG was proposed [25, 26]. Six distinct variants of CDG in group I have been described to date (types Ia–If; table 2) and the defects have been localized to deficiencies in the assembly of the dolichylpyrophosphate-linked oligosaccharide N-glycan precursor and its transfer to asparagine residues on the nascent polypeptides. Two variants of CDG group II (types IIa and IIb; table 2) have been identified as defects in the processing of protein-bound N-glycans. CDG patients in which the defect has not yet been determined (table 2) will not be discussed here.

CDG group I (CDG-I)

The following discussion is based primarily on papers published prior to the separation of CDG group I patients into separate types. Since CDG-Ia is the most common type of CDG-I, the discussion of clinical and pathological features refers primarily to CDG-Ia patients. However, the section on clinical biochemistry is relevant to all CDG-I types.

Clinical and pathological features

CDG-I occurs worldwide and affects both sexes [27–34]. The patients show moderate to severe neurological disease, a characteristic dysmorphism, and variable involvement of other organs [24, 27, 32, 35–38]. In the neonatal period, the patients may show slow head movements, and in infancy, alternating internal strabismus, abnormal eye movements, axial hypotonia and hyporeflexia. Feeding problems, vomiting and diarrhea may occur, resulting in severe developmental delay and failure to thrive [39, 40]. Infants may show a distinctive lipodystrophy (peculiar distribution of subcutaneous fat), nipple retraction, and hypogonadism. Some infants show liver failure, cardiac insufficiency, pericardial effusion [41–43], nephrotic syndrome, and multiorgan failure [43–46]. Older children usually develop cerebellar ataxia and marked psychomotor retardation [47]. Retinitis pigmentosa [48, 49], joint contractures, skeletal deformities [50], stroke-like episodes, epilepsy, and peripheral neuropathy may also develop. About 20% of the patients die within the first year. Some adults show premature aging [51]. Language and motor development are severely delayed and walking without support is rarely achieved. The IQ ranges from 40 to 60 and the children usually have an extroverted and cheerful disposition.

Table 1. Autosomal recessive congenital disorders with defective N-glycan synthesis.

Name of disease	Type of disease	Enzyme defect	Gene	OMIM*	Locus Link*
Congenital disorders of Glycosylation	severe developmental abnormalities	see table 2			
HEMPAS (congenital dyserythropoietic anemia type II, CDA II)	relatively mild disease with mild anemia and hemosiderosis	alpha-mannosidase II deficiency; other genes	<i>MAN2A1</i>	224100 154582	4124
Leukocyte adhesion deficiency type II (LAD II)	immunodeficiency and severe developmental abnormalities	(a) GDP-fucose synthesis (b) GDP-fucose transport		266265	
Inclusion cell disease (I-cell disease or mucopolipidosis II)	lysosomal glycoprotein storage disease with severe developmental abnormalities	N-acetylglucosamine-1-phosphotransferase required for synthesis of Man-6-phosphate targeting signal	<i>GNPTA</i>	252500	2795
Pseudo-Hurler polydystrophy (mucopolipidosis III)	A milder form of I-cell disease	different lesion in same gene as I-cell disease	<i>GNPTA</i>	252600	2795
Galactosemia type I	failure to thrive, liver disease, mental retardation, cataracts	galactose-1-phosphate uridylyltransferase	<i>GALT</i>	230400	2592
Galactosemia type II		galactokinase 1	<i>GALK1</i>	230200 604313	2584
Galactosemia type III		UDP-Gal-4-epimerase	<i>GALE</i>	230350	2582

* OMIM, Online Mendelian Inheritance in Man; Locus Link summarizes all the known information on a particular gene. Databases can be accessed at <http://www.ncbi.nlm.nih.gov/>

Table 2. Congenital disorders of glycosylation (CDG).

Type	Enzyme defect	Gene	OMIM*	Locus Link*	Acronym
Ia	phosphomannomutase 2	<i>PMM2</i>	212065 601785	5373	CDG-Ia
Ib	phosphomannose isomerase	<i>MPI</i>	602579 154550	4351	CDG-Ib
Ic	dolichyl-PP-Glc:Man ₆ GlcNAc ₂ -PP-dolichyl alpha-1,3-glucosyltransferase	<i>ALG6</i>	603147 604566	29929	CDG-Ic
Id	dolichyl-PP-Man:Man ₅ GlcNAc ₂ -PP-dolichyl alpha-1,3-mannosyl-transferase	<i>ALG3</i> <i>NOT56L</i>	601110	10159	CDG-Id
Ie	dolichol-P-Man synthase 1	<i>DPM1</i>	603503	8813	CDG-Ie
If	dolichol-P-Man utilization defect 1; SL15, suppressor of Lec15 and Lec35	<i>MPDU1</i>	604041	9526	CDG-If
Ix	Genetic basis unknown		603585 212067		CDG-Ix
IIa	UDP-GlcNAc:alpha-6-D-mannoside beta-1,2-N-acetylglucosaminyltransferase II (GnT II)	<i>MGAT2</i>	212066 602616	4247	CDG-IIa
IIb	alpha-1,2-glucosidase I	<i>GCSI</i>	601336	7841	CDG-IIb

* OMIM, Online Mendelian Inheritance in Man; Locus Link summarizes all the known information on a particular gene.

Both databases can be accessed at <http://www.ncbi.nlm.nih.gov/>

Group I: defects in N-linked protein glycosylation due to deficiencies in the assembly of the dolichylpyrophosphate linked oligosaccharide and/or its transfer to asparagine residues on the nascent polypeptides.

Group II: defects in the processing of N-glycans or addition of other glycans to proteins.

Table 3. Other diseases involving abnormal glycosylation.

Name of disease	Type of disease	Enzyme defect	Gene	OMIM*	Locus Link*
Paroxysmal nocturnal hemoglobinuria (PNH)	acquired hematologic disorder with complement-mediated red cell hemolysis	synthesis of N-acetylglucosaminyl phosphatidylinositol (GlcNAc-PI)	<i>PIGA</i>	311770	5277
Tn polyagglutinability	acquired hematologic disorder with anemia, leukopenia and thrombocytopenia	beta-1,3-D-galactosyltransferase involved in O-glycan core 1 synthesis		230430	
Ehlers-Danlos syndrome, progeroid form	congenital disease with delayed mental development, connective tissue abnormalities, loose skin, hypotonia	xylosylprotein beta-1,4-D-galactosyltransferase involved in dermatan sulfate proteoglycan synthesis	<i>XGPT1</i> <i>B4GALT7</i>	130070 604327	11285

* OMIM, Online Mendelian Inheritance in Man; Locus Link summarizes all the known information on a particular gene. Databases can be accessed at <http://www.ncbi.nlm.nih.gov/>

Computerized tomography (CT), nuclear magnetic resonance imaging (MRI), and postmortem studies of the brain often show olivopontocerebellar atrophy (OPCA) and a small brain stem [27, 37, 52–57]. Other postmortem findings may include pericarditis, renal cysts, fibrosis of the testes and lymph node abnormalities. Peripheral nerves may show multivacuolar myelinoid bodies in the Schwann cells. Endo- and epineurial fibroblasts may contain cytoplasmic inclusions [27, 58]. The liver may show fibrosis, intracellular lipid vacuoles, and lysosomal inclusions.

Clinical biochemistry

The basic defect in CDG-I is defective N-glycosylation of proteins throughout the body with resultant multisystemic disease. Diagnosis is made by examination of the complex N-glycans on serum transferrin, but other glycoproteins can also be used. Serum transferrin has only two asparagine N-glycosylation sites per molecule, both of which are normally occupied by complex N-glycans, primarily of the disialo-biantennary N-acetylglucosamine type with smaller amounts of monosialo-biantennary, disialo-triantennary, trisialo-triantennary, and tetrasialo-tetraantennary N-glycans [37, 59–65]. Normal serum transferrin therefore exists as a series of glycoforms containing two to seven sialic acid residues per mole of protein (designated S2–S7). Isoelectric focusing and other techniques can be used to determine the relative amounts of serum transferrin glycoforms. Most CDG-I sera show reductions in S4 and S5 and increases in S0 and S2 (table 4). The presence of appreciable amounts of normal S4 indicates that the CDG-I mutations are leaky.

The N-glycan structures on transferrin glycoforms S4, S2, and S0 from Japanese CDG-I patients have been analyzed by mass spectrometry and other methods [37,

66–69]. The only N-glycans detected on S4 and S2 were normal complex N-glycans, while S0 was completely devoid of carbohydrate. These and other studies show that each glycosylation site on transferrin is either occupied by a normal N-glycan or is not occupied (an ‘all-or-none’ pattern), indicating that the addition of oligosaccharide to Asn is the defective step. The serum glycoprotein glycoform patterns are normal in the CDG-I fetus and, therefore, pre-natal diagnosis is not possible by this method [70]. Abnormal glycoform patterns appear in the second to third weeks of post-natal life.

Performing a detailed glycoform analysis is important, since carbohydrate-deficient serum transferrin also occurs in other conditions such as chronic alcohol intake

Table 4. Distribution of transferrin glycoforms in normal and CDG sera.

Transferrin glycoform*	Percent distribution		
	Normal [23, 29, 66, 235–237]	CDG-I [23, 27, 29, 82, 236, 238, 239]	CDG-IIa [63, 64, 165]
S0	0	2–29	~ 0
S1		+	+
S2	1–7	14–37	95
S3	4–17	0–19	~ 4
S4	46–73	18–57	~ 0
S5	10–30	5–17	~ 0
S6	0–9	0–6	~ 0
S7	trace		

* The designations S0–S7 refer to serum transferrin glycoforms with 0–7 sialic acid residues per mole of protein, respectively. The data are based on papers published prior to the separation of CDG group I patients into separate types. Since CDG-Ia is the most common type of CDG-I, the data refer primarily to CDG-Ia patients. However, the other CDG-I types (table 2) present with very similar transferrin glycoform patterns.

[71], galactosemia [72–74], untreated fructosemia [75, 76], and hepatic disease [71].

Due to the great variations in clinical presentations of CDG (discussed below), screening for carbohydrate-deficient transferrin glycoforms is recommended for patients not only with psychomotor retardation and hypotonia, but also in unexplained feeding problems, failure to thrive, liver fibrosis, coagulopathy, and intestinal disease, even in the absence of severe neurological disease.

Many glycoproteins not only in serum but also in cerebrospinal fluid [23, 77] and other tissues show incomplete glycosylation. The levels of various serum glycoproteins may be decreased or increased, probably secondary to damage to the liver and other organs, or to other factors. Significant abnormalities have been observed in the levels of plasma proteins which modify coagulation [78–83]. This may contribute to the hemorrhages, venous thromboses, and stroke-like episodes reported in some CDG-I patients. Abnormal plasma hormone levels have been reported [22, 84, 85]. Female patients may show a hypergonadotrophic hypogonadism associated with dysfunctional follicle-stimulating hormone bioactivity. In males, testosterone levels tend to be low with normal or slightly raised gonadotrophin values.

Hypoglycosylation of glycosyltransferases and glycosidases may affect their activity or intracellular localization, thereby producing secondary alterations in carbohydrate structure that may result in misleading glycoform patterns [86]. For this and other reasons, some CDG-I patients do not show the typical ‘all-or-none’ serum transferrin glycoform pattern [87, 88].

CDG type Ia (CDG-Ia)

The biochemical defect in CDG-Ia

As described above, the ‘all-or-none’ serum transferrin glycoform pattern in CDG-I suggests that the addition of oligosaccharide to Asn is the defective step. This step is catalyzed by an oligosaccharyltransferase which transfers $\text{Glc}_3\text{Man}_9\text{GlcNAc}_2$ from dolichol-pyrophosphate- $\text{Glc}_3\text{Man}_9\text{GlcNAc}_2$ (Dol-PP- $\text{Glc}_3\text{Man}_9\text{GlcNAc}_2$) to the asparagine residue of the protein [89, 90]. Oligosaccharyltransferase activity was shown to be normal in fibroblasts from four CDG-Ia patients [91] suggesting a defect in the synthesis of Dol-PP-oligosaccharide [92] (fig. 1).

Earlier studies showing that CDG-Ia fibroblasts are impaired in their ability to incorporate exogenous mannose into both protein- and dolichol-linked oligosaccharides [87, 93–96] led to the eventual demonstration that CDG-Ia cells and tissues are markedly deficient ($\leq 10\%$ of the control activity) in phosphomannomutase (PMM) activity (fig. 1) [97–99]. PMM deficiency results in reduced synthesis of Man-1-phosphate, GDP-Man, Dol-P-

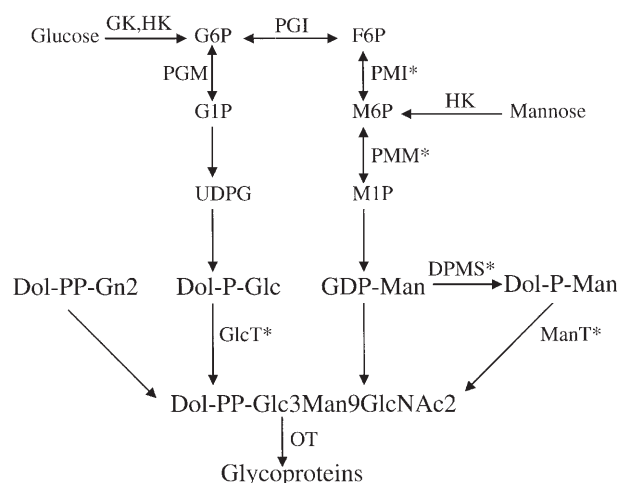


Figure 1. Metabolic pathway from glucose and mannose to dolichol pyrophosphate oligosaccharide. Enzymes: HK, hexokinase; GK, glucokinase; PGI, phosphoglucosomerase; PGM, phosphoglucomutase; PMI, phosphomannoisomerase; PMM, phosphomannomutase; GlcT, α -1,3-glucosyltransferase; ManT, α -1,3-mannosyltransferase; DPMS, Dol-P-Man synthase; OT, oligosaccharyltransferase. Asterisks on PMM, PMI, GlcT, ManT, and DPMS denote enzyme defects in CDG types Ia, Ib, Ic, Id, and Ie respectively. Intermediates: G6P, glucose-6-phosphate; G1P, glucose-1-phosphate; F6P, fructose-6-phosphate; M6P, mannose-6-phosphate; M1P, mannose-1-phosphate; UDPG, UDP-glucose; Dol-P-Glc, dolichol phosphate glucose; Dol-P-Man, dolichol phosphate mannose; Dol-PP-Gn2, dolichol pyrophosphate N-acetylchitobiose; Dol-PP-Glc₃Man₉GlcNAc₂, dolichol pyrophosphate Glc₃Man₉GlcNAc₂. Dol-PP-Glc₃Man₉GlcNAc₂ is assembled by the addition of Man from both GDP-Man and Dol-P-Man and Glc from Dol-P-Glc to dolichol pyrophosphate N-acetylchitobiose.

Man, and truncated dolichol-linked oligosaccharides (fig. 1). The oligosaccharyltransferase that transfers $\text{Glc}_3\text{Man}_9\text{GlcNAc}_2$ from Dol-PP- $\text{Glc}_3\text{Man}_9\text{GlcNAc}_2$ to the asparagine residue of the protein can also use shorter lipid-linked oligosaccharides as donor substrates but does so very inefficiently [89, 95, 100]. The lowered rate of oligosaccharyltransferase activity in PMM-deficient CDG-Ia cells leaves some Asn-X-Ser/Thr sequons unglycosylated. Any truncated oligosaccharides that are transferred to protein will be processed to normal N-glycan structures either by the usual pathway or by an ‘alternate pathway’ independent of α -mannosidase II [101] resulting in the ‘all-or-none’ pattern of transferrin glycosylation described above.

Intracellular GDP-Man levels are low in CDG-Ia and Ib fibroblasts, and the addition of exogenous Man to the cells can correct this deficiency [102]. Addition of exogenous Man, but not Glc, to CDG-Ia fibroblasts also corrects both the low amount and small size of lipid-linked oligosaccharides and normalizes protein N-glycosylation [94, 103, 104]. Although Man can utilize the Glc transporter, a distinct Man-specific Glc-independent transporter has been demonstrated in mammalian cells [105]. When fibroblasts are provided with physiological con-

centrations of mannose, they use the mannose rather than glucose to supply most of the mannose needed for glycoprotein synthesis [106, 107]. Serum from CDG-Ia patients has considerably reduced mannose levels (5–40 mM) compared to normal controls (40–80 mM) [103, 108]. Ingested mannose is efficiently absorbed and increases blood mannose levels in both normal subjects and CDG patients [109]. However, oral or intravenous mannose administration has not been successful in reversing either the clinical or biochemical signs of CDG-Ia [110–113].

The genetic defect in CDG-Ia

CDG-Ia is inherited in an autosomal recessive manner. Linkage and haplotype analyses of DNA from 86 CDG-Ia pedigrees of Scandinavian, German, Belgian, and other origins have localized the gene to chromosome 16p13.3–p13.12 [114–116]. There are two human PMM isozymes (PMM1 and PMM2) encoded by two genes, *PMM1* on chromosome 22q13 [117–119] and *PMM2* on chromosome 16p13 [120, 121], respectively. The identification of 26 different *PMM2* mutations in 74 CDG-Ia patients from different geographical origins and with a documented PMM deficiency proves that PMM2 deficiency is the basis for CDG-Ia [99, 120–124]. Mutation and linkage analyses with polymorphic markers have been used to perform prenatal diagnoses for CDG-Ia [125–127]. The number of molecularly characterized cases is steadily increasing. A recent collation of data on *PMM2* mutations from six research and diagnostic laboratories lists 58 different mutations in 249 patients from 23 countries [128]. Demographic data and the number of deceased patients have been recorded (data available at <http://www.kuleuven.ac.be/med/cdg>).

The most frequent mutation (R141H) never occurs in homozygous alleles, whereas patients homozygous for other mutations have been found [122, 124, 129]. Seven mutant forms of human PMM2 have been produced in *Escherichia coli* and purified [130]. R141H was the least active protein, indicating that R141H homozygosity and a total lack of PMM2 are incompatible with life. Only limited correlations have to date been possible between genotype, PMM activities, and the clinical severity of the disease [88].

The carrier frequency of R141H in two normal Dutch and Danish populations was found to be 1/60, a figure in disequilibrium with the estimated CDG-Ia frequency of 1/80,000–1/20,000 in these populations [129]. Haplotype analysis of 43 patients with the R141H mutation of different geographic origins indicated that it is an old mutation in the Caucasian population. The data indicate that CDG-Ia is probably underdiagnosed.

PMM2 converts mannose 1-phosphate into mannose 6-phosphate about 20 times more rapidly than glucose 1-

phosphate to glucose 6-phosphate, whereas PMM1 displays identical V_{\max} values with both substrates [131]. PMM2 is the only detectable isozyme in most rat tissues except brain and lung, where PMM1 accounts for about 66 and 13% of the total activities, respectively.

Diagnosis of CDG-Ia

Once a diagnosis of CDG-I has been confirmed by demonstration of the typical transferrin glycoform pattern (table 4), PMM assays should be carried out on cultured fibroblast or lymphoblast extracts, fresh leukocytes, or liver biopsies [97, 99]. PMM activities in CDG-Ia patients may vary from less than 5 to 30% of normal values [122]. Diagnoses can also be made by PMM assays on parental leukocytes [126]. The diagnosis should be completed by mutational analysis.

Prenatal testing should be limited to families with a documented PMM deficiency and a known *PMM2* mutation [126]. PMM can be measured in chorionic villus samples, cultured chorionic villus cells, and cultured amniocytes [127].

CDG type Ib (CDG-Ib)

About 20% of patients with a type I transferrin glycoform pattern do not show PMM deficiency (table 2) [132]. CDG-Ib is due to defective phosphomannoisomerase (PMI; fig. 1) [133–136]. The clinical presentations vary but all show a type I transferrin glycoform pattern without neurological disease. Niehues et al. [133] reported a 6-year-old boy who appeared normal at birth and first developed signs at about 1 year of age, i. e., failure to thrive, recurrent and severe hypoglycemia, thrombotic episodes, protein-losing enteropathy, severe vomiting, and diarrhea. Serum albumin and antithrombin III were persistently low, first suggesting CDG. There were no signs of developmental delay, neuropathy, dysmorphism, or abnormal skeletal features. Anti-coagulant therapy to reduce his thrombotic episodes led to life-threatening intestinal bleeding. Oral mannose therapy was initiated and proved to be effective. The patient has been on oral mannose (0.1–0.15 g/kg) three to five times a day for several years. His symptoms have reversed and all his biochemical abnormalities, including his abnormal transferrin pattern, returned to normal within 11 months. Assays of fibroblast and leukocyte lysates showed an 85–95% deficiency in PMI. Heterozygous relatives showed PMI levels at 34–65% of normal. The genetic lesion in the *PMI* gene was heterozygous, a point mutation (R219Q) on one allele (from the father) and an unidentified mutation from the mother. Transfection of the mutant gene into COS cells showed no enzyme activity. Other CDG-Ib patients have presented with different *PMI* mutations [134, 135]

and similar, but not identical, signs and symptoms. Three siblings were found to have congenital hepatic fibrosis associated with a deficiency of the enzyme PMI and recurrent attacks of persistent vomiting with diarrhea and mild hepatomegaly [137].

The phosphomannoisomerase gene (*MPI*) is composed of eight exons and spans only 5 kb [136]. Eight different mutations were found in seven patients with a confirmed PMI deficiency.

PMM (CDG-Ia) and PMI (CDG-Ib) both affect the synthesis of Dol-P-Man but have very different clinical presentations. Conversion of free Man to Dol-P-Man depends on PMM but not on PMI (fig. 1) and this pathway supplies most of the Man for N-glycosylation of proteins. The clinical differences between CDG-Ia and Ib may be related to the fact that both the Glc and Man paths to Dol-P-Man are defective in CDG-Ia but not in Ib.

Since CDG-Ib is potentially lethal and mannose therapy appears to be curative, patients with idiopathic congenital hepatic fibrosis [137, 138], hypoglycemia [139, 140], coagulopathies, and failure to thrive should be tested for CDG with a serum transferrin glycoform analysis.

CDG type Ic (CDG-Ic)

CDG-Ic patients have a defect in the Dol-P-Glc:Dol-PP-Man₉GlcNAc₂ α 1,3-glycosyltransferase (α 1,3-Glc-T) that converts Dol-PP-Man₉GlcNAc₂ to Dol-PP-Glc₁Man₉GlcNAc₂ (fig. 1). Burda et al. [86] presented biochemical data on four related patients. The clinical presentation is similar to CDG-Ia but milder. Fibroblasts from all four patients showed a specific deficiency in α 1,3-Glc-T. The resulting non-glycosylated dolichol-linked oligosaccharides are suboptimal substrates for the oligosaccharyltransferase (fig. 1). The limited availability of GDP-Man in PMM-deficient CDG-Ia cells decreases not only the synthesis of N-glycans but also the synthesis of GDP-Fuc, the glycosylphosphatidylinositol anchors [141], and O-mannosylated [142, 143] and C-mannosylated [144] proteins. The fact that the α 1,3-Glc-T defect in CDG-Ic does not affect synthesis of these components may account for the milder clinical presentation in this subtype.

Körner et al. [145] described a form of CDG, originally designated type V, which clinically resembles CDG-Ia but with normal PMM and a defect in α 1,3-Glc-T. The defect is leaky and allows for residual synthesis of small amounts of normally glycosylated lipid-linked oligosaccharides. The patient, a 7-year-old girl, had been noted in her first year to have a convergent squint, recurrent edema of the upper eyelids, and recurrent infections. Muscular hypotonia, ataxia, and mental and motor developmental retardation were present at the age of 6 months. Beginning at the age of 11 months, seizures occurred dur-

ing infections. Nerve conduction velocity was always normal. A slight general atrophy of the cerebrum and cerebellum was noted at the age of 4 years. Sequencing of the α 1,3-Glc-T gene (see below) from this patient revealed an in-frame deletion of three nucleotides leading to the loss of isoleucine 299 [146].

Imbach et al. [147] cloned the human orthologs of the yeast genes encoding Dol-P-Glc synthase (*ALG5*) and the α 1,3-Glc-T (*ALG6*) [148]. No mutations were found in the Dol-P-Glc synthase gene of the four CDG-Ic patients studied by Burda et al. [86] but a point mutation (A333V) was found in the α 1,3-Glc-T gene of all four patients. Normal human α 1,3-Glc-T cDNA can partially complement a yeast strain with a deletion of α 1,3-Glc-T (*ALG6*) but the CDG-Ic α 1,3-Glc-T cDNA was unable to do so, indicating that the CDG-Ic mutation inactivates the gene. Imbach et al. [149] recently described seven additional cases of CDG-Ic among a group of 35 untyped CDG patients. Analysis of lipid-linked oligosaccharides in patient fibroblasts showed accumulation of Dol-PP-Man₉GlcNAc₂. Three additional mutations in the α 1,3-Glc-T gene were detected. The detrimental effect of these mutations on α 1,3-Glc-T activity was confirmed by complementation of *alg6* yeast mutants. Haplotype analysis of CDG-Ic patients revealed a founder effect for the *ALG6* allele bearing the A333V mutation.

The clinical presentation of eight CDG-Ic patients homozygous for an A333V mutation [150] was mainly neurological with developmental retardation, muscular hypotonia, and epilepsy. Several signs commonly seen in CDG-Ia such as inverted nipples, abnormal fat distribution and cerebellar hypoplasia were not observed. Although the serum transferrin glycoform pattern was the same in CDG-Ia and Ic sera, beta-trace protein in cerebrospinal fluid showed a less pronounced hypoglycosylation pattern in CDG-Ic patients than in CDG-Ia patients.

Although more than 80% of CDG are type Ia, CDG-Ic may be the second-most common form of the disease.

CDG type Id (CDG-Id)

In 1995, Stibler et al. [151] presented two unrelated infants with a clinically and biochemically novel form of CDG. The first case was a German boy and the second a Turkish girl born to first-cousin parents. Both children were microcephalic and developed intractable seizures. The boy had optic atrophy and a coloboma of the iris. Both children had abnormalities of the uvula and high-arched palates. The girl had hypoplasia of the cerebellum, as is seen in CDG-Ia.

Körner et al. [152] demonstrated that the biochemical defect in these patients is a deficiency in Dol-P-Man:Dol-PP-Man₅GlcNAc₂ α -1,3-mannosyltransferase (α -1,3-Man-T) which transfers Man from Dol-P-Man to Dol-PP-

Man₅GlcNAc₂. The defect is leaky, since there is formation of some full-length Dol-PP-oligosaccharide.

The yeast *alg3* gene product, the functional ortholog of human α -1,3-Man-T, shares 30% sequence homology with the human Not56-like protein (NOT56L). NOT56L complements the glycosylation defect in a yeast strain with a disrupted *alg3* gene, showing that NOT56L is the human ortholog of yeast ALG3. Sequencing of the gene encoding NOT56L from the male CDG-Id patient showed a missense mutation (G118D). The mutation reduces but does not abolish α -1,3-Man-T activity. The patient was homozygous for the G118D mutation and his parents were heterozygous.

CDG type Ie (CDG-Ie)

Kim et al. [153] reported that fibroblasts from two patients with clinical and laboratory findings indicative of type I CDG accumulated Dol-PP-Man₅GlcNAc₂. Addition of 0.25 mM Man to the culture medium corrected the size of the truncated oligosaccharide. Microsomes from fibroblasts of these patients were approximately 95% deficient in Dol-P-Man synthase (fig. 1) with an apparent K_m for GDP-Man approximately sixfold higher than normal. The *DPM1* gene, coding for the catalytic subunit of Dol-P-Man synthase, was altered in both patients. One patient was homozygous for the R92G mutation. This patient was seen at age 10 months because of developmental delay, hypotonia, seizures, and acquired microcephaly. Telangiectases on the eyelids and hemangiomas of the occiput and sacrum were observed. The other patient also had the R92G mutation but was a compound heterozygote for a 13-bp deletion in exon 4 that presumably resulted in an unstable transcript. This patient was born at 29 weeks of gestation. The post-natal course was complicated by hydrops, respiratory distress, apnea, patent ductus arteriosus and transient hypertension. The infant later developed generalized intractable seizures. At 3 years of age, the child had no speech, was cortically blind, had strabismus, and swallowed poorly.

Human and mouse *DPM1* cDNAs were first cloned by homology screening using the sequence of the yeast *dpm1* gene [154]. The human protein shares approximately 30% identity with yeast *DPM1*. Mammalian cells require *DPM1* and an additional protein (*DPM2*) for synthesis of Dol-P-Man. *DPM1* is the catalytic subunit and *DPM2* is the membrane-anchored subunit. Colussi et al. [155] have cloned human, rat, nematode, and *Schizosaccharomyces pombe* *DPM1* cDNAs.

Imbach et al. [156] reported a brother and sister who were hospitalized at ages 3 years and 19 months, respectively, after repeated seizure episodes. Microcephaly developed in early childhood. Hypertelorism, gothic palate, small hands with dysplastic nails and knee contractures were

observed. Nipples were not inverted. Seizures began in the girl at the age of 5 weeks and in her brother at the age of 6 months. Both children were hypotonic and showed severe global developmental delay. There was no visual fixation, and they were unable to interact socially.

Biochemical analysis showed hypoglycosylation of serum transferrin and cerebrospinal fluid beta-trace protein and an accumulation of Dol-PP-Man₅GlcNAc₂ in their fibroblasts. The fibroblasts showed reduced Dol-P-Man synthase activity. Both siblings were found to be compound heterozygotes for two mutations in the *DPM1* gene, the R92G mutation identified by Kim et al. [153] and a 628delC deletion which caused a premature stop of translation. Complementation analysis using *DPM1*-null murine cells confirmed the detrimental effect of both mutations on enzymatic activity. Mannose supplementation failed to improve the glycosylation status of *DPM1*-deficient fibroblasts, thus precluding a possible therapeutic application of mannose in the patients [102].

CDG type If (CDG-If)

Lec15 and Lec35 are recessive mutant Chinese hamster ovary (CHO) cell lines characterized, respectively, by defects in the synthesis and utilization of Dol-P-Man. Lec35 cells accumulate Dol-PP-Man₅GlcNAc₂ due to their inability to utilize Dol-P-Man (fig. 1). Lec15 mutant CHO cells, which lack the *DPM2* subunit of Dol-P-Man synthase but express a functional Lec35 gene, also accumulate Dol-PP-Man₅GlcNAc₂ but can utilize Dol-P-Glc to add some glucose to the terminal Man- α 1,2 residue of the lipid-linked oligosaccharide [157]. This indicated that the Lec35 gene is required for both Dol-P-Man and Dol-P-Glc utilization. Lec35 mutant cells are indeed defective in both Dol-P-Man-dependent synthesis of lipid-linked oligosaccharides, glycosylphosphatidylinositols, and C-linked mannosylation of tryptophan, and Dol-P-Glc-dependent glycosylation of lipid-linked oligosaccharides [158, 159].

Ware and Lehrman [160] cloned a suppressor (SL15) of the Lec15 and Lec35 mutations from a CHO cDNA library. SL15 has two potential membrane-spanning regions and a likely C-terminal endoplasmic reticulum retention signal. SL15 corrects both the defective mannosylation and glycosylation in Lec35 cells but exhibits a preference for Dol-P-Man over Dol-P-Glc. SL15 is neither Dol-P-Man synthase nor an inhibitor of mannosyltransferases [158]. The function of the protein is not known but it is probably required for Dol-P-Man transport. The gene for the human homolog of SL15 has been mapped to chromosome 17p13.1–p12 [161].

Schenk et al. [162] recently reported three unrelated patients with a novel CDG type (CDG-If). The patients showed a typical type I serum transferrin glycoform pattern and normal PMM and PMI activities. Patient fibro-

blasts accumulated truncated dolichol-pyrophosphate-linked oligosaccharides (predominantly $\text{Man}_5\text{GlcNAc}_2$ and $\text{Man}_3\text{GlcNAc}_2$ with smaller amounts of the glucosylated forms of these oligosaccharides). Sequence analysis of cDNA encoding the human homolog of the CHO Lec35 protein (SL15) showed distinct mutations in all three patients. The accumulation of Dol-PP- $\text{Man}_5\text{GlcNAc}_2$ and its glucosylated form in patient fibroblasts indicates that the Lec35 mutations are leaky.

CDG type IIa (CDG-IIa)

Two CDG patients have been described who differ from the classic picture of CDG-I described above, an Iranian girl [163] and a Belgian boy [164, 165]. Both patients, designated as CDG-IIa, have inactivating point mutations in the gene encoding UDP-GlcNAc: α -6-D-mannoside β -1,2-N-acetylglucosaminyltransferase II (GnT II; fig. 2) [64, 166–169]. The first committed step in the conversion of oligomannose to complex and hybrid N-glycans is catalyzed by GnT I (fig. 2). Processing of the product of GnT I by α 3/6-mannosidase II (MII; fig. 2) to form the

substrate for GnT II is the first committed step in the conversion of hybrid to complex N-glycans [101, 170–173]. GnT II is a typical type II transmembrane protein [174, 175], the gene for which has been mapped to human chromosome 14q21.

Clinical features and clinical biochemistry of CDG-IIa

The CDG-IIa patients had severe psychomotor retardation but there was no peripheral neuropathy and the cerebellum was normal on nuclear MRI. Both patients had a similar dysmorphism particularly of the face (coarse features, low-set ears), widely spaced nipples, a ventricular septal defect, a striking stereotypic behaviour (tongue thrusting, hand washing and other movements), generalized hypotonia and limb weakness, and normal deep-tendon reflexes. The girl was lost from follow-up after the age of 3. The boy's speech was limited to a few monotonous sounds at 10 years. He suffered from frequent infections in infancy and epilepsy developed at 6 years. The diagnosis of CDG was not made until he was 9.5 years old when an investigation of bleeding gums revealed a typical CDG coagulopathy.

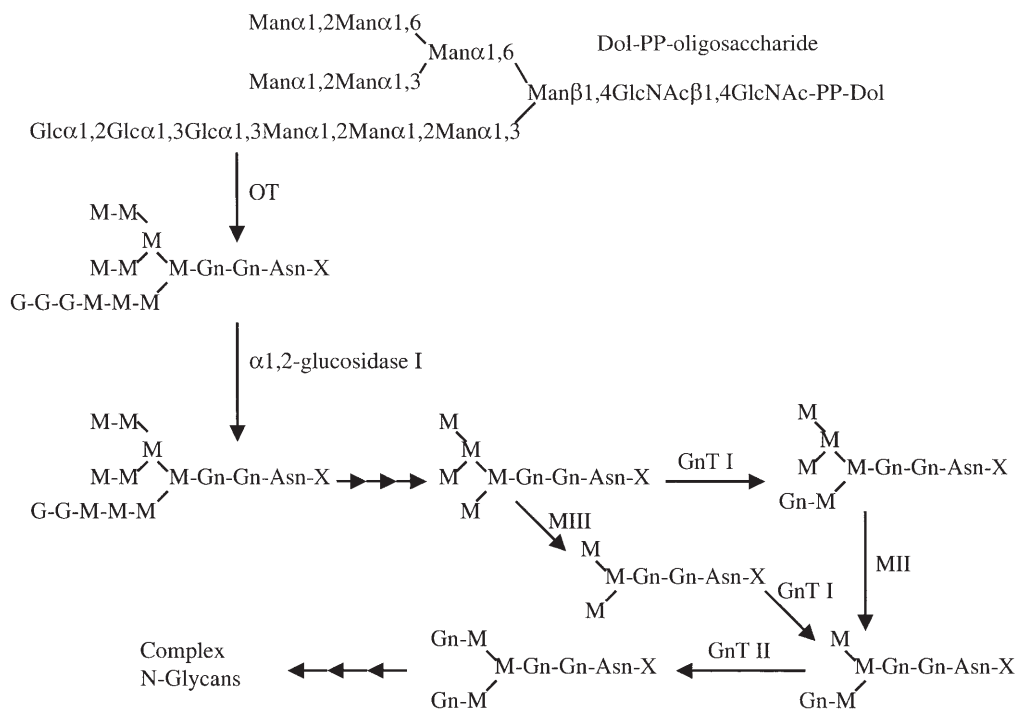


Figure 2. Pathway from dolichol pyrophosphate oligosaccharide to complex N-glycans. Oligosaccharyltransferase (OT) transfers $\text{Glc}_3\text{Man}_5\text{GlcNAc}_2$ from dolichol pyrophosphate oligosaccharide to an Asn residue in a nascent protein chain in the rough endoplasmic reticulum (RER). The glycosylated protein is released from the ribosome into the RER lumen where $\alpha 1,2$ -glucosidase I and $\alpha 1,3$ -glucosidase II remove the three Glc residues. ER $\alpha 1,2$ -mannosidase, and Golgi $\alpha 1,2$ -mannosidases I remove four Man residues to produce $\text{Man}_5\text{GlcNAc}_2$ -protein; $\alpha 1,3$ -glucosidase II, ER $\alpha 1,2$ -mannosidase, and Golgi $\alpha 1,2$ -mannosidases I are represented by three arrows together. In the medial Golgi compartment, the successive actions of GnT I, $\alpha 3,6$ -mannosidase II (MII), and GnT II convert $\text{Man}_5\text{GlcNAc}_2$ -protein to the biantennary complex N-glycan $\text{GlcNAc}_2\text{Man}_3\text{GlcNAc}_2$ -protein. HEMPAS, CDG-IIa, and CDG-IIb are due, respectively, to defects in Golgi MII (at least in some cases), Golgi GnT II, and endoplasmic reticulum $\alpha 1,2$ -glucosidase I. MIII is a GnT I-independent $\alpha 3/6$ -mannosidase which provides an alternate pathway that does not require MII.

Biochemical differences from CDG-I are the absence of proteinuria, a deficiency of clotting factors IX and XII, decreased β -glucuronidase, and normal serum glutamic pyruvic transaminase activity, albumin, cholesterol, and arylsulfatase A. As occurs in CDG-I, the CDG-IIa patient showed decreased levels of many serum glycoproteins (thyroxine-binding globulin, clotting factor XI, anti-thrombin III, proteins C and S, heparin cofactor II, β -galactosidase, α 1-anti-trypsin, apolipoprotein B, haptoglobin). Serum IgM and cerebrospinal fluid protein were elevated. Radiological examination showed osteopenia and other skeletal abnormalities. MRI revealed no cerebellar atrophy but delayed myelination and global cortical atrophy.

The CDG-IIa serum transferrin isoelectric focusing pattern differs markedly from that in CDG-I (table 4). Electrospray-mass spectrometry of CDG-IIa serum transferrin showed no or minimal amounts of asialo-, tetrasialo-, pentasialo- and hexasialotransferrins, low amounts of monosialotransferrin, a moderate amount (about 4%) of trisialotransferrin and a large amount (95%) of disialotransferrin [63, 64, 165]. Carbohydrate analysis and high-resolution proton nuclear magnetic resonance spectroscopy of CDG-IIa serum transferrin [63] showed that the major N-glycan is $\text{Man}\alpha 1-6[\text{NeuNAc}\alpha 2-6\text{Gal}\beta 1-4\text{GlcNAc}\beta 1-2\text{Man}\alpha 1-3]\text{Man-R}$ where R is $-\beta 1-4\text{GlcNAc}\beta 1-4\text{GlcNAc-Asn-X}$. Each glycosylation site of the major disialotransferrin (S2) component is occupied by this truncated monosialo-monoantennary N-glycan. The presence of truncated N-glycans clearly differentiates the CDG-IIa transferrin glycoform pattern from the 'all-or-none' model described above for CDG-I (table 4). The parents of the CDG-IIa patients showed a normal pattern.

The large amount of normal transferrin glycoform S4 in CDG-I serum indicates that this mutation is leaky. In contrast, the mass spectrometry data [63] indicate that there is little, if any, normal S4 in CDG-IIa serum. Thus the mutation in CDG-IIa appears to be stringent.

The biochemical and genetic defects in CDG-IIa

The truncated monosialo-monoantennary N-glycan described above suggested that CDG-IIa patients may have a defect in GnT II. Indeed, GnT II activity was reduced by over 98% in fibroblast extracts from the two unrelated CDG-IIa patients [165] and there was no detectable GnT II activity in mononuclear cell extracts from the male patient [166]. There were two different point mutations in the catalytic domain of GnT II, S290F and H262R, in the girl and boy, respectively [167]. Both mutations occur in the C-terminal catalytic domain [172, 176] at locations which are conserved between rat and human GnT II [175]. Both patients are homozygous for their respective mutations and have therefore inherited the same allele

from each parent. The father, mother, and brother of the boy show one normal allele and one allele with the CDG-IIa mutation.

Both mutant forms of GnT II were expressed in the baculovirus/Sf9 system [167] and showed less than 1% of the enzyme activity of normal GnT II. Thirteen blood relatives of the patient were identified as heterozygotes and showed a significant reduction (33–68%) in mononuclear cell GnT II activity. CDG-IIa is a recessive autosomal disease located at chromosome 14q21.

Over 60% of mouse embryos lacking the GnT II gene develop fully but 99% of newborns die during the first week of post-natal development [6]. The few surviving mice are runted and exhibit facial dysmorphism, kyphoscoliosis, muscular atrophy, tremors, and osteopenia. Patho-histologic findings indicate reduced ossification at the growth plates, increased prevalence of skeletal cartilage, and a calcified bone density that is reduced by over 30%. This appears with a significant increase in the frequency of osteoclasts. Although the surviving female 'nul' mice are fertile, surviving males are infertile with a block in spermatogenesis. Some serum coagulation factors are reduced. The production of T and B lymphocytes is reduced, hypocalcemia is observed, and a ventral septal defect of the heart was noted in one of the surviving mice. The majority of the 'null' mice die with gastrointestinal blockage. Gastrointestinal hemorrhages and alterations in microbial colonization of the gastrointestinal tract were observed in some animals. Like the GnT II-null mice, the majority of humans with CDG-IIa probably die in gestation or shortly after birth, and the surviving GnT II-null mouse is likely very similar to the human CDG-IIa patient in many pathologic and biochemical features. Although a third case of CDG-IIa has been described recently [177], it is a very rare disease.

CDG type IIb (CDG-IIb)

Glucosidase I is an endoplasmic reticulum N-glycan-processing enzyme which removes the distal $\text{Glc}\alpha 1,2$ residue from the $\text{Glc}_3\text{Man}_9\text{GlcNAc}_2\text{-Asn}$ -protein after oligosaccharyltransferase-catalyzed transfer of oligosaccharide from Dol-PP-oligosaccharide to an Asn residue (fig. 2). A glucosidase I defect has recently been described in a neonate with severe generalized hypotonia and dysmorphic features [178]. The clinical course was progressive and characterized by the occurrence of hepatomegaly, hypoventilation, feeding problems, seizures, and fatal outcome at 74 days after birth. An accumulation of $\text{Glc}\alpha 1-2\text{Glc}\alpha 1-3\text{Glc}\alpha 1-3\text{Man}$ in the patient's urine first indicated a possible glycosylation disorder. Studies on liver tissue and cultured skin fibroblasts revealed a severe glucosidase I deficiency (<3% of control values). Glucosidase I activities in cultured skin fibroblasts from both pa-

rents were found to be 50% of control values. Tissues from the patient subjected to Western blot analysis revealed strongly decreased amounts of glucosidase I protein in the homogenate of the liver, and a less-severe decrease in cultured skin fibroblasts. The patient was a compound heterozygote for two missense mutations in the glucosidase I gene, R486T and F652L. The mother and father were heterozygous for the R486T and F652L mutations, respectively.

Surprisingly, the serum transferrin isoelectric focusing pattern was reported to be normal. The action of Golgi endo- α 1,2-mannosidase [179, 180] accounts for the presence of Glc α 1-2Glc α 1-3Glc α 1-3Man in the patient's urine and provides a by-pass alternate pathway towards complex N-glycans. However, the severity of the clinical picture indicates severe problems in complex N-glycan formation in many organs of the infant's body; the normal serum transferrin glycoform pattern is thus difficult to explain.

Hereditary erythroblastic multinuclearity with a positive acidified-serum lysis test; congenital dyserythropoietic anemia type II (HEMPAS)

Clinical features

Ineffective and morphologically abnormal erythropoiesis is called dyserythropoiesis and results in anemia if the output of erythrocytes by the bone marrow is significantly reduced. In 1966 in Toronto, Crookston et al. [181] reported a young man (MF) with a life-long history of dyserythropoietic anemia. His bone marrow showed marked hyperplasia and multinuclear erythroblasts. His erythrocytes were lysed by acidified sera from other donors but not by his own serum. The disorder was later found in several other patients, including two sisters (CL, LF) and was determined to be a congenital dyserythropoietic anemia (CDA). The disease was named hereditary erythroblastic multinuclearity with a positive acidified-serum lysis test (HEMPAS) [182]. Three major types of CDA have been classified [183]. HEMPAS is type II CDA and is distinguished from types I and III CDA primarily on the basis of multinuclear erythroblasts and a positive serum lysis test.

In 1987, there were over 120 known cases of HEMPAS [184], but there are probably about 300 reported cases to date [185, 186]. HEMPAS consists of a group of autosomal recessive disorders, the age of diagnosis varies from infancy to old age, and the anemia varies from slight to severe. Jaundice, hepatosplenomegaly, diabetes, and gallstones are common. The body iron stores in HEMPAS are usually increased; hepatic hemosiderosis is common and hepatic cirrhosis has been reported. Electron microscopy shows that the red cell membrane is 'duplicated' and covered with pits and plaques [187, 188]. HEMPAS manifests itself primarily as a disease of erythroblasts and

erythrocytes although some patients express biochemical defects in leukocytes and other organs [189].

Structural studies on HEMPAS erythrocyte glycans

About 30% of normal individuals have in their serum an antibody which when acidified can lyse HEMPAS red cells. HEMPAS serum does not contain this antibody. HEMPAS red cells also react strongly with antibodies against poly-N-acetyllactosamines [182, 184, 187, 188] suggesting that the abnormal antigen may be carbohydrate in nature. Several laboratories have reported decreased erythrocyte membrane protein glycosylation [190–193].

Whereas normal red cells have bands 3 and 4.5 that are rich in poly-N-acetyllactosamines, Fukuda et al. [194] found that there was no detectable poly-N-acetyllactosamine on bands 3 and 4.5 of HEMPAS erythrocytes. HEMPAS red cells, however, show the concomitant appearance of large amounts of a poly-N-acetyllactosamine-bearing compound identified as a macroglycolipid [191, 194–196]; normal red cells have a negligible quantity of macroglycolipid.

Fukuda et al. [197] reported varying amounts of the following protein-bound carbohydrate structures on erythrocytes from four HEMPAS patients: NeuNAc α 2-6Gal β 1-4GlcNAc β 1-2Man α 1-3[Man α 1-6]Man-R (R is - β 1-4GlcNAc β 1-4GlcNAc-Asn-X; glycopeptide 1), suggesting a defect in GnT II (fig. 2), and NeuNAc α 2-6Gal β 1-4GlcNAc β 1-2Man α 1-3[Man α 1-6(Man α 1-3)Man α 1-6]Man-R (glycopeptide 2), suggesting a defect in α 3,6-mannosidase II (MII; fig. 2). Glycopeptides 1 and 2 were major constituents in patients TO and GC, respectively [197, 198].

Analysis of HEMPAS lymphocytes and lymphoblasts

Lymphocytes from HEMPAS patient TO showed GnT II levels 10% of normal [197], and patient GC lymphoblasts had almost no detectable MII activity [198], findings compatible with the accumulation of glycopeptides 1 and 2, respectively. Northern blot analysis of mRNA from cultured transformed lymphoblasts using a probe for human MII showed that GC had levels of message less than 10% of normal [198]. These results suggest that GC cells contain a mutation in the *MII* gene that results in inefficient expression of MII mRNA, either through reduced transcription or message instability. Recently, a second human *MII*-like gene called *MIIx* has been described, but its role in HEMPAS remains to be elucidated [199].

The genetic defect in HEMPAS

Normal adult human erythrocyte band 3 carries a single biantennary N-glycan with poly-N-acetyllactosamine

chains on both antennae [200], whereas band 3 from all HEMPAS patients studied to date lacks poly-N-acetylglucosamine chains [194, 197, 198, 201–203]. Since there are poly-N-acetylglucosamine chains on the Man α 1-3 arm of the normal band 3 N-glycan, a defect in either GnT II or MII should not result in complete absence of poly-N-acetylglucosamine chains. Indeed, band 3 from CDG-IIa patients (lacking GnT II, see above) retains about 50% of its poly-N-acetylglucosamine content [166], consistent with the fact that there is no preferential attachment of poly-N-acetylglucosamine chains to either of the arms of a biantennary N-glycan although preferential attachment to the Man α 1-6 arm has been reported for tri- and tetra-antennary N-glycans [3, 204]. The relatively benign clinical picture of HEMPAS is completely different from the severe abnormalities found in CDG-IIa. Therefore, lack of GnT II is not likely to be the primary defect in HEMPAS.

Linkage analysis and cytogenetic studies in 12 southern Italian families [205, 206] located the CDA II gene (*CDAN2*) to chromosome 20q11.2 and excluded the genes encoding GnT II (chromosome 14q21 [175]), MIIx (chromosome 15q25 [199]) and MII (chromosome 5q21-q22 [199]). Northern analyses of mRNA from several Italian HEMPAS patients showed a reduction of MII and GnT II mRNAs suggesting a secondary effect, such as defective transcription or mRNA maturation involving both the genes for GnT II and MII [185, 206]. The authors suggest that the HEMPAS mutation may alter the properties of a tissue-specific cellular factor which specifies the utilization of distinct polyadenylation signals within the 3' untranslated region of both mRNAs. However, Fukuda [186, 203] did not find a reduction in GnT II or MII transcripts in southern Italian HEMPAS cases and suggested that a defect exists in a Golgi or cytoplasmic protein regulating membrane trafficking, and that this defect affects glycosylation.

Genetic heterogeneity in CDA II was demonstrated by Iolascon et al. [207] who found two unrelated families from southern Italy in which CDA II was not linked to the *CDAN2* locus. The HEMPAS gene of patient GC (described above), with over 90% decrease in MII expression [198], is probably also not linked to the *CDAN2* locus. The mutation responsible for the lowered MII mRNA levels in patient GC has not yet been determined. Fukuda [186, 203] has reported preliminary evidence, published only in reviews, that another HEMPAS case (LF) may also have a defect in MII. LF is a compound heterozygote with a deletion in one allele and an insertion in the other. GC and LF are descended from British and Irish families, respectively. There are probably HEMPAS variants which involve neither the *CDAN2* locus nor *MI*I [207–210].

Since the *MI*I gene is normally expressed in a variety of cells and tissues, the HEMPAS defect is not restricted to erythroid cells. However, there are cells and tissues that

are not affected by the HEMPAS genetic defect, suggesting that there may be other tissue-specific MII isozymes. Another possibility is the presence of alternate processing pathways which are independent of MII action: (i) lack of Dol-P-Man synthase [101, 211], glucose starvation [212], or energy deprivation [101] all cause defective Dol-P-Man synthesis which leads to the synthesis of truncated oligosaccharides that do not require MII action; (ii) rat brain and liver have a membrane-bound α 3/6-mannosidase which can cleave protein-bound Man₅GlcNAc₂ to Man₃GlcNAc₂ [213–216] without the need for GnT I or MII.

As explained above, lack of MII should not result in complete absence of poly-N-acetylglucosamine chains from erythrocyte band 3. It is possible that poly-N-acetylglucosamine chains can be added to protein-bound Man₃GlcNAc₂ but not to protein-bound Man₅GlcNAc₂. Data from the MII-null mouse [12] support the hypothesis that MII lack can cause HEMPAS. The mice developed a dyserythropoietic anemia, splenomegaly, reticulocytosis, and other features similar to HEMPAS, concurrent with loss of erythrocyte complex N-glycans. Non-erythroid cell types continued to produce complex N-glycans by an alternate pathway comprising a distinct α 3/6-mannosidase (*MI*II, fig. 2) which converts protein-bound Man₅GlcNAc₂ to Man₃GlcNAc₂ [215, 216]. The MII mutant mice, unlike HEMPAS patients, do not show multinucleated erythroblasts, hepatomegaly, liver cirrhosis, or hemosiderosis. Neither normal nor mutant mouse erythrocytes have protein-bound poly-N-acetylglucosamine chains.

Leukocyte Adhesion Deficiency Type II (LAD II)

Leukocyte adhesion deficiency type II (LAD II) is a rare disorder characterized by recurrent infections, persistent leukocytosis, and severe mental and growth retardation [217]. In 1992, two supposedly unrelated Arab Moslem boys (3 and 5 years old) were reported with a distinctive syndrome (Rambam-Hasharon syndrome) comprising unusual facial appearance, severe mental retardation, microcephaly, cortical atrophy, seizures, hypotonia, dwarfism, and recurrent infections with a high leukocyte count and without the formation of pus [218, 219]. Autosomal recessive inheritance is strongly suggested by the fact that both of the patients were the offspring of consanguineous parents.

Both patients manifested the Bombay (*hh*) phenotype caused by a lack of H blood group α 1,2-fucosyltransferase (*FUT*1, [220]) action. Both children were also non-secretors (*sese*, due to lack of activity of the secretor α 1,2-fucosyltransferase, *FUT*2 [221]), and Lewis-negative (*lele*, due to lack of activity of the Lewis blood group α 1,3/4-fucosyltransferase, *FUT*3 [222]). However, the

above fucosyltransferase activities were expressed at normal levels. A general defect in fucose metabolism was therefore suggested [218, 223, 224].

The immune defect in the patients is due to the absence of fucosylated selectin ligands [225] with a resultant defect in the adhesion of leukocytes to endothelia and lack of recruitment of neutrophils to sites of inflammation [see ref. 4 for a review of leukocyte adhesion]. LAD II neutrophils are deficient in expression of selectin ligand activity and exhibit a correspondingly diminished ability to roll on endothelium and to traffic to inflammatory sites *in vivo*. Neutrophils from LAD II patients bind minimally or not at all to E- or P-selectin [225]. Cell surface expression of fucosylated glycoconjugates was induced by exposure of lymphoblastoid cell lines, human umbilical vein endothelial cells, and fibroblasts from LAD II patients to exogenous fucose [226]. GDP-mannose-4,6-dehydratase, the first of two enzymes in the *de novo* GDP-L-fucose biosynthesis pathway, was reported to show altered kinetics in cell lysates from a LAD II patient compared with controls [227], but no mutations were identified in patient cDNA encoding the dehydratase. Furthermore, the levels of immunoreactive enzyme in cell lysates were comparable in the patient and controls, suggesting that the LAD II defect was due to a mutation affecting an unidentified dehydratase-regulating protein.

Lübke et al. [228] recently reported a patient of Turkish origin with a new type of LAD II due to decreased import of GDP-fucose into the Golgi with resultant decreased fucosylation of glycoproteins. *In vitro* assays of cytosolic extracts from leukocytes and fibroblasts of the patient demonstrated a normal GDP-L-fucose biosynthesis from GDP-D-mannose [229]. Analysis of the two enzymes involved in the pathway, GDP-mannose 4,6-dehydratase and FX protein, revealed normal numbers of transcripts without any detectable mutations within the coding regions of either gene. However, the saturable, high-affinity import of GDP-fucose into Golgi-enriched vesicles was deficient in the patient, while import of UDP-Gal and the activity of GDPase (which generates the nucleoside phosphate GMP required for antiport of GDP-fucose) were normal [228]. Addition of L-fucose to the medium of fibroblasts restored the fucosylation of glycoproteins. The rat liver Golgi membrane GDP-fucose transporter has been identified and purified [230]. Transport was stimulated two to three-fold after pre-loading proteoliposomes with GMP, the putative antiporter.

Sialyl-Lewis X was absent from the surface of polymorphonuclear neutrophils from this patient and cell binding to E- and P-selectins was severely impaired, causing an immunodeficiency [231]. Elevation of peripheral neutrophil counts occurred within several days after birth. A severe hypofucosylation of glycoconjugates was present in all cell types investigated. Since the fucosylation defect in the patient's fibroblasts can be corrected by addi-

tion of L-fucose to the culture medium [228], oral fucose therapy of the patient was attempted [232, 233]. This resulted in dramatic improvement in fucosylation of the selectin ligands and other glycoproteins and an overall improvement in clinical condition. There was no hemolysis (a possibility due to the presence of antibodies against blood group H in the sera of LAD II patients) or other side effects. During 9 months of treatment, infections and fever disappeared, elevated neutrophil counts returned to normal and psychomotor capabilities improved.

A recent review [234] reported that five LAD II patients have been reported to date, four of Arabic origin living in Israel (which include the original two patients described above) and one of Turkish origin (also described above). A defect in the transport of GDP-Fuc into Golgi vesicles was observed in one of the Arab patients [234] but the kinetics were different from those observed in the Turkish patient. While oral fucose was an effective treatment for the Turkish patient, it was ineffective in the Arab patient.

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