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Congenital disorders of glycosylation (CDG): Quo vadis?

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ABSTRACT

The survey summarizes in its first part the current status of knowledge on the Congenital Disorders of Glycosylation (CDG) with regard to their phenotypic spectrum, diagnostic and therapeutic strategies, and pathophysiology. It documents the clinical and basic research activities, and efforts to involve patients and their families. In the second part, it tries to look into the future of CDG. More specific biomarkers are needed for fast CDG diagnosis and treatment monitoring. Whole genome sequencing will play an increasingly important role in the molecular diagnosis of unsolved CDG. Epigenetic defects are expected to join the rapidly expanding genetic and allelic heterogeneity of the CDG family. Novel treatments are urgently needed particularly for PMM2-CDG, the most prevalent CDG. Patient services such as apps should be developed e.g. to document the natural history and monitor treatment. Networking (EURO-CDG, the European Reference Networks (MetabERN)) is an efficient tool to disseminate knowledge and boost collaboration at all levels. The final goal is of course to improve the quality of life of the patients and their families.

1. Introduction

Approximately half of all proteins typically expressed in a cell undergo glycosylation to achieve their full functionality. There are mainly two categories of glycosylation: N-glycosylation and O-glycosylation. N-glycans are linked to the amide group of asparagine, while O-glycans are linked to the hydroxyl group of serine or threonine. The synthesis of N-glycans proceeds in three stages: formation of nucleotide-linked sugars, assembly (in cytosol and ER), and processing (in the Golgi). The synthesis of O-glycans does not involve processing, and occurs mainly in the Golgi. Besides, there is also lipid glycosylation and synthesis of glycosylphosphatidylinositol anchors. Congenital Disorders of Glycosylation (CDG) are genetic defects in the synthesis and attachment

of glycoprotein and glycolipid glycans. Initially, mutations were found in genes encoding glycosyltransferases, remodelling glycosidases, and sugar nucleotide transporters, that are all known to have a direct role in glycosylation. However, new forms of CDG have recently been identified with defects in vesicular trafficking, pH homeostasis or Mn^{2+} homeostasis. Various approaches have been developed for the efficient diagnosis of these diverse types of CDG (see section 2.2 for more details). Since their first clinical description in 1980, 105 types of CDG have been identified, and that number keeps rising. Their clinical spectrum is extremely broad, covers nearly all known phenotypes, and comprises new phenotypes. Research into CDG received an enormous boost since 1999 thanks to the consecutive, collaborative initiatives of EUROGLYCAN and EUROGLYCANET, that were originally funded by

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the European Commission's Framework Programmes. In 2011, our group (Berlin, Brussels, Heidelberg, Leuven, Lille (Villeneuve d'Ascq), Madrid, Nijmegen, and Paris) has successfully replied to the E-Rare-2 Call for Proposals with the EURO-CDG project. Research in the context of EURO-CDG has yielded improved diagnostic methodologies resulting in the identification of an increasing number of CDG, shortening of the time to diagnosis, and CDG diagnosis in patients who remained 'unsolved' for many years. In addition, cellular models have been used to study the pathophysiology of disease and to identify molecular pathways that can be targeted for therapy. Within the network, more than 1300 CDG patients received a definite diagnosis (with PMM2-CDG representing 62% of the recorded patients, and 30 other CDG representing the remaining 38%).

Efforts are now guided towards the development of therapeutic approaches for PMM2-CDG, the most frequent CDG, but also for the more rare CDG. The functional characterization of disease-causing mutations in PMM2-CDG patients led to the identification of pharmacological chaperones to rescue the folding of the mutant PMM2 enzyme. In parallel, oral D-galactose therapy has been shown to be beneficial in CDG with hypogalactosylation. We initiated a multicentre clinical trial to characterize the effects of D-galactose supplementation in different genetic conditions affecting Golgi glycosylation, including PGM1-CDG, TMEM165-CDG and SLC35A2-CDG. The European network for research on CDG wants to build on its past achievements and is committed to explore different possibilities to improve treatment and quality of life of the patients and their families. It will of course also share efforts to this aim with other researchers interested in CDG. Open, international meetings, often in parallel with patients and parents meetings, are meant to exchange experience and results, and to promote progress in CDG.

2. CDG at present

2.1. Phenotypic spectrum

Table 1 tabulates the known CDG (in alphabetical order) with the main associated organ involvement and symptomatology. For a recent general review on CDG and a selection of reviews on organ/tissuespecific CDG and specific CDG/CDG groups see Jaeken and Morava 2016; Jaeken and Péanne 2017. The fact that five novel CDG have been reported in the first half of 2017 illustrates the rapid expansion of this disease family: ATP6V1A-CDG (Van Damme et al., 2017), ATP6V1E1- CDG (Van Damme et al., 2017), PIGC-CDG (Edvardson et al., 2017), TRAPPC11-CDG (Matalonga et al., 2017), and OGT-CDG (Willems et al., 2017). Also, a novel regulatory mutation has been presented, with a defect in the PMM2 promoter (Cabezas et al., 2017). In recent years, it has become clear that some CDG can present totally different phenotypes depending on the types of mutation. Striking examples are PMM2-CDG (a dysmorphism-disability syndrome; polycystic kidney disease with hyperinsulinemic hypoglycaemia; isolated tendency to thrombosis), ALG9-CDG (a dysmorphism/neuro-hepato-renal syndrome; a skeletal phenotype with death in utero), EXT2-CDG (exostoses; seizures-scoliosis-macrocephaly syndrome), PIGA-CDG (intellectual disability and seizures without dysmorphism; ferro-cerebrocutaneous syndrome; Simpson-Golabi-Behmel syndrome type 2; early onset epileptic encephalopathy with severe muscular hypotonia, dysmorphism, multiple congenital anomalies and early death (MCAHS2)), and POGLUT1-CDG (skin disease; muscular dystrophy). No defects have yet been reported in many genes of the glycosylation machinery, as for instance in the Golgi mannosidases (except MAN1B1), in MGAT1, B4GAT1, …which have been candidate genes, right from the beginning. We reckon that patients with defects in these genes are extremely rare and highly underestimated, or may not survive until birth.

There is an increasing number of reports on adult features of CDG such as PMM2-CDG (up to 67 years; Monin et al., 2014; Barone et al., 2015), SRD5A3-CDG (up to 45 years; Kahrizi et al., 2011; Kara et al.,

2014; Wheeler et al., 2016), PGM3-CDG (up to 35 years; Sassi et al., 2014; Zhang et al., 2014), a.o. This helps in answering the often asked question of parents: what is the future of my child?

2.2. CDG frequency and registry

The standard test for the diagnosis of N-glycosylation disorders with sialic acid deficiency is still isoelectrofocusing of serum transferrin (Tf IEF), which is only N-glycosylated. A type 1 pattern (decreased tetrasialotransferrin, increased disialo- and asialotransferrin) points to an assembly defect or a defect in the transfer to the peptide chain (CDG-I), whilst a type 2 pattern (increase also of threesialo- and monosialotransferrin) suggests a remodelling defect (CDG-II). Note that in normal infants up to about 6 weeks, the serum transferrin bands are slightly more intense than later on (looking like a mild type 2 pattern). In case of a typical MPI-CDG or PMM2-CDG presentation, enzymatic testing can be performed in leukocytes or fibroblasts although it is more cumbersome than direct mutation analysis of the MPI and PMM2 genes respectively. In addition, we have evidence that false negative PMM2 measurements in fibroblasts occur (G. Matthijs, E. Van Schaftingen and co-workers, unpublished). Hence, we propose to sequence the PMM2 gene first in all CDG type I cases. In the other cases with a type 1 pattern, there is a tendency to first perform a targeted CDG panel analysis, and when negative, whole genome/exome sequencing. Lipidlinked oligosaccharide analysis (LLO) in fibroblasts for type 1 is a cumbersome and expensive test that not always provides accurate results (see below). In patients with a type 2 pattern, mass spectrometry of transferrin glycans can first be performed but this rarely yields a specific pattern. Isoelectrofocusing of serum apolipoprotein C-III (which is only O-glycosylated) can detect some O-glycosylation disorders. A flowchart summarizing the approach to obtain molecular diagnosis in unsolved CDG is depicted in Fig. 1.

Since there is no worldwide CDG registry, information about frequency is lacking. In order to fill up this gap, in November 2016 the different laboratories in Europe offering CDG diagnosis were asked to fill an informal excel table with (i) the actual number of patients for each type of molecularly diagnosed CDG-I and CDG-II; (ii) and for the types with less than 4 patients, the initials and nationality of the patients, to avoid double counting of patients with a very rare CDG that could have been studied by more than one laboratory; and (iii) the number of 'unsolved' patients (indicating: positive screening for abnormal glycans, negative targeted sequencing or negative exome results). Thus only the CDG with an abnormal transferrin IEF were included in this study (for example not alpha-dystroglycanopathies).

The following laboratories accepted to share their data: Barcelona, Catania, Heidelberg, Leuven, Lille, Lyon, Madrid, Nijmegen, Paris, Porto, Prague and Tallinn. The number of molecularly diagnosed patients was 1350, distributed among 94% CDG-I and 6% CDG-II. Twentytwo different types of CDG-I and 15 of CDG-II were reported. Fig. 2 shows the distribution of the patients. As to CDG-I (Fig. 2A), PMM2- CDG, as expected, was by far the most frequent (62%; n: 834). ALG6- CDG was the second most frequent (8%; n: 101), followed by SRD5A3- CDG (n: 43), ALG1-CDG (n: 41) and MPI-CDG (n: 36). Regarding CDG-II (Fig. 2B), MANB1-CDG was the type with the largest number of patients (n: 18), followed by COG7-CDG (n: 10). The different COG deficiencies (COG1-CDG COG4-CDG to COG8-CDG) together comprised 33 patients. The distribution of some specific types was strikingly different within the different laboratories. For example, almost all of the TMEM165- CDG patients (n: 5/6) were reported by Leuven, the SRD5A3-CDG patients mainly by Nijmegen. Importantly, it is worth mentioning that some patients may have been counted twice, as samples traveled extensively especially in the early days of genetic diagnostics.

Finally, the number of reported molecularly unsolved cases was relatively small (less than 100). The total number of diagnosed CDG patients in Europe might reasonably exceed 2500 when adding those from the United Kingdom, Ireland, and the countries of Northern and

Table 1

Overview of CDG organ involvement and symptoms/signs Items before the semicolon are clinical symptoms and signs, and the items after the semicolon are results of paraclinical investigations.

ALG1-CDG^{*}

ALG2-CDG^{*}

ALG3-CDG^{*}

ALG6-CDG^{*}

ALG8-CDG^{*}

ALG9-CDG^{*}

Gillessen-Kaesbach-Nishimura syndrome

 \star

ALG12-CDG^{*}

ALG13-CDG^{*}

Epileptic encephalopathy, early infantile, 36

ALG14-CDG^{*}

ATP6AP1-CDG^{*}

ATP6V0A2-CDG^{**}

Cutis laxa, autosomal recessive, type IIA

Wrinkly skin syndrome

B3GALNT2-CDG

Muscular dystrophy-dystroglycanopathy (congenital with brain and eye anomalies), type A, 11

B3GAT3-CDG

B3GAT3-CDG
Multiple joint dislocations, short stature, craniofacial dysmorphism, with or without congenital heart defects
Expositional contract contract and proportional line colored

B4GALNT1-CDG

Spastic paraplegia 26, autosomal recessive

B4GALT7-CDG

Ehlers-Danlos syndrome with short stature and limb anomalies

B3GALTL-CDG

Peters-plus syndrome

CAD-CDG

Epileptic encephalopathy, early infantile, 50

$CCDC115-CDG$ **

CHSY1-CDG

Temtamy preaxial brachydactyly syndrome

$COG2-CDG$ **

$COG4-CDG$ **

$COGS-CDG$ **

$\frac{\text{COG6-CDG}^{**}}{\sqrt{25}}$

COG7-CDG^{**}

$COG8$ -CDG $***$

DDOST-CDG^{*}

DHDDS-CDG^{*}
Retinitis pigmentosa 59

Multisystem disease

DOLK-CDG^{*}

DPAGT1-CDG^{*}

Myasthenic syndrome, congenital, 13, with tubular aggregates

DPM1-CDG^{*}

DPM2-CDG^{*}

DPM3-CDG^{*}

EOGT-CDG

EXT1-CDG

Chondrosarcoma Skeleton

chondrosarcoma of the pelvic bone, fibulae, and femora

EXT2-CDG
Exostoses, multiple, type 2

FKRP-CDG

Muscular dystrophy-dystroglycanopathy (congenital with brain and eye anomalies), type A, 5

Muscular dystrophy-dystroglycanopathy (congenital with or without mental retardation), type B, 5 mental disability, hypotonia; cerebellar cysts
wasting and weakness of shoulder girdle muscles and upper limbs, facial weakness $Brain$

Muscular dystrophy-dystroglycanopathy (limb-girdle), type C, 5

FKTN-CDG

Cardiomyopathy, dilated, 1X

Muscular dystrophy-dystroglycanopathy (congenital with brain and eye anomalies), type A, 4

Muscular dystrophy-dystroglycanopathy (congenital with or without mental retardation), type B, 4

Muscular dystrophy-dystroglycanopathy (limb-girdle), type C, 4

GANAB-CDG

GFPT1-CDG

GMPPA-CDG

GMPPB-CDG

Muscular dystrophy-dystroglycanopathy (congenital with mental retardation), type B, 14

Muscular dystrophy-dystroglycanopathy (limb-girdle), type C, 14

GNE-CDG

Nonaka myopathy

Sialuria

ISPD-CDG

Muscular dystrophy-dystroglycanopathy (congenital with brain and eye anomalies), type A, 7

LARGE-CDG

LFNG-CDG

MAN1B1-CDG^{**}

MGAT2-CDG^{**}

MOGS-CDG

MPDU1-CDG^{*}

MPI -CDG^{*}

NANS-CDG
Spondvloeni

PGAP1-CDG

PGAP2-CDG

PGAP3-CDG
Hyperphosphatasia with mental retardation syndrome 4

PGM1-CDG^{**}

PGM3-CDG
Immunodeficiency 23

PIGA-CDG

PIGC-CDG

Muscles

PIGL-CDG
CHIME syndrome

hyporeflexia

PIGM-CDG

PIGN-CDG

PIGO-CDG

DICP-CDC

PIGT-CDG

Multiple congenital anomalies-hypotonia-seizures syndrome 3

PIGV-CDG

Hyperphosphatasia with mental retardation syndrome 1

PIGW-CDG

$PMM2-CDG$ ^{*}

POFUT1-CDG

POGLUT1-CDG
Dowling-Dogos dis

POMGNT1-CDG

Muscular dystrophy-dystroglycanopathy (congenital with brain and eye anomalies), type A, 3

Muscular dystrophy-dystroglycanopathy (congenital with mental retardation), type B, 3:

Muscular dystrophy-dystroglycanopathy (limb-girdle), type C, 3:

Retinitis pigmentosa 76

POMT1-CDG

Muscular dystrophy-dystroglycanopathy (limb-girdle), type C, 1

POMT2-CDG

Muscular dystrophy-dystroglycanopathy (congenital with mental retardation), type B, 2

Muscular dystrophy-dystroglycanopathy (limb-girdle), type C, 3

PRKCSH-CDG

RFT1-CDG^{*}

SEC23B-CDG

$SLC35A1$ -CDG $**$

SLC35A2-CDG^{**}

SLC35D1-CDG

SLC39A8-CDG^{**}

SRD5A3-CDG^{*}

Kahrizi syndrome

SSR4-CDG^{*}

ST3GAL3-CDG

ST3GAL5-CDG

STT3A-CDG^{*}

STT3B-CDG^{*}

TMFM199-CDG **

TMEM5-CDG

Muscular dystrophy-dystroglycanopathy (congenital with brain and eye anomalies), type A, 10

TRAPPC11-CDG[#]

TUSC3-CDG^{*}

 \mathbf{I}

VPS13B-CDG

XYLT1-CDG

XYLT2-CDG
Spondylo-ocular syndrome

* refers to a type 1 serum transferrin pattern, while ** refers to a type 2. $^{\#}$ indicates that the glycosylation of serum transferrin has not been investigated.

Fig. 1. Updated diagnostic flowchart for unsolved CDG. IEF: isoelectrofocusing; NGS: next generation sequencing (CDG panel, exome or genome sequencing). #: we recommend to perform serum transferrin IEF twice, using independent serum samples.

Eastern Europe. The prevalence of CDG in Europe could then approach 0.1–0.5/100,000, which is far from the one of only PMM2-CDG calculated on the basis of carrier frequencies (1/20 000; Schollen et al., 2000, 1/77 000; Vals et al., 2017). Thus, CDG is still largely underdiagnosed, even in Europe, the most active region with regard to CDG screening worldwide. This under-diagnosis leads to under-treatment since some CDG are treatable, in particular MPI-CDG (mannose; de Lonlay et al., 2001), and PGM1-CDG and SLC35A2-CDG (galactose; Morava, 2014; Dörre et al., 2015).

The number of molecularly unsolved CDG patients (after exclusion of galactosemia and fructosemia, see section 2.3 for more details) decreases thanks to targeted and whole exome sequencing. As expected, CDG-I appeared to be much more frequent than CDG-II. This is logical since 30 of the known 105 CDG show a Tf IEF type 1 pattern, while only 18 CDG show a type 2 pattern (48 in total; review in Jaeken and Péanne, 2017). Thus only about half of the known CDG are picked up by this test. Among these 48 CDG, eleven did not show up in this survey performed by our network.

In conclusion, these preparatory results on CDG frequency will be a helpful tool in accompanying the development of new therapeutics for CDG patients and should be followed by setting up a patient register containing full clinical and biological data.

2.3. Treatment

2.3.1. Therapeutic trials in cells

An important pitfall in the field of many inherited metabolic disorders is the lack of good cellular models for testing therapeutic drugs. The cells most commonly used are patient-derived fibroblasts. However in diseases such as CDG these cells are not representative for the cells that are involved in CDG pathophysiology. Furthermore, for testing mutation-specific therapies cellular models are needed with specific mutations. Recently, the generation of induced pluripotent stem cells (iPSCs) and the number of reports on its applications have rapidly increased because these cells provide a unique platform to carry out in vitro drug screening tests (Thiesler et al., 2016). Nevertheless, the generation of a battery of iPSCs bearing different mutations for successful therapeutic evaluation is a complex task. This prompted B. Pérez and coworkers to develop other cellular models. They have generated a biobank of patient-derived fibroblasts overexpressing hypomorphic mutant alleles. This cellular model allows a rapid screening of potential drugs to be selected for further evaluation in neurons or hepatocytes derived from iPSCs and, in the last step, for evaluation in animal models (unpublished results). In addition, methodologies to generate knock-out cell lines for specific gene defects have been established within the EURO-CDG network, including Hap1, HEK293 and C2C12 cells.

Fig. 2. Distribution among twelve European laboratories of (A) CDG-I patients, and (B) CDG-II patients. For more clarity, only the CDG-I with a frequency higher than 3% (left panel) or the CDG-II with a frequency higher than 5% (right panel) are displayed.

2.3.2. Treatment strategies in patients

MPI-CDG was the first CDG with a fairly effective treatment. Initial studies showed significant clinical improvement on dietary intervention with oral mannose (1 g/kg per day divided in 3–4 doses), improving the serum transferrin isoform pattern, coagulation anomalies, hyperinsulinism and the protein losing enteropathy. Mannose therapy acts by its transformation into mannose-6-phosphate, thus restoring the defective pathway. Some patients require higher doses and a few patients do not tolerate mannose due to recurrent hemolysis. Although mannose reduces serum transaminase levels, it does not cure the liver disease in MPI-CDG. Several MPI-CDG patients are known with progressive liver cirrhosis and liver failure on mannose therapy. Liver transplantation has been shown to be beneficial in a few patients with full clinical recovery (Janssen et al., 2014).

PGM1-CDG involves several metabolic pathways, including glycogenolysis, glycolysis and glycosylation. Galactose therapy has been introduced based on the hypogalactosylation pattern of protein glycans in this disorder. It improves the mixed type of N-glycosylation defect. While the Tf IEF type 2 pattern normalizes quickly, a full restoration is rarely observed. Depending on the patient, dietary galactose in a dose of 0.5–1.5 g/kg per day decreased serum transaminase levels and increased coagulation factors, especially antithrombin. Some patients showed better endocrine control, and a decrease in the frequency of hypoglycemia and rhabdomyolysis. Muscle weakness and cardiomyopathy seem to be unaffected by the galactose intervention in PGM1 deficiency. In a few patients uridine was added, but the effect hereof is not clear yet (Tegtmeyer et al., 2014; Morava, 2014; Wong et al., 2017).

CAD-CDG is a disorder in the pyrimidine biosynthesis, important for glycosylation through its role in nucleotide biosynthesis. Both the severe seizures and the microcytic anemia are treatable by oral uridine supplements (Koch et al., 2017). Uridine is an efficient treatment because it is a product of the defective pathway. Monosaccharide supplementation is a partial treatment for individual patients in several other N-glycosylation disorders. Oral galactose supplementation improved seizures and a few blood parameters including Tf IEF in a subset of SLC35A2-CDG patients (Dörre et al., 2015), and the bleeding diathesis, endocrine function and Tf IEF in TMEM165-CDG (Morelle et al., 2017). Both galactose and manganese improved the transferrin isoforms and the seizure disorder in SLC39A8-CDG (Park et al., 2015). The treatment with mannose, galactose, manganese, and a possible treatment with chaperones for PMM2-CDG is illustrated in Fig. 3. Oral fucose treatment improved the immune disorder and decreased infection frequency in a few patients with SLC35C1-CDG (Wild et al., 2002).

Besides in MPI-CDG, liver transplantation has also been performed with partial success in CCDC115-CDG (Jansen et al., 2016a, 2016b). Heart transplantation was successful in 2 children with mild DOLK-CDG (Kapusta et al., 2013), and bone marrow transplantation led to improvement of the immune disease in PGM3-CDG (Stray-Pedersen et al., 2014). Other potential therapeutic approaches aim at specific symptoms like hypoglycemia, hypothyroidism, pericarditis. Congenital myasthenia such as in DPAGT1-CDG can be treated with cholinesterase inhibitors (Finlayson et al., 2013).

2.4. Pathophysiology

A disordered glycosylation machinery does not only influence the glycoprotein and glycolipid homeostasis, but can also have a significant secondary impact on other cellular pathways. The other way around, some metabolic diseases such as galactosemia and fructose intolerance, cause a secondary glycosylation disorder. They show a type 1 pattern. Equally, alcoholism show a type 1 pattern while infections with neuraminidase-producing bacteria cause a type 2 pattern.

Although these hypoglycosylation devious side effects were expected, they were somewhat out of the scope and began to gain center stage just recently. First of course is the polyisoprenoid (or mevalonate) pathway which is necessary for the synthesis of cholesterol and the oligosaccharide lipid-carrier dolichol. Both are directly associated with and influenced by the glycosylation process. A group of CDG, most prominently exemplified by the COG-related CDG, is secondary to perturbation of the in- and outward vesicular trafficking at the Golgi apparatus (Reynders et al., 2011). Since these transport processes play central roles independent of protein glycosylation, the related disorders are probably caused by a combination of protein hypoglycosylation and defects in exo- and endocytosis, lysosomal function, and/or autophagy. There is also a rising interest in pathways leading to the generation of other metabolites such as aminoacids, acylcarnitines and lipids. In a patient with ATP6AP1-CDG, dysregulated levels of several amino acids (e.g. arginine) and strong up-regulated levels of acylcarnitines of the long and very long species were found. Besides, within the main and minor lipid classes reduced amounts of e.g. phosphatidylcholine in combination with abnormalities of the plasmalogens were detected (C. Thiel and co-workers, unpublished results).

It is worth mentioning that, as in CDG, defects in the metabolism of amino acids and in the biosynthesis and remodelling of phospholipids, sphingolipids and complex fatty acids can lead to pathology of the nervous system and many other organs (de Koning, 2013; Lamari et al.,

Fig. 3. Schematic representation of some promising CDG treatments. Even if more treatments are being investigated (for instance for SLC35A2-CDG, CAD-CDG, SLC39A8-CDG or SLC35A1-CDG), only the therapeutic approaches developed within the European EURO-CDG network are illustrated.

2015). More metabolomic analyses of patient material as well as of CDG animal models will help to further elucidate the role of glycosylation in other pathways. This will be of major help in understanding the complex pathophysiology underlying a glycosylation deficiency and in establishing new therapeutic approaches.

2.5. Patients and parents involvement

The parents have been very active in raising awareness for CDG and in helping families. They have also contributed to the commitment of the basic and clinical research community for CDG. At the risk of not being comprehensive and forgetting to honour several organisations that have been active in CDG – and the people that are the drivers behind these associations - we want to name a few that have contributed significantly. First, there have been parents associations in Denmark (Den Danske CDG Forening), in Germany (Glycokids[®]), in Sweden (Svenska CDG-Föreningen) and later associations were founded in Canada (Foundation Glycosylation (the FoG)), France (Les P'tits CDG), the Netherlands (CDG Netherlands), Portugal (Associação Portuguesa CDG, APCDG), Spain (AES CDG), and the UK (CDG UK), who have been very active at the national level. Prior to these, the American CDG Family Network Inc. has organized meetings in association with the EUROGLYCAN, EUROGLYCANET and EURO-CDG networks, a.o. in Leuven (1999) and in Worms (2008).

In 2013, the Portuguese CDG Association has organised in Barcelona the first World Conference on CDG, a gather of patients, parents, policy makers, representatives from industry and scientists. The second and third World Conference took place in Lyon in 2015 and in Leuven in 2017, the latter again in conjunction with EURO-CDG. Reports and videos of these gatherings are available [\(http://www.apcdg.com/](http://www.apcdg.com/)). Thanks to joint programs for parents, clinicians and basic scientists, a strong impetus is given to research in the field of CDG. A very interesting leaflet providing general information on CDG to parents has been developed by clinicians, scientists from the Barcelona Hospital Sant Juan de Déu, together with the parents (see [http://www.euroglycanet.](http://www.euroglycanet.org/uz/digitalAssets/1006_P05-Barcelona-Triptico_CDG.pdf) [org/uz/digitalAssets/1006_P05-Barcelona-Triptico_CDG.pdf\)](http://www.euroglycanet.org/uz/digitalAssets/1006_P05-Barcelona-Triptico_CDG.pdf). Other information is available at the patients' and parents' association websites. For information on 'inclusive education' see <https://www.includ-ed.eu/> , <http://aaate.net/> and [https://www.european-agency.org/.](https://www.european-agency.org/)

3. The future of CDG

3.1. Developments in the diagnostics of CDG: protein-specific glycoprofiling and metabolic labelling as functional diagnostic tools

About 50 genetic glycosylation defects are known that can be screened for by Tf IEF (Jaeken and Péanne, 2017). The identification of novel types of CDG-I, with a defect in the cytosol or endoplasmic reticulum (ER), has been very successful thanks to direct metabolic labeling of cultured CDG patients' cells with radioactive [2-(³H)] mannose (Péanne et al., 2013). Following lipid-linked oligosaccharide (LLO) analysis, the culprit gene could relatively easily be identified thanks to the high level of conservation of the N-glycosylation pathway in the ER between humans and yeast. Next-generation sequencing, via wholeexome sequencing or targeted gene panels, has replaced LLO analysis for gene identification. In combination with clinical phenotyping, an efficient diagnostic protocol for CDG-I subtyping has been achieved. For identification of CDG-II defects, glycan structural analysis by glycomics has been instructive to define genetic defects, such as MGAT2-, SLC35C1-, SLC35A1-, B4GALT1-and MAN1B1-CDG, that are directly associated with enzymes and transporters involved in the Golgi processing of glycans (Jaeken and Péanne, 2017). However, the newer forms of CDG-II with defects in vesicular trafficking and ion homeostasis are clearly more difficult to elucidate. The discovery of a CDG-II patient with COG7 –deficiency increased the awareness of the impact of abnormal trafficking on glycosylation in humans (Reynders et al., 2011;

Wu et al., 2004). Similarly, the identification of mutations in the V-ATPase complex (ATP6V0A2, ATP6V1E1, and ATP6V1A) and in V-A-TPase assembly factors (ATP6AP1, CCDC115 and TMEM199) extended the causes of CDG to intracellular compartmental pH defects (Jansen et al., 2016a, 2016b; Kornak et al., 2008; Van Damme et al., 2017). This is also true for defects in TMEM165 and SLC39A8, two genes that link CDG to deficiency of the trace element manganese (Park et al., 2015; Potelle et al., 2017). These observations suggest that any defect that disturbs the function and organization of the Golgi complex may lead to abnormal glycosylation and thus to CDG. As a result, the number of candidate genes becomes very large. In the majority of cases, glycomics profiling of total serum N-linked glycoproteins does not result in sufficiently specific signatures to directly diagnose the respective CDG-II defects. Since plasma biomarkers are highly relevant and easily accessible for CDG diagnostics and subtyping, future efforts will aim at the development of proteome-wide analysis of glycopeptides to identify protein-specific CDG biomarkers. For example, immunoglobulin glycosylation was shown to be affected in MOGS-CDG, while transferrin remained unaffected (Sadat et al., 2014).

Exome sequencing has greatly facilitated the search for novel genes and is now commonly used in CDG-II diagnostics. On the other hand, disorders like EXT1-and EXT2-CDG, which are not captured by testing for abnormal serum protein glycosylation, indicate that there may be many more monogenic disorders with relevant tissue-specific glycosylation deficiencies. The confirmation of this kind of effect of genetic variants is highly challenging, due to the limited availability of easy read-out systems for visualization and analysis of glycosylation deficiencies in patient material. The advent of bioorthogonal click chemistry with the emergence of metabolic oligosaccharide engineering (MOE) has opened a completely new field of investigation (Ovryn et al., 2017). This extremely powerful strategy allows via a chemical reaction to decipher in living cells a specific metabolic pathway without interfering with it. The available chemical toolbox and the strategies to study glycosylation in normal and pathophysiological conditions are constantly growing. In the field of CDG, the use of two unprotected monosaccharide reporters, namely N-4-pentynoylneuraminic acid (SiaNAl) and N-(4-pentynoyl) mannosamine (ManNAl) has proved to be an effective method to track glycoconjugate sialylation defects (Vanbeselaere et al., 2013; Gilormini et al., 2016). Such labeling strategies, coupled to the use of different azido functionalized fluorescent probes allowed to quantitatively measure the Golgi glycosylation efficiency in CDG patient cells. This assay was successfully applied in COG-, TMEM165-, CCDC115- and TMEM199-CDG patient fibroblasts (Vanbeselaere et al., 2013; Jansen et al., 2016a, 2016b), showing a drastically reduced incorporation of monosaccharide reporters, which was restored upon complementation with wild-type gene. This novel approach will be also facilitate the confirmation of novel CDG-II defects in Golgi homeostasis, as still many Golgi defects are expected to be discovered.

3.2. Beyond genetics: epigenetic studies

Epigenomics or alterations to chromatin (modifications of DNA and histones) can be divided in chromatin marks (individual chemical modifications) and features (multiple linked modifications and more complex elements). Examples of the first are DNA methylations and histone acetylations, and of the latter chromatin interactions, RNA modifications and non-coding RNAs (reviewed in Stricker et al., 2017). A large body of literature documents epigenetic regulation of glycosylation, mostly by showing aberrant glycosylation in cancer. A change in cytosine methylation within the promotor of certain glyco-genes is responsible for the expression of cancer-associated carbohydrate antigens, in gastrointestinal, pancreatic and breast cancer. Other examples of epigenetic regulation of glyco-genes include FUT7 in leukocytes and the transcription factor HNF1A, a master regulator of plasma protein fucosylation (Zoldoš et al., 2013; Lauc et al., 2014). Treatments of cultured cells with epigenetic inhibitors reveal that N-glycome profiles drastically change, which indicates that many glycosylation-related genes are regulated by DNA and histone modifications (Saldova et al., 2011). To the best of our knowledge, there are no clear examples of CDG caused by epigenetic changes, probably because we are not looking for such defects. However, we are quite convinced that epigenetic disorders will become an important CDG chapter.

3.3. In search for novel treatments

The functional characterization of phosphomannomutase 2 (PMM2) disease-causing mutations has suggested that PMM2-CDG could be a conformational disease and that therapies addressed to improve the protein folding would be able to ameliorate the clinical symptoms (Yuste-Checa et al., 2015). From a 10,000 compound library screening, 8 possible pharmacological chaperone (PCs) were selected. The compound 1-(3-chlorophenyl)-3-3-bis(pyridine-2-yl)urea stood out, based on its pharmacochemical properties, the absence of inhibitory effect on PMM enzymatic activity and the improved stability of a number of destabilizing mutant proteins. PMM activity assays were performed with soluble cell extracts from healthy and patient-derived fibroblasts overexpressing wild type PMM2 or PMM2 with the mutations p.Asp65Tyr, p.Pro113Leu, p.Arg162Trp and p.Thr237Met. These results have provided the first proof-of-concept of a possible treatment for PMM2-CDG and identified a promising chemical structure as a starting lead for the development of therapeutic agents against this severe orphan disease (Yuste-Checa et al., 2017). Future clinical trials aim at Dgalactose use in different CDG, liposomal mannose-1-phosphate and chaperone therapy in PMM2-CDG (Fig. 2), and possibly PMM enzyme replacement therapy. However, there are major hurdles for enzyme replacement, because it is difficult to target deficiencies in the cytosol, the endoplasmic reticulum or the Golgi compartment. The finding that GDP-mannose levels are tightly controlled by a feedback loop involving GMPPA (Koehler et al., 2013) opens the possibility that PMM2 defects could be treated by pharmacological intervention aimed at suppressing the inhibition exerted by GMPPA on GMPPB, the catalytic subunit of GDP-mannose pyrophosphorylase.

3.4. CDG reference network

MetabERN is a European non-profit network established by the EU to facilitate access to the best available care and to address the needs of all European patients affected by any rare inherited metabolic disease (IMD) and their families. MetabERN already involves 69 specialized metabolic centers from 19 countries and is continuously growing. It aims to promote prevention, accelerate diagnosis and improve standards of care across Europe for patients with an IMD. It is entirely patient- and expert-led. The 7 subnetworks focus on disorder groups, one of which is disorders of glycosylation and intracellular trafficking. This subnetwork aims at initiating natural history studies and therapeutic trials in different CDG.

3.5. eHealth at the service of the patient

Nanotechnology is invading daily life and this should profit the patients. The CDG patient community as well as the researchers involved in CDG would benefit from the development and use of specific apps for the follow-up of patients. Indeed, CDG is characterized by frequent and often severe clinical events throughout the life of the patients. Examples are seizures, bleeding, infections, but also events like hospitalisation, change of drug treatment, frequency of physical therapy sessions, etc. A detailed, online registration would allow the collection of data necessary for the natural history of the different types of CDG. A mobile tool would be especially welcome, given the extreme genetic heterogeneity of CDG, the broad clinical spectrum and variable symptoms, the rarity of most of the types of the disease and the large

geographical distribution of the patients. The different compounds of the app should be developed in collaboration with clinicians and patients' representatives, and the data collected in accordance with national and international laws on medical records and privacy. The app should be useful to inform caretakers of critical events, and allow rapid clinical action if needed (alert function).

4. Conclusion

CDG are a family of, largely not yet treatable, genetic diseases. Like for all patients, it is of utmost importance to provide the best possible care and support to these patients and their families. These include a well-organized, multidisciplinary medical approach and follow-up, optimal paramedical services (physiotherapy, speech therapy, social service a.o.), regularly updated information (via meetings, letters, social media), and practical help e.g. by specific apps. The patients/families, caregivers, and researchers should form a strong community at the service of the patients. The EURO-CDG initiatives are prominent examples of such collaboration and take the lead in this undertaking. We hope that this survey may contribute to this goal.

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References

- [Barone, R., Carrozzi, M., Parini, R., et al., 2015. A nationwide survey of PMM2-CDG in](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref1) [Italy: high frequency of a mild neurological variant associated with the L32R muta](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref1)[tion. J. Neurol. 262, 154](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref1)–164.
- Cabezas, O.R., Flanagan, S.E., Stanescu, H., et al., 2017. Polycystic kidney disease with hyperinsulinemic hypoglycemia caused by a promoter mutation in phosphomannomutase 2. J. Am. Soc. Nephrol. <http://dx.doi.org/10.1681/ASN.2016121312>.
- [de Koning, T.J., 2013. Amino acid synthesis de](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref3)ficiencies. Handb. Clin. Neurol. 113, 1775–[1783](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref3).
- [de Lonlay, P., Seta, N., Barrot, S., et al., 2001. A broad spectrum of clinical presentations](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref4) [in congenital disorders of glycosylation I: a series of 26 cases. J. Med. Genet. 38,](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref4) 14–[19](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref4).
- [Dörre, K., Olckzak, M., Wada, Y., et al., 2015. A new case of UDP-galactose transporter](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref5) defi[ciency \(SLC35A2-CDG\) : molecular basis, clinical phenotype, and therapeutic](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref5) [approach. J. Inherit. Metab. Dis. 38, 931](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref5)–940.
- [Edvardson, S., Murakami, Y., Nguyen, T.T., et al., 2017. Mutations in the phosphatidy](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref6)[linositol glycan C \(PIGC\) gene are associated with epilepsy and intellectual disability.](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref6) [J. Med. Genet. 54, 196](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref6)–201.
- [Finlayson, S., Palace, J., Belaya, K., et al., 2013. Clinical features of congenital myasthenic](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref7) syndrome due to mutations in DPAGT1[. J. Neurol. Neurosurg. Psychiatry 84,](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref7) 1119–[1125](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref7).
- [Gilormini, P.A., Lion, C., Vicogne, D., et al., 2016. A sequential bioorthogonal dual](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref8) [strategy: ManNAl and SiaNAl as distinct tools to unravel sialic acid metabolic path](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref8)[ways. Chem. Commun. \(Camb\) 52, 2318](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref8)–2321.
- [Jaeken, J., Morava, E., 2016. Congenital disorders of glycosylation, dolichol and glyco](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref9)[sylphosphatidylinositol metabolism. In: Saudubray, J.-M., Baumgartner, M.R.,](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref9) [Walter, J. \(Eds.\), Inborn Metabolic Diseases Diagnosis and Treatment, sixth ed.](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref9) [Springer, Berlin chap 41](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref9).
- Jaeken, J., Péanne, R., 2017. What is new in CDG. J. Inherit. Metab. Dis. [http://dx.doi.](http://dx.doi.org/10.1007/s10545-017-0050-6) [org/10.1007/s10545-017-0050-6.](http://dx.doi.org/10.1007/s10545-017-0050-6)
- [Jansen, J.C., Cirak, S., van Scherpenzeel, M., et al., 2016a. CCDC115 de](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref11)ficiency causes a [disorder of Golgi homeostasis with abnormal protein glycosylation. Am. J. Hum.](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref11) [Genet. 98, 310](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref11)–321.
- Jansen, E.J., Timal, S., Ryan, M., et al., 2016b. ATP6AP1 deficiency causes an immunodeficiency with hepatopathy, cognitive impairment and abnormal protein glycosylation. Nat. Commun. 7, 11600. <http://dx.doi.org/10.1038/ncomms11600>.
- [Janssen, M.C., de Kleine, R.H., van den Berg, A.P., et al., 2014. Successful liver trans](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref13)[plantation and long-term follow-up in a patient with MPI-CDG. Pediatrics 134,](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref13) e279–[e283.](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref13)
- [Kahrizi, K., Hu, C.H., Garshasbi, M., et al., 2011. Next generation sequencing in a family](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref14) [with autosomal recessive Kahrizi syndrome \(OMIM 612713\) reveals a homozygous](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref14) frameshift mutation in SRD5A3[. Eur. J. Hum. Genet. 19, 115](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref14)–117.
- [Kapusta, L., Zucker, N., Frenckel, G., et al., 2013. From discrete dilated cardiomyopathy](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref15) [to successful cardiac transplantation in congenital disorders of glycosylation due to](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref15) dolichol kinase defi[ciency \(DK1-CDG\). Heart Fail. Rev. 18, 187](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref15)–196.
- Kara, B., Ayhan, Ö., Gökçay, G., Başboğaoğlu, [N., Tolun, A., 2014. Adult phenotype and](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref16)

[further phenotypic variability in SRD5A3-CDG. BMC Med. Genet. 15, 10](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref16).

[Koch, J., Mayr, J.A., Alhaddad, B., et al., 2017. CAD mutations and uridine-responsive](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref17) [epileptic encephalopathy. Brain 140 \(Pt2\), 279](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref17)–286.

- [Koehler, K., Malik, M., Mahmood, S., et al., 2013. Mutations in GMPPA cause a glyco](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref18)[sylation disorder characterized by intellectual disability and autonomic dysfunction.](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref18) [Am. J. Hum. Genet. 93, 727](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref18)–734.
- [Kornak, U., Reynders, E., Dimopoulou, A., et al., 2008. Impaired glycosylation and cutis](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref19) [laxa caused by mutations in the vesicular H+-ATPase subunit ATP6V0A2. Nat.](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref19) [Genet. 40, 32](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref19)–34.
- [Lamari, F., Mochel, F., Saudubray, J.-M., 2015. An overview of inborn errors of complex](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref20) [lipid biosynthesis and remodelling. J. Inherit. Metab. Dis. 38, 3](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref20)–18.

Lauc, G., Vojta, A., Zoldoš[, V., 2014. Epigenetic regulation of glycosylation is the](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref21) [quantum mechanics of biology. Biochim. Biophys. Acta 1840, 65](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref21)–70.

[Matalonga, L., Bravo, M., Serra-Peinado, C., et al., 2017. Mutations in TRAPPC11 are](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref22) [associated with a congenital disorder of glycosylation. Hum. Mutat. 38, 148](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref22)–151.

[Monin, M.-L., Mignot, C., De Lonlay, P., et al., 2014. 29 French adult patients with PMM2](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref24) [congenital disorder of glycosylation: outcome of the classical pediatric phenotype](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref24) [and depiction of a late-onset phenotype. Orphanet J. Rare Dis. 9, 207.](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref24)

[Morava, E., 2014. Galactose supplementation in phosphoglucomutase-1 de](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref25)ficiency: re[view and outlook for a novel treatable CDG. Mol. Genet. Metab. 112, 275](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref25)–279.

Morelle, W., Potelle, S., Witters, P., et al., 2017. Galactose supplementation in TMEM165- CDG patients rescues the glycosylation defects. J. Clin. Endocrinol. Metab. [http://dx.](http://dx.doi.org/10.1210/jc.2016-3443) [doi.org/10.1210/jc.2016-3443.](http://dx.doi.org/10.1210/jc.2016-3443)

[Ovryn, B., Li, J., Hong, S., Wu, P., 2017. Visualizing glycans on single cells and tissues.](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref27) [Curr. Opin. Chem. Biol. 39, 39](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref27)–45.

[Park, J.H., Hogrebe, M., Grüneberg, M., et al., 2015. SLC39A8 de](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref28)ficiency: a disorder of [manganese transport and glycosylation. Am. J. Hum. Genet. 97, 894](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref28)–903.

[Péanne, R., Vanbeselaere, J., Vicogne, D., 2013. Assessing ER and Golgi N-glycosylation](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref29) [process using metabolic labeling in mammalian cultured cells. Methods Cell Biol.](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref29) [118, 157](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref29)–176.

[Potelle, S., Dulary, E., Climer, L., et al., 2017. Manganese-induced turnover of TMEM165.](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref30) [Biochem. J. 474, 1481](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref30)–1493.

[Reynders, E., Foulquier, F., Annaert, W., Matthijs, G., 2011. How Golgi glycosylation](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref31) meets and needs traffi[cking: the case of the COG complex. Glycobiology 21, 853](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref31)–863.

[Sadat, M.A., Moir, S., Chun, T.W., et al., 2014. Glycosylation, hypogammaglobulinemia,](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref51) [and resistance to viral infections. N. Engl. J. Med. 370, 1615](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref51)–1625.

[Saldova, R., Dempsey, E., Garay-Perez, M., et al., 2011. 5-AZA-2](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref32)'-deoxycytidine induced demethylation infl[uences N-glycosylation of secreted glycoproteins in ovarian cancer.](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref32) [Epigenetics 6, 1362](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref32)–1372.

[Sassi, A., Lazaroski, S., Wu, G., et al., 2014. Hypomorphic homozygous mutations in](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref33) [phosphoglucomutase 3 \(PGM3\) impair immunity and increase serum IgE levels. J.](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref33) [Allergy Clin. Immunol. 133, 1410](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref33)–1419.

[Schollen, E., Kjaergaard, S., Legius, E., Schwartz, M., Matthijs, G., et al., 2000. Lack of](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref34) [Hardy-Weinberg equilibrium for the most prevalent PMM2 mutation in CDG-Ia](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref34)

[\(congenital disorder of glycosylation type Ia\). Eur. J. Hum. Genet. 8, 367](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref34)–371.

Stray-Pedersen, [A., Backe, P.H., Sorte, H.S., et al., 2014. PGM3 mutations cause a con](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref35)[genital disorder of glycosylation with severe immunode](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref35)ficiency and skeletal dys[plasia. Am. J. Hum. Genet. 95, 96](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref35)–107.

[Stricker, S.H., Köferle, A., Beck, S., 2017. From pro](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref36)files to function in epigenomics. Nat. [Rev. Genet. 18, 51](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref36)–66.

[Tegtmeyer, L.C., Rust, S., van Scherpenzeel, M., et al., 2014. Multiple phenotypes in](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref37) phosphoglucomutase 1 defi[ciency. N. Engl. J. Med. 370, 533](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref37)–542.

Thiesler, C.T., Cajic, S., Hoff[mann, D., 2016. Glycomic characterization of induced](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref38) [pluripotent stem cells derived from a patient su](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref38)ffering from phosphomannomutase 2 [congenital disorder of glycosylation \(PMM2-CDG\). Mol. Cell Proteomics 15,](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref38) 1435–[1452](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref38).

Vals, M.A., Pajusalu, S., Kals, M., Mägi, R., Õunap, K., 2017 Jul 7. The prevalence of PMM2-CDG in Estonia based on population carrier frequencies and diagnosed patients. JIMD Rep. [http://dx.doi.org/10.1007/8904_2017_41.](http://dx.doi.org/10.1007/8904_2017_41) [Epub ahead of print].

[Vanbeselaere, J., Vicogne, D., Matthijs, G., Biot, C., Foulquier, F., Guerardel, Y., 2013.](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref40) [Alkynyl monosaccharide analogues as a tool for evaluating Golgi glycosylation e](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref40)ffi[ciency: application to Congenital Disorders of Glycosylation \(CDG\). Chem. Commun.](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref40) [\(Camb\) 49, 11293](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref40)–11295.

[Van Damme, T., Gardeitchik, T., Mohamed, M., et al., 2017. Mutations in ATP6V1E1 or](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref41) [ATP6V1A cause autosomal-recessive cutis laxa. Am. J. Hum. Genet. 100, 216](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref41)–227.

[Wheeler, P.G., Ng, B.G., Sanford, L., et al., 2016. SRD5A3-CDG: expanding the phenotype](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref42) [of a congenital disorder of glycosylation with emphasis on adult onset features. Am.](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref42) [J. Med. Genet. A 170, 3165](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref42)–3171.

[Wild, M.K., Lühn, K., Marquardt, T., Vestweber, D., 2002. Leukocyte adhesion de](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref43)ficiency [II: therapy and genetic defect. Cells Tissues Organs 172, 161](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref43)–173.

Willems, A.P., Gundogdu, M., Kempers, M.E.J., et al., 2017. Mutations in N-acetylglucosamine (O-GlcNAc) transferase in patients with X-linked intellectual disability. J. Biol. Chem. <http://dx.doi.org/10.1074/jbc.M117.790097>.

Wong, S.Y., Gadomski, T., van Scherpenzeel, M., et al., 2017. Oral D-galactose supplementation in PGM1-CDG. Genet. Med. [http://dx.doi.org/10.1038/gim.2017.41.](http://dx.doi.org/10.1038/gim.2017.41)

[Wu, X., Steet, R.A., Bohorov, O., et al., 2004. Mutation of the COG complex subunit gene](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref46) [COG7 causes a lethal congenital disorder. Nat. Med. 10, 518](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref46)–523.

[Yuste-Checa, P., Gámez, A., Brasil, S., et al., 2015. The e](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref47)ffects of PMM2-CDG-causing [mutations on the folding, activity, and stability of the PMM2 protein. Hum. Mut. 36,](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref47) 851–[860](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref47).

- [Yuste-Checa, P., Brasil, S., Gámez, A., et al., 2017. Pharmacological chaperoning: a po](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref48)[tential treatment for PMM2-CDG. Hum. Mut. 38, 160](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref48)–168.
- [Zhang, Y., Yu, X., Ichikawa, M., et al., 2014. Autosomal recessive phosphoglucomutase 3](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref49) [\(PGM3\) mutations link glycosylation defects to atopy, immune de](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref49)ficiency, auto[immunity, and neurocognitive impairment. J. Allergy Clin. Immunol. 133,](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref49) 1400–[1409](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref49).
- Zoldoš, V., Novokmet, M., Beč[cheli, I., 2013. Genomics and epigenomics of the human](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref50) [glycome. Glycoconj. J. 30, 41](http://refhub.elsevier.com/S1769-7212(17)30494-9/sref50)–50.