O-glycosylation disorders pave the road for understanding the complex human O-glycosylation machinery
Walinka van Toi¹,², Hans Wessels² and Dirk J Lefeber¹,²

Over 100 human Congenital Disorders of Glycosylation (CDG) have been described. Of these, about 30% reside in the O-glycosylation pathway. O-glycosylation disorders are characterized by a high phenotypic variability, reflecting the large diversity of O-glycan structures. In contrast to N-glycosylation disorders, a generic biochemical screening test is lacking, which limits the identification of novel O-glycosylation disorders. The emergence of next generation sequencing (NGS) and O-glycoproteomics technologies have changed this situation, resulting in significant progress to link disease phenotypes with underlying biochemical mechanisms. Here, we review the current knowledge on O-glycosylation disorders, and discuss the biochemical lessons that we can learn on 1) novel glycosyltransferases and metabolic pathways, 2) tissue-specific O-glycosylation mechanisms, 3) O-glycosylation targets and 4) structure-function relationships. Additionally, we provide an outlook on how genetic disorders, O-glycoproteomics and biochemical methods can be combined to answer fundamental questions regarding O-glycan synthesis, structure and function.

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Introduction
Glycosylation, the addition of carbohydrate chains to proteins, is the most common post-translational and co-translational modification. It is initiated by the cytosolic synthesis of activated sugars (with the exception of CMP-N-acetylneuraminic acid) that are subsequently transported to the endoplasmic reticulum (ER) and Golgi apparatus, where glycans are assembled and modified on proteins. Glycosylation affects many aspects of protein function, including protein folding, enzyme activity and cell-to-cell and cell-to-extracellular matrix (ECM) interactions. Therefore, it is not surprising that glycosylation disorders present with a broad range of clinical phenotypes.

Currently, over 100 different Congenital Disorders of Glycosylation (CDG) have been described [1,2], the majority affecting the N-glycosylation pathway. Broad availability of an adequate screening assay for abnormal N-glycosylation, isofocusing of serum transferrin (TIEF), has resulted in the identification of defects in glycosyltransferases, nucleotide sugar transporters and enzymes involved in sugar metabolism, which are all directly linked to glycosylation. In recent years, more complex mechanisms have been identified underlying abnormal N-glycosylation related to Golgi trafficking, homeostasis and vesicular transport [3,4,5].

In contrast to N-glycosylation defects, the identification of O-glycosylation disorders is much more challenging. In humans, O-glycans are initiated by seven different monosaccharides that can be further extended to complex O-glycan structures. For mucin O-glycosylation (O-linked N-acetylgalactosamine, O-GalNAc), the most common form of O-glycosylation, over 20 polypeptide GalNAc transferases are known with tissue and substrate-specific activities [6,7]. Isofocusing of ApoC-III was developed to detect defects in mucin type O-glycosylation [8]. Although many of the Golgi homeostasis disorders showed abnormal mucin type O-glycosylation of ApoC-III, only mutations in polypeptide GalNAc transferase 2 (GALNT2) could be detected with this test. So far, the complexity of O-glycan structures renders it impossible to design a single screening test for diagnostics of O-glycosylation disorders.

O-glycans are important for protein structure, folding, stability, recognition, expression, and processing, and they are known to modulate enzyme activity [9,10,11,12–15]. Furthermore, highly negatively charged O-mucin glycans can bind water, forming protective layers and preventing bacterial adhesion [16]. The function of an O-glycan can be tissue, protein, and site-specific, alongside mediating different functions throughout development [17]. That, O-glycans play not only
important, but also complex roles, is illustrated by the vast amount of O-glycan enzymes that upon knockout, caused embryonic lethality or tissue-specific phenotypes in mice [18,19]. Mice knockout systems have provided invaluable lessons about O-glycan function, for example, the role of O-fucosylation of thrombospondin type 1 repeats (TSRs) by POFUT2 in epithelial organization and expression of signaling factors during gastrulation [20].

In humans, a more complete understanding of the human O-glycosylation machinery can be accomplished by studying genetic defects in O-glycosylation. Identification of an increasing number of genetic O-glycosylation disorders has been facilitated by the emergence of next generation sequencing (NGS) [2]. Furthermore, recent developments in glycopeptide analysis revealed previously unidentified O-glycosylation enzymes and their targets, which can be linked to disease. 3D structural models of human glycosyltransferases are rare, especially since these types of proteins are embedded in the membrane of the ER and Golgi apparatus making crystallization extremely daunting. However, in recent years, some structures have been resolved and modeled. Taken together, new opportunities arise to link findings from genetic disease with fundamental research to increase our understanding of the mechanisms of O-glycosylation. In this review, we illustrate the importance of inherited O-glycosylation disorders to elucidate the structural aspects of the O-glycosylation machinery (Figure 1). Glososaminoglycan biosynthesis disorders are not discussed and have been described in great detail by others [21]. For elaborate descriptions of O-glycosylation disorder phenotypes, we recommend the reviews of Wopereis et al. [22], Hennet [21] and Jaecken and Péanne [3].

**O-glycosylation disorders: current status and screening methods**

Most of the currently known O-glycosylation disorders have been identified through genetic techniques. The clinical phenotypes are highly variable, which is linked to the large number of different O-glycan types. O-glycosylation defects have now been identified for each type of O-glycan, and an overview of the known O-glycosylation disorders is provided in Figure 1 and Table 1. Thus far, assays for functional validation of mutations are largely lacking, except for the dystroglycanopathies. This is a group of disorders affecting the α-mannosyl glycan on the α-dystroglycan (αDG) protein that is essential for binding to extracellular matrix components (Table 1; α-mannose). Functional confirmation of α-mannosylation defects is possible by histochemical detection of the α-mannosyl glycan of αDG in muscle biopsies [23]. Together with NGS of patients, this has resulted in the identification of novel Golgi glycosyltransferases, while mass spectrometry of recombinant αDG has recently resolved the complete α-mannose glycan structure [24,25,26].

Thus, together with NGS, functional tests are highly warranted for a more rapid identification of inherited O-glycosylation disorders, and to increase our understanding of O-glycosylation mechanisms. O-glycomics, the profiling of the complete set of glycans produced by specific cell types, offers potential as a generic functional test. Methods have been developed for the comparative analysis of O-glycans from complex samples [27–30]. Unfortunately, O-glycomics has thus far not contributed to the functional confirmation of O-glycosylation disorders. This can be explained by the fact that O-glycosylation is highly dependent on the specific attachment site, and O-glycans do not have a general consensus sequence with the exception of O-fucose glycans (C2X5,3S/TC3 and WX3CX2S/TCX2G; C = conserved cysteines of epidermal growth factor (EGF)-like or TSRs, S/T = serine or threonine, X = any residue) and O-gucose glycans (C1XSXPC2). Therefore, it is essential to study O-glycan structures in their protein context. Identification of aberrant O-glycopeptides by direct LC–MS/MS analysis of intact O-glycopeptides in patient samples or model systems would be preferred, thus providing a complete overview of the affected O-glycans and O-glycosylation sites. Despite the challenges in the field of O-glycoproteomics (reviewed in Ref. [31]), first studies have demonstrated the potential of LC–MS/MS for holistic O-glycopeptide profiling. In 2016, Hoffmann et al. [32] analyzed intact O-glycopeptides in human blood plasma in an untargeted fashion by analyzing HILIC enriched and fractionated glycopeptides by reversed phase LC–MS/MS using multistage collision induced dissociation (CID) and electron transfer dissociation (ETD) fragmentation experiments. In total, 31 O-GalNAc sites and regions from 22 proteins were identified, which included 11 novel O-glycosylation sites and regions. More recently, King et al. [33] performed high collision energy dissociation (HCD) and ETD LC–MS/MS analysis of de-sialylated glycopeptides purified by lectin chromatography from AB RhD-positive platelets and blood plasma. Their analysis detected 1123 O-GalNAc sites from 649 glycoproteins, which not only provided novel biological insights but above all demonstrated the feasibility of holistic O-glycoproteomics.

Although functional tests still need to be developed, the O-glycosylation disorders that have been identified have aided structural biology in a number of ways. Despite the fact that O-glycan disorders are very heterogeneous, patients generally show tissue-specific phenotypes, hinting toward tissue-specific O-glycan targets and function. Studying O-glycosylation disorders has 1) led to the discovery of new glycosyltransferases and metabolic pathways, 2) provided insight in tissue-specific glycosylation pathways, 3) aided in the discovery of O-glycosylation targets and 4) elucidated structure-function relations of O-glycosyltransferases and nucleotidyltransferases (Figure 1). Below, we will provide recent examples of
Mechanistic insights from human O-glycosylation disorders

Characterization of O-glycosylation disorders is indispensable to accomplish a better understanding of the human O-glycosylation mechanisms. Phenotypic heterogeneity of the O-glycosylation disorders reflects the high diversity of O-glycan structures with a high tissue-specificity. Phenotypic characterization and modern omics techniques such as genomics, glycomics, and glycoproteomics complement each other in the
each type of discovery in the O-glycosylation field, covering the majority of the O-glycosylation disorder core types.

**Discovery of new glycosyltransferases and metabolic pathways**

Firstly, genetic defects in O-glycosylation with a characteristic phenotype have aided the discovery of new O-glycosylation gene candidates. For example, NGS has resulted in the identification of new genes causing dystroglycanopathy that is characterized by muscular dystrophy and, in severely affected individuals, eye and brain abnormalities. Dystroglycanopathies are caused by defective O-mannosylation of αDG, leading to aberrant cell-to-ECM connections. Genetic analysis of patients with dystroglycanopathy features has revealed mutations in *ISPD* (CRPPA), *FKTN* and *TMEM5(RXYLT1)* [34–37] (Table 1; O-mannose). The function of these proteins has been elucidated in the last three years [24,26*,38,39,40]. Identification of ISPD as a cytosolic ecdysyne transferase even led to the discovery of a new mammalian nucleotide sugar: CDP-ribitol [38]. Soon after, FKTN and FKRP were identified as ribitol 5-phosphate (Rbo5P) glycosyltransferases, and Rbo5P moieties were detected on the functional O-mannosyl glycan of αDG [24,26*,39*]. TMEM5 was identified as a B1,4-xyllosyltransferase, adding xylose onto the second Rbo5P of unique O-mannosyl glycans on αDG [24,40]. Subsequently, mass spectrometry of genetically engineered αDG led to the discovery of glycopolysaccharide (Gro3P) on the glycan, indicating the existence of a CDP-glycerol biosynthesis pathway [25*]. This was further supported by the finding that FKRPs and FKTN can use CDP-glycerol as substrates for glycosylation [41*]. If CDP-glycerol and Gro3P have a regulatory role in O-mannosyl glycan extension remains to be investigated [25*]. An interesting observation is that these findings on αDG show high overlap with the wall teichoic acids in gram-positive bacteria, that contain repeating units of Rbo5P and Gro3P [42]. The O-mannosylation disorders are a classical example of how we learn about novel mechanisms and even completely new human metabolic pathways, initiated by genetic screening of patients with distinct O-glycosylation disorder phenotypes.

**O-glycosylation disorders can provide insight in tissue-specific pathways**

Secondly, the phenotypes associated with O-glycosylation disorders can provide important insights about tissue-specific glycosylation mechanisms. This is nicely illustrated by *POFUT1* (Table 1; O-fucose) and *POGLUT1* (Table 1; O-glucose) deficiency, both resulting in Dowling-Degos disease. The shared phenotype, characterized by reticular pigmentation of the skin [43,44], indicates a similar underlying pathomechanism. Indeed, both enzymes are involved in the regulation of Notch signaling; however, by the addition of different glycan types. *POFUT1* stabilizes EGF-like repeats by the addition of O-fucose glycans, and *POGLUT1* through the addition of O-glucose glycans [11*]. Interestingly, *POGLUT1* also shows O-xyllosyltransferase activity, but the function of O-xylene on EGF-like domains remains to be investigated [45,46*]. The O-fucose glycan initiated by POFUT1 is extended with N-acetylgalactosamine (GlcNAc) by LNFG [reviewed in Ref. 47]. Interestingly, LNFG patients present with a completely different phenotype of vertebral malformation, spondylolisthesis (DDO) [48,49]. This phenotype is also associated with defects in Notch signaling, and other types of DDO are all caused by defects in proteins involved in Notch1 signaling [50]. Another recent article reports that the *POGLUT1* D233E mutation causes muscular dystrophy [51]. Investigating other POGLUT1 targets could shed light on the mechanisms underlying the different phenotypes. The different phenotypes for *POFUT1* and *POGLUT1* deficiency provide opportunities to investigate tissue-specific targets and O-glycosylation mechanisms.

**Patient phenotypes aid in the identification of O-glycosylation targets**

The phenotype of some O-glycosylation deficiencies resembles the phenotype of genetic defects in potential target proteins. Hence, phenotypic characterizations can point to potential glycosylation targets. For instance, mutations in *FGF23* cause familial tumoral calcinosis paired with increased re-adsorption of phosphate by the renal proximal tubule. Interestingly, patients carrying mutations in the polypeptide GalNAc transferase *GALT3* present with exactly the same phenotype [52–57] (Table 1; O-GalNAc), suggesting a shared mechanism of disease. Indeed, Kato et al. [13] demonstrated that the phosphatinon FGF23 is O-glycosylated at Thr178 by *GALT3*, preventing the furin protease cleavage of FGF23 and regulating phosphate re-absorption [13]. There are over 20 polypeptide GalNAc transferases. Some share substrate specificities and have overlapping expression in different tissues [6,7]. Nevertheless, O-GalNAc glycosylation of FGF23 seems a non-redundant function of *GALT3* [13]. Despite the large number of *GALT3s*, only *GALT3* and *GALT2* deficiency have been reported. Khetarpal et al. showed that loss of function of *GALT2* lowered high-density lipoprotein
cholesterol (HDL-C) levels in human, mice, rats and cynomolgus monkeys. GALNT2 exhibited species-specific glycosylation targets, including PLTP, a regulator of HDL metabolism in plasma [58]. PLTP activity was altered by absence of GALNT2 O-GalNAc modifications, explaining the findings in GALNT2 patients. The involvement of additional GALNT2 targets in the disease phenotype remains to be investigated.

Likewise, mutations in OGT (O-GlcNAc-transferase) and HCF1 (host cell factor 1, a transcriptional regulator of the cell cycle) cause similar intellectual disability (ID) phenotypes [59,60,61,62] (Table 1: O-GlcNAc). OGT is a unique O-GlcNAc transferase that modifies nucleocytoplasmic proteins, a process that can be reversed by OGA (O-GlcNAcase) [63–65]. All five patient mutations that have been described so far reside in the N-terminal tetratricopeptide (TPR) repeats of OGT, which are involved in the substrate recognition and specificity of OGT [66]. OGT patient-derived cells and model cell lines with patient mutations showed normal O-GlcNAcylation [59,60,62]. This homeostasis was suggested to be maintained by a reduced expression of OGA [59,60] or by temporal dynamics in O-GlcNAcylation kinetics [62]. In addition, OGT is involved in proteolytic maturation of HCF1 [14,67], and it has been suggested that the

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Table 1

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Table 2

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O-Glucose

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EGF-like domain fucosylation

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EGF-like domain fucosylation

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Genetics, ELISA of properdin serum levels

X-linked ID in some OGT patients is linked to insufficient activated HCF1 [60*]. Taken together, it is plausible that ID genes are regulated or glycosylated by OGT, and this should be addressed in further studies for a better understanding of the disease mechanisms.

For a long time, POMT1 and POMT2 were believed to be the only human O-mannosyltransferases. In 2017, glycoproteomics in HEK293 knock-out cells revealed that the O-mannosylation of cadherins and protocadherins is independent of these two enzymes [68]. Using a similar approach, four new O-mannosyltransferases were identified. TMTC1-4, which specifically glycosylate cadherins and protocadherins, and thus have different targets than the POMT1/POMT2 glycosyltransferases (Table 1: O-mannose) [68,69**]. Interestingly, patients with TMTC2 and TMTC3 mutations have very different phenotypes. TMTC3 mutations are associated with lissencephaly (6 families, 9 patients) and periventricular nodular heterotopia with ID and epilepsy (three siblings) [70,71]. Both phenotypes are associated with deficient neuronal migration. TMTC2 deficiency is associated with sensorineural hearing loss [72,73], suggesting that the TMTCs have different, tissue-specific targets. Mutations in Cadherin-23 and Protocadherin-15 cause Usher syndrome, which is characterized by deafness and blindness, and can cause non-syndromic recessive hearing loss [74–76]. Hence, it is tempting to speculate that TMTC2 is involved in the O-mannosylation of these proteins. However, direct demonstration of enzyme activity of the TMTCs is still lacking and whether the TMTC3 and TMTC2 disease phenotypes are directly related to

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<td>WWS, MEB, LGMD, non-syndromic retinitis pigmentosa</td>
<td>Muscle, brain, eye, heart</td>
<td>Genetics, IIH6/VIA4-I on muscle biopsy, O-Man β-1,2 GlcNAc-transferase activity assay</td>
</tr>
<tr>
<td>TMTC3**</td>
<td>Putative O-mannosyltransferase</td>
<td>617218</td>
<td>Cobblestone lissencephaly</td>
<td>Brain, minimal muscle and eye involvement</td>
<td>Genetics</td>
</tr>
<tr>
<td>TMTC2**</td>
<td>Putative O-mannosyltransferase</td>
<td>615856</td>
<td>Periventricular nodular heterotopia</td>
<td>Cochlea or auditory nerve</td>
<td>Genetics</td>
</tr>
</tbody>
</table>
hypomannosylation of cadherins, protocadherins or other proteins remains to be investigated.

Finally, B3GLCT deficiency leads to Peter’s Plus syndrome, a severe disorder characterized by anterior eye chamber defects (Table 1: O-fucose). B3GLCT attaches glucose via a β-1,3 linkage to O-fucose (synthesized by POFUT2) on TSRs of proteins. In search for B3GLCT targets linked to the eye defects, Dubail et al. [77] found that ADAMTS9 haploinsufficient mice showed a similar eye phenotype [77]. Glycosylation with glucose-β-1,3-fucose by POFUT2 and B3GLCT ensures proper secretion of ADAMTS9 during development. Taken together, the identification of new genetic O-glycosylation disorders can provide important insights about the targets and functions of specific O-glycans.

**Modeling mutations to study structure-function relations of O-glycosylation proteins**

In the last few years, crystal structures have been solved of enzymes related to O-glycosylation disorders, for example of OGT [78], POMK [79], POMGNT1 [80] and ISPD [38]. Known disease-causing mutations can be modeled in 3D structures, helping to understand the function of specific enzymatic domains and with it, underlying disease mechanisms. For example, the crystal structure of ISPD revealed a N-terminal cytidylytransferase domain and a C-terminal domain connected via a linker helix [38]. Surprisingly, the C-terminal domain did not share homology with any known enzyme domains. No missense mutations have been reported in the C-terminal domain, but the c.1114_1116del (p.Val372del) mutation is reported for five patients. The absence of the Val residue leads to relatively mild phenotype (LGMD) compared to larger deletions like a deletion of exon 6–8 or 9–10 (WWS). Taken together, this demonstrates that the C-terminal domain is important for ISPD function, either contributing to the stability of the enzyme, or having a enzymatic function on its own [38], a question that so far remains unanswered. For POMGNT1, one study has reported a correlation between mutations closer to the 5’ end of the gene with more severe hydrocephalus than mutations near the 3’ end. However, correlations with enzymatic activity or structure have not been established yet [81]. Taken together, much work remains to elucidate the 3D structure of many O-glycosylation enzymes. However, if such models are accomplished, structure-function relationships can be studied utilizing described O-glycosylation patient mutations. Additionally, this will lead to a better understanding of disease mechanisms, and will hopefully be accompanied by the emergence of new treatment opportunities.

**Conclusions**

We illustrated that studying the complex phenotypes of O-glycosylation disorders has enabled the elucidation of O-glycosylation proteins, targets, and O-glycan structure and function. Nevertheless, many questions remain to be answered about the O-glycosylation machinery. Although we know in many diseases which O-glycan core structure is affected, for most, their exact attachment site and tissue-specific protein targets remain to be elucidated. In the future, the development of more advanced O-glycopeptide profiling methods is essential to facilitate these discoveries. Ideally, untargeted O-glycoproteomics LC–MS/MS technology will evolve to enable robust high-throughput analysis for the in-depth characterization of intact O-glycopeptides in biological samples. The screening of patient groups with similar clinical presentations or with different genetic O-glycosylation defects (e.g. in different GALNT3) with genomics and O-glycoproteomics will lead to the discovery of glycosylation genes and tissue-specific targets, respectively. As illustrated in this review, comparing the phenotypes of other known disorders to the phenotype of O-glycosylation disorders can hint to the respective targets.

So far, most O-glycosylation defects that have been identified affect the core sugar of O-glycans. In the last few years, NGS has been applied more frequently, and probably will lead to the identification of additional disorders that affect more distal monosaccharides on O-glycan structures. Functional validation of these disorders will require developments in the glycoproteomics field, since large scale in-depth characterization of the exact glycan structure of intact glycopeptides is still challenging. Furthermore, it is important to develop *in-silico* approaches to identify differential O-glycopeptides and interpret complex glycobiology by novel bioinformatic approaches. Combined analysis of O-glycopeptide data and patient meta data by machine learning is of particular interest to associate protein specific O-glycosylation changes to the physiopathology of O-glycosylation disorders. Taken together, understanding the disease mechanisms of the O-glycosylation disorders will contribute to our understanding of O-glycosylation mechanisms, while versa, new mechanistic insights are highly warranted to develop new therapeutic strategies.

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**Conflict of interest statement**

Nothing declared.

**References and recommended reading**

Papers of particular interest, published within the period of review, have been highlighted as:

- of special interest
- of outstanding interest


This review highlights recently discovered CDG. The authors also give a complete overview of all currently known CDG and their phenotypes.


Using HEK293T cells, the authors demonstrate that Notch1 expression is dependent on PQG1UT1 and POFUT1 expression. Subsequently, they show that O-fucose and O-glucose glycans added by these enzymes stabilize EGFR repeats in an additive manner. Finally, they solve the crystal structure of an EGF repeat with O-glucose. This is the first paper comparing the function of O-fucose and O-glucose glycans in human Notch trafficking.


This review summarizes the glycosylation genes that are not only necessary for mouse embryonic development, but also for pathway-specific glycosylation genes, of which deletion causes a much milder phenotype. Stanley points the lessons that we have learned from these mouse models and also discusses general strategies for generating and interpreting the phenotype of mice in relation to human CDG.


Using nano-LC-MS/MS analysis of glycopeptides of a recombinant α-dystroglycan protein expressed in HCT116 colon cancer cells, the authors compare the glycan structure of the functionalα-mannosylglycan in different knockout cells. They confirm the functions of ISPD, FKTN, and FKRP in CDP-ribitol synthesis and RbsP5 transfer. Interestingly, TME5 was also required for RbsP5 transfer. In addition, this is the first paper demonstrating glycerol phosphate moiety on α-dystroglycan.


This was the first paper that demonstrated the presence of RbsP5 moieties on the functionalα-mannosyl glycan of the α-dystroglycan protein using MALDI-TOF mass spectrometry. Major finding of this paper is that FKTN and FKRP, that were long known to cause dystroglycanopathy when mutated, are the Golgi transferences adding RbsP5 to this glycan.


The authors applied a more holistic O-glycoproteomic approach of blood plasma proteins to analyze site-specific glycosylation with short mucin-type core-1 and core-2 O-glycans. They identified 31 O-glycosylation sites and regions belonging to 22 glycoproteins.


This study identified the largest O-glycoproteome from native tissue so far. The authors used human plasma, platelets and endothelial cells, demonstrating 1123 O-glycosylated sites on 649 glycoproteins. Interestingly, they found that many O-glycans were located close to proteolytic cleavage sites. This was confirmed with in vitro peptide assays where cleavage of proteins was inhibited by the presence of O-glycans.


This paper demonstrated for the first time the presence of CDP-ribitol in mammalian cells and tissues. Furthermore, ribitol supplementation in mice caused this metabolism to increase. Interestingly, in fibroblasts of some ISPD patients the-O-glycosylation of α-dystroglycan could be restored, proposing ribitol as a potential therapy for ISPD dystroglycanopathy.


The authors demonstrated within vitro enzyme reactions that CDP-lygrolcerol can be used as a substrate by the transferases FKTN and FRKP. The addition of glycerol 3P to the O-mannosyl glycan on α-dystroglycan inhibited the further extension toward a completely functional glycan. In addition, CDP-lygrolcerol inhibits the transfer of RboSP from CDP-ribitol by FKTN in vitro. How CDP-lygrolcerol is synthesized in mammalian cells remains unclear. In addition, the question remains whether glycerol 3P moieties on the glycan have a regulatory function in healthy cells.


The structure of human POGLUT1 in complex with three different EGFR-like domains is reported. The structures of the substrate and product complexes show the mechanisms of how local conformational states are likely responsible for the ability of POGLUT1 to transfer both glucose and xylose to serine residues on EGFR-domains. This study demonstrated how the structure of glycosyltransferases can shed light on the substrate specificity and glycosylation mechanisms.


Here, pholipid unaffected, rodents showed that processing the O-linked beta-N-acetylglucosaminyl (O-GlcNAc) transferase gene that segregates with X-linked intellectual disability. J Biol Chem 2017, 292:6948-6963.

This paper is describing a L254F mutation in O-GlcNAc transferase (OGT), leading to X-linked intellectual disability (XLID). Interestingly, in cells from these patients, a decrease in steady-state OGT protein levels was observed but steady-state global O-GlcNAc levels were not altered, and the decrease in OGT activity was compensated by decreased O-GlcNAcase (OGA) promoter activity. The mutation did not affect the capability of OGT to splice HCF1. However, the authors do demonstrate that the L254F mutation in OGT affects the expression of a subset of genes, including ones linked to intellectual disability, suggesting this as the underlying disease mechanism.


Here, two other mutations in human OGT are described to XLID. OGT and OGA levels were slightly reduced and global O-GlcNAc levels were unaffected, as was also independently demonstrated by Vaidyabhanth et al. [59] in cells from another patient. Recombinant OGT with the p.Arg84Pro mutation had reduced glycosylation activity and showed reduced proteolytic processing of the HFC1 protein. The reduced processing of HFC1 is suggested to be part of the underlying disease mechanism.


Here, two novel mutations in OGT are identified. All known mutations of OGT were engineered into a human embryonic stem cell line using CRISPR/Cas9. In these cells, O-GlcNAc, OGT, and OGA levels were unaltered when assessed using western blot, analyses of the differential transcriptomes of the OGT variant-expressing stem cells showed that genes involved in cell fate determination and liver X receptor (retinoid X receptor) signaling were deregulated, potentially contributing to the clinical phenotypes of OGT patients.


The authors apply O-glycosyproteomics approach on “SimpleCells”. HEK239 with knockout of COSMC and POMGNT1 that have truncated O-GalNAc and O-mannose glycans. Additional knockout of POMT1/2 or a combination of POMT1-2 and the TMC1-4 showed that the TMCs are putative protein O-mannosyltransferases of specifically cadherins and proteoglycans. This clearly shows how O-glycosylation can be used to study the function of putative glycosyltransferases. The underlying disease mechanisms of TMC2 and TMC3 deficiency should be further explored.


The authors aim to investigate the underlying disease mechanism of Peters Plus Syndrome caused by mutations in B3GLCT. Their mouse model with Adamts9 haploinsufficiency demonstrated congenital corneal opacity and Peters anomaly. Mass spectrometry of recombinant B3GLCT expressed in HEK293F cells demonstrated that TSSR of ADAMTS9 carry the glucose1-1fucosse disaccharide. Secretion of ADAMTS9 was reduced upon B3GLCT knockdown, proposing this as the underlying disease mechanism of Peters anomaly.

