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Glycoconjugates: Synthesis, Functional Studies, and Therapeutic Developments

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Abstract

Glycoconjugates are major constituents of mammalian cells that are formed *via* covalent conjugation of carbohydrates to other biomolecules like proteins and lipids and often are expressed on the cell surfaces. Among the three major classes of glycoconjugates, proteoglycans and glycoproteins contain glycans linked to the protein backbone *via* amino acid residues such as Asn for *N*-linked glycans and Ser/Thr for *O*-linked glycans. In glycolipids, glycans are linked to a lipid component such as glycerol, polyisoprenyl pyrophosphate, fatty acid ester, or sphingolipid. Recently, glycoconjugates have become better structurally defined and biosynthetically understood, especially those associated with human diseases, and are accessible to new drug, diagnostic, and therapeutic developments. This review describes the status and new advances in the biological study and therapeutic application of natural and synthetic glycoconjugates, including proteoglycans, glycoproteins, and glycolipids. The scope, limitations, and novel methodologies in the synthesis and clinical development of glycoconjugates including vaccines, glyco-remodeled antibodies, glycan-based adjuvants, glycan-specific receptor-mediated drug delivery platforms, *etc.*, and their future prospectus are discussed.

Graphical Abstract

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1. INTRODUCTION

1.1. Glycoconjugates in Biological Systems

Carbohydrates are often attached to proteins or lipids to form glycoproteins or glycolipids on the cell surfaces.^{1–3} Because of their structural heterogeneity and functional complexity, the roles of glycans in biology have historically been underexplored compared with other biomolecules.^{4,5} Carbohydrates can be conjugated to proteins or lipids to form the adduct as glycoprotein bearing *N*-/*O*-linked phosphorylated glycans, glycosaminoglycans (GAGs), and glycosylphosphatidylinositol (GPI) anchors, or as glycolipid such as glycosphingolipids (GSLs) (Figure 1).^{3,5–8} Oligosaccharides are formed by linking one sugar unit to another *via* a glycosidic bond between the hydroxyl group of one sugar and the anomeric carbon of another in *a* or β stereochemistry that led to tremendous diversity.⁹ In addition, each monosaccharide can be linked at any of the several positions with another monosaccharide, allowing for a staggering variety in connectivity and branching. Finally, the glycans can be further modified, for example, through selective oxidation, acetylation, phosphorylation, and sulfation, which greatly expand the diversity and complexity, to generate biological information that is read out by receptors on other cells.^{10–12}

Protein glycosylation begins in the endoplasmic reticulum (ER) and Golgi apparatus, while the final processing occurs in the cis-, medial-, and trans-Golgi compartments.^{8,13} During the synthesis of *N*-glycoprotein, an oligosaccharide is first assembled on dolichol pyrophosphate (Dol-PP) then transferred to the Asn residue of a Asn-X-Ser/Thr sequon where the X residue is not proline, or to the aromatic sequon (Phe/Trp-X-Asn-X-Ser/Thr).¹⁴

Next, the enzymatic processing of *N*-glycans by differentially expressed glycosidases and glycosyltransferases (GTs) occur in the ER and Golgi.¹³ This glycosylation process is very complex and cell-dependent, so the *N*-glycans of a mature glycoprotein expressed in different cells are very heterogeneous and have different patterns and compositions. The *O*-glycosylation process begins in the late ER or early Golgi that also produces heterogeneous glycoforms with an enormous structural complexity.¹⁵ Most of the *O*-glycoproteins carry glycans initiated by *N*-acetylglucosamine (GlcNAc) or *N*-acetyl galactosamine (GalNAc) linked to Ser or Thr residue.^{16,17} Mucins are the glycoproteins carrying numbers of *O*-GalNAc glycans, known as mucin-type *O*-glycans. The *O*-GalNAc glycans generally consist of GalNAc, galactose (Gal), GlcNAc, fucose (Fuc), and sialic acid (Neu5Ac), whereas mannose (Man), glucose (Glc), or xylose (Xyl) residue is not present.¹⁸ Sialic acid may be further modified by *O*-acetylation, and oxidation at the *N*-acetyl group to the glycolyl group, and sulfation can occur on Gal and GlcNAc residues.¹⁹ *O*-GalNAc glycans may vary in length from a single GalNAc to more than 20 sugar residues including blood group and other glycan epitopes.²⁰

GAGs are *O*-linked glycans with huge structural diversity.²¹ Proteoglycans contain chains of GAGs linked to a serine residue of proteins through the glucuronic acid (GlcA) containing tetrasaccharide (GlcA) β 1–3Gal β 1–3Gal β 1–4Xyl, except for keratan sulfate, which is linked to *N*- and *O*-glycans. GAGs are longer polysaccharides containing repeating units of the disaccharide with GalNAc or GlcNAc linked to GlcA or Gal.²² Based on the structure of the disaccharide, GAGs are subdivided into three types: (a) dermatan sulfate (DS) and chondroitin sulfate (CS) (GlcA-GalNAc), (b) heparin/heparan sulfate (HS) (GlcA-GlcNAc), and (c) keratan sulfate (KS) (Gal-GlcNAc).²³ In DS and heparin/HS, GlcA can be present as the epimerized form of iduronic acid. The additional heterogeneity of GAGs arises from variable *O*-sulfations, including, for example, uniform sulfation in heparin or specific sulfation in heparin sulfate (HS). Deacetylation and *N*-sulfation of GlcNAc can also occur in heparin or HS.²⁴

GSLs are a subclass of glycolipids, consisting of carbohydrate moieties linked to the 1hydroxyl group of a ceramide backbone *via* a β -linkage.²⁵ GSLs are ubiquitously embedded in the cell plasma membrane. The astonishing structural diversity of GSLs arises from linking hundreds of different glycan heads to tens of different ceramide chains, which are responsible for various biological activities, like regulation of cell growth, differentiation, and signaling.²⁶ Among mammalian GSLs, 90% of GSLs are derived from glucosyl ceramide (GlcCer) and the rest are from galactosyl ceramide (GalCer). The GalCer series GSLs are composed of GalCer itself, 3-*O*-sulfate ester, sulfatide (sulfogalactosyl ceramide), and galabiosyl ceramide. The GlcCer series GSLs are further subclassified into gangliosides (GalNAc- β 1,4-Gal), globosides (Gal- β 1,4-Gal), lactosides (Gal- β 1,3-GlcNAc- β 1,3-Gal), and neolacto (Gal- β 1,4-GlcNAc- β 1,3-Gal) series GSLs (Figure 2).²⁷

In the Golgi apparatus, various Golgi-resident GTs transfer a specific sugar residue to specific acceptors such as a ceramide the oligosaccharide on ceramide.²⁶ Lactosyl ceramide (LacCer), which is the branching point for the synthesis of GlcCer series GSLs, is generated from GlcCer, after it is translocated to the luminal leaflet of Golgi by β 1,4-galactosyl transferases 5/6 (B4GALT5/6).²⁸ Once produced, the LacCer cannot be translocated

back to the cytosolic phase of cell membranes. Galactose can be added to the 4-O or 3-O position of LacCer as *a*-galactoside, resulting in the synthesis of the globo-series Gb3 or isoglobo-series iGb3. For the synthesis of lacto-series GSLs, the enzyme β 1,3-*N*acetylglucosaminyltransferase 5 (B3GNT5) catalyzes the addition of GlcNAc to LacCer to form intermediate Lc3,²⁹ whereas, in the case of the ganglio-series GSLs, β 1,4-GalNAc transferase (B4GALNT1) catalyzes the addition of GalNAc residue to the hydroxy group of galactose on LacCer to form asialo-GM1. In the synthesis of o-, b-, and c-series gangliosides, GM3 is the key intermediate that is formed by *a* 2,3-sialyltransferase 5 (ST3GAL5) catalyzed addition of sialic acid to LacCer (Figure 2).³⁰ The precursors such as Gb3, iGb3, Lc3, sialo-GM2, and GM3 are modified by various GTs to generate GSLs as asialo-, ganglio-, globo-, isoglobo-, lacto-, and neolacto-series. In the case of GalCer series GSLs, the precursor GalCer is transported to the Golgi complex where it can be sialylated to produce GM4 ganglioside or sulfated to produce sulfogalactolipids.²⁵

Glycosylphosphatidylinositol (GPI) often links to a glycan and acts as an anchor for a variety of cell surface proteins³¹ as part of a post-translational protein modification process and is present in diverse eukaryotic species.^{32,33} The GPI anchor consists of a phosphoethanolamine moiety linked to the terminal mannose of a highly conserved core glycan Man α 1–2Man α 1–6Man α 1–4GlcNH₂ α 1–6*myo*-inositol, and the phospholipid tail (Figure 1).³⁴ The GPI-anchored protein is linked to the amine group of the phosphoethanolamine moiety on the glycan core, while the phospholipid tail inserts into the cell membrane. The GPI anchored protein synthesized in the ER first moved to the lumen where the coupling of protein C-terminal to GPI anchor and insertion of phosphatidylinositol into the lipid membrane takes place.^{35,36} During the maturation process, the Man3 glycan on GPI anchored protein may undergo further glycosylations³⁷ and involved in many functions such as protein transportation, signal transduction, cell adhesion, and protection.³⁸

1.2. Biological Significance of Glycoconjugates

In eukaryotes, glycolipids and glycoproteins are anchored to the cell membrane, while proteoglycans cover the extracellular matrix that leads to the highly glycosylated environment essential for intracellular signaling.^{12,14,39} Therefore, cell surface glycans engage in numerous aspects of cell–cell interactions with self-molecules and invaded pathogens (Figure 3a).^{40,41}

Glycan-binding proteins (GBPs) are classified into: lectins and sulfated GAG-binding proteins.⁴² Animal lectins include the C-type, P-type, S-type, and I-type lectins, differing in the affinity of their carbohydrate recognition domain (CRDs) toward the glycan residues such as Man, Gal, GalNAc, GlcNAc, Fuc, and Neu5Ac. CRDs can exist as proteins in monomeric form or as a multidomain protein. GBPs containing specific CRDs that confers glycan-binding specificity often recognize complementary glycans on cell surfaces.⁴³ The first discovered animal lectin, asialo-glycoprotein receptor (ASGPR), is involved in the rapid clearance of asialo-glycoproteins with exposed Gal residues by liver *via* a cell surface receptor that recognizes terminal Gal or GalNAc in β -linkage.⁴⁴ Other examples of glycan-specific receptors involved in glycoprotein clearance include mannose 6-phosphate receptor

(CI-MPR) and mannose receptors (MR or CD206) that removes glycoproteins with terminal Man, Fuc, and GlcNAc residue from the circulation.⁴⁵

Upon glycan binding, the other functional domains on GBPs translate the binding into appropriate downstream signaling.⁴³ Some of the classical examples include glycans and GBPs on the surfaces of immune cells involved in immune activation, deactivation, pathogen recognition, and regulation within a dynamic pathogen landscape.^{46,47} Extracellular carbohydrates and GBPs interact with certain molecules in the matrix or the adjacent glycan to regulate intracellular signaling.⁴⁸ GBPs on the surface of immune cells are involved in modulation of leukocyte trafficking, pathogen recognition, antigen processing, and immune regulation.^{47,49} For example, surface glycoproteins and glycolipids on immune cells and GBPs and other molecules can help the immune system to sense environmental changes.⁵⁰

Many receptors present on immune cells interact with glycan-containing molecules on pathogens⁵¹ such as bacterial lipopolysaccharides (LPS), capsular polysaccharides, mannans on fungal surfaces, and peptidoglycans. These glycan-based epitopes on microbial surfaces have been utilized in vaccine design.^{52,53}

1.2.1. Role of Glycoconjugates in Immune Regulation.—In the adaptive immune system, the interaction of specific cell surface glycan ligands with extracellular or secreted proteins, like siglecs, galectins, selectins, CD43, and CD45, plays a critical role in B- and T-cell differentiation.^{54,55} The glycoproteins CD43 and CD45 that are highly expressed on the surface of B/T cells contain both *O*- and *N*-glycans which are important for the modulation of cell motility, downstream signaling, cell survival, and apoptosis.^{56,57} The interactions between CD43 or CD45 with their ligands are thus greatly influenced by the glycosylation pattern.

Galectins.: Galectins are carbohydrate-binding proteins that contain a conserved CRD specific for β -galactosides including galactose, lactose, poly lactosamine, and N-acetyllactosamine (LacNAc).⁵⁸ Structurally, galectins have a conserved CRDs, with a six-stranded β -sheet that binds β -galactosides and a five-stranded β -sheet.⁵⁹ Galectins in the extracellular domain recognize the galactosylated oligosaccharides in a bi- or multivalent manner, resulting in cross-linking of cell surface glycoconjugates and activation of programmed cell death, cytokine production, cell adhesion, and migration.⁶⁰ The glycan binding specificities of galectins and their occurrence on immune cells are summarized in Table 1.61 Both intracellular and cell-surface galectins are associated with many cellular functions including cancer metastasis, immune response, and cell death.^{62–64} The binding affinity of galectins is dependent on glycan structure that regulates the signals induced by galectin binding. For example, terminal sialylation affects galectin binding, a2,6-sialic acid capping prevents binding to galectin-2, whereas galectin-1 binds a_2 , 3- but not a_2 , 6-sialylated glycans, and galectin-3 binds to some glycans terminating with either $a_{2,3}$ - or $a_{2,6}$ -sialic acid.⁶⁵ The functional role of galectins in regulating various biological activities has been used as a promising therapeutic option for treatment of inflammatory diseases and cancers. For example, the interaction between galectin-3 binding protein and galectin-1 is important for breast cancer metastasis, Galectin-8 N-domain binds α 2,3-sialylated galactoside while the C-domain binds galactosides, and numerous galectin antagonists are currently under

clinical evaluation.⁶⁶⁻⁶⁸ Galectin Therapeutics developed Belapectin (GR-MD-02), a new polysaccharide comprising of galacturonic acid, galactose, arabinose, rhamnose, and smaller amounts of other sugars, as an inhibitor of galectin-1 and -3 for treatment of NASH cirrhosis. In addition, Belapectin in combination with Keytruda is in advanced clinical trials for treating metastatic melanoma and head and neck cancer.⁶⁹⁻⁷²

Siglecs.: Sialic acid-binding immunoglobulin-like lectins (siglecs) are type 1 membrane proteins, displaying an amino-terminal V set IgG domain that binds to sialic acid-containing glycoproteins and glycolipids.⁷³ Based on their sequence similarity, siglecs are classified into (a) sialoadhesin (siglec-1), CD22 (siglec-2), myelin-associated glycoprotein (MAG, siglec-4), and siglec-15, and (b) CD33-related siglecs such as CD33 (siglec-3), Siglecs-5-15 and -16. Most of the siglecs contain a tyrosine-based signaling motif, especially an immunoreceptor tyrosine inhibitory motif (ITIM), in their cytosolic domains that are implicated in endocytosis and cell siglaling.⁷⁴ Because sialic acid-containing glycans are abundant in mammalian cells, siglecs, such as siglec-5, -7, -9, -10, and -15 act as immune check points on immune cells to differentiate self vs nonself signals and to avoid unwanted immune responses.^{46,75} Despite their common *N*-terminal V domain, each member of the siglec family represents defined specificity toward terminal sialic acid residues on glycoproteins or glycolipids (Table 1).⁷⁵ Sialic acid can be linked *via* a2-3 or a2-6 linkage to an inner galactose residue, or via a2-8 or a2-9 linkage to an inner sialic acid residue. There are several possible elements in the sialylated glycoproteins that can be recognized by siglecs to induce biological responses consequently,⁷³ including terminal sugar linkage, composition of oligosaccharide, and other modifications like sulfation or N-acetylation.

CD22 (siglec-2) is the most studied siglec on B cells that recognize *a*2,6-sialyted motifs to control B cell receptor (BCR) signaling following antigen binding.^{76,77} Regulation of BCR signaling is essential for maintaining self-tolerance. CD22 deficiency may cause autoimmune diseases and therefore offered an effective mean to autoimmune diseases.⁷⁶ CD169 (also known as siglec 1) is an essential member of siglec family that binds to *a*2,3 sialylated *N*- and *O*-glycoproteins and glycolipids.^{78,79} CD169 receptor shows a low binding affinity toward monomeric sialic acid; hence, to have an effective interactions, its ligand must be heavily sialylated to form a multivalent sialoside.⁸⁰ CD169 is a macrophage marker and plays a critical role in initiating antibacterial and antiviral immune responses and in development of autoimmune diseases.⁸¹ Human T cells generally lack siglecs, however, recent studies showed that, siglecs such as siglec-5, siglec-7, siglec-9, and siglec-10 are present and negatively control T cell functions.^{82,83}

Cancer cells escape from the attack of macrophages by overexpressing antiphagocytic molecules called "do not eat me" signals, such as CD47/signal regulatory protein *a* (SIRP*a*), PD-L1/PD-1, and the β -2 macroglobulin subunit of the major histocompatibility class I complex (B2M)/leukocyte immunoglobulin like receptor B1 (LILRB1).^{84,85} Blocking the interactions between macrophage receptor and the tumor associated do not eat me molecule using antibodies has shown significant therapeutic prospect for cancer immunotherapy. Recently, the Weissman group demonstrated that tumor expressing CD24 stimulates macrophage mediated phagocytosis through interactions with siglec-10 specifically expressed on tumor associated macrophages (TAMs) in ovarian and breast

cancer. In addition, elimination of CD24 or siglec-10 genetically or antibody mediated blocking of CD24-siglec 10 interaction drastically improved the phagocytosis of all CD24⁺-tumors, indicating that blockade of CD24-siglec-10 interaction has the potential for cancer treatment.⁸⁶ Siglec-15 is mainly present on a subclass of myeloid cells that binds specifically to the sialyl-Tn glycan and is a promising target for osteoporosis treatment because of its involvement in osteoclast differentiation.^{87,88} Recent studies revealed the unexpected role of siglec-15 in microbial infection and the cancer microenvironment.⁸⁹

Selectins.: The selectins are glycan-binding transmembrane glycoproteins found on the surface of endothelial cells, platelets, and leukocytes, that bind to sialylated, fucosylated glycan ligands and sometimes to a subset of heparan sulfateGAGs.⁹⁰ This family of GBP comprises E-selectin, P-selectin, and L-selectin.⁹¹ Selectins are important for the trafficking of immune cells, T lymphocytes, and platelets.⁹² During inflammation, selectins on epithelial cells enable the initial attachment of leukocytes to epithelial cells from the bloodstream, which causes leukocyte movement along the endothelium via adhesive interactions referred to as leukocyte rolling. The absence of selectins or their ligands cause a significant health concerns like recurrent bacterial infections and progression. L-selectin is a 74–100 kDa glycoprotein mainly involved in the early stages of the adhesion cascade by mediating lymphocyte homing and adhesion to endothelial cells.⁹³ Inflammatory stimulation of endothelial cells triggers overexpression of P-selectin on platelets and endothelial cells. In leukocyte rolling, P-selectin interacts with the P-selectin glycoprotein ligand-1 (PSGL-1) consisting of a sialyl Lewis x (sLex) glycan and a sulfate group on tyrosine expressed on all leukocytes, facilitate leukocyte rolling along the venular endothelium.⁹⁴ E-Selectin is expressed only on endothelial cells activated by cytokines TNF-a and IL-1 β . E-Selectin recognizes sialylated glycan ligands on glycoproteins, especially sLex expressed on specific immune cells. Adhesion of these cells to the acute and chronic inflammatory sites is associated with expression of E-selectin, suggesting the role of E-selectin in mediating immune cell recruitment to inflammatory sites.⁹⁵ The inhibition of selectins has been investigated in a mice to model for the treatment of sickle cell disease. For example, an inhibitor of P- and L-selectin, GMI 1070, has been evaluated in clinical studies for the treatment of sickle cell anemia, and the result showed that GMI 1079 effectively suppressed vascular occlusion.⁹⁶ Inclacumab is a fully human mAb that selectively targets P-selectin and was shown to reduce vaso-occlusive crisis in sickle cell disease.⁹⁷ These examples support that these selectins are potential targets for the treatment of inflammatory diseases.

1.2.2. Glycoconjugates in Signal Transduction.—Binding of small protein ligands like hormones, cytokines, and growth factors to specific cell receptors triggers intracellular signaling events, which ultimately lead to the activation or inhibition of gene transcription.⁹⁸ Most of these receptors are highly glycosylated membrane associated proteins, whereas their ligands are also glycoproteins.⁹⁹ The glycans on the receptors affect their conformational flexibility and ligand binding. Receptor–ligand binding on a cell surface results in clustering of the receptor followed by phosphorylation of the cytoplasmic domain and activation of the downstream signaling events that control protein expression.^{100,99}

Carbohydrates at extracellular domain are critical for many signaling pathways. For example, (1) the extracellular region of the Notch receptor carries many epidermal growth factor like repeating units which are glycosylated with *O*-fucose and *O*-glucose, as well as *N*-glycans. Activation of Notch receptors by Notch ligand regulates cell fate decisions in metazoa, however, disruption of *O*-fucose glycan leads to Notch signaling defects.¹⁰¹ (2) In the injured adult nervous system, myelin-associated glycoprotein (MAG) binds to receptors such as gangliosides (GD1a and GT1b) and GPI-anchored Nogo receptors (NgRs) on axons, forming signaling complexes that inhibit axonal outgrowth and limit functional recovery.¹⁰² (3) Some cell surface carbohydrates are important mediators of the signal transduction pathways for B-cell receptor activation and T-cell apoptosis.^{103,104} (4) Sialylation of EGFR inhibits EGFR dimerization and signaling associated with drug resistance.¹⁰⁵ (5) *O*-GlcNAc addition to histone lysine methyl transferase EZH2 or MLL5 causes activation of this enzyme for methylation of histone and thereby leads to tumor suppression or cell lineage determination.^{106,107}

1.2.3. Glycoconjugates in pathogenic infections.—Host–pathogen interactions (HPIs) during infection are highly complex regarding their mechanism and relation with the progression of infectious diseases. HPIs are facilitated via cell surface protein-protein interactions between hosts and pathogens. Recognition and attachment to specific cell surface carbohydrates is the first and critical step in viral entry.⁵¹ Cell surface carbohydrates are utilized by a wide variety of viruses as a receptor and most of these structures are negatively charged, such as sialic acid-containing glycans or polysulfated proteoglycans. One of such classical examples is hemagglutinin, an influenza glycoprotein, which binds to sialic acid-containing glycans on human airways epithelium to facilitate viral entry into the host. Upon replication, a large number of viral particles bud out from infected cells and are released by removal of surface sialic acid by sialidase and then infect another fresh target cell.¹⁰⁸ The rational design of transition state analogues as sialidase inhibitors led to development of the anti-influenza drugs Relenza (GlaxoSmithKline) and Tamiflu (Genentech).^{109,110} These drugs inhibit the activity of sialidase so that the freshly budded virions do not disseminate from infected cells and thus stop further infection. In humans, α^{2} , 6-sialylated glycans are more predominant in the upper respiratory tract than the lower respiratory tract, whereas a2,3-sialylated glycans are dominant in avian species. The presence of both a2,6/2,3-sialylated glycans in swine makes them vulnerable to influenza viruses of human and avian origin.^{111,112} Glycan microarray profiling of influenza strains has provided a new understanding of the specificity of hemagglutinins, especially the specificity of binding toward the internal glycan beyond the sialyl galactose linkage.^{113,114} Different virus families and their preference for carbohydrate structures as receptors for entry are presented in Table 2. Most of the members of these virus families bind to glycoepitopes containing terminal sialic acids of sulfated glycan motifs of proteoglycan chains.^{115–119} Protein–glycan interactions also occur during the infection of many other pathogens.

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is a member of the *Coronaviridae* family, which causes the COVID-19 pandemic.^{120,121} The SARS-CoV-2 S protein exists as a trimer on viral surface, and each monomer is composed of S1 and S2

subunits with a total of 1273 amino acids. The receptor binding domain (RND) in S1 is responsible for viral entry into the host cell by interaction with the angiotensin-converting enzyme 2 (ACE2) receptor, while fusion of viral and host cell membrane is mediated by the S2 subunit.^{122,123} Recently, Clausen *et al.* showed that the cell surface heparan sulfate interacts with SARS-CoV-2 S protein and triggers a conformational change to favor the high affinity binding with ACE2 receptors on the host cell.^{124–126} To facilitate viral entry, engagement of both cell surface HS and ACE2 is critical, indicating that heparan sulfate acts as a coreceptor.¹²⁴ The SARS-CoV-2 S protein contains 22 *N*-linked and at least two *O*-linked glycosites that are important for proper protein folding, binding to receptor, and escape from host's immune response and antibody neutralization.¹²⁷

Many bacterial lectins function as adhesins for attachment to host and invasion. For example, type 1 fimbrin D-mannose specific adhesin (FimH) from Escherichia coli (E. coli) preferentially binds to oligomannose type glycans on host cells in urinary tract infections.¹²⁸ FimH has been shown to bind with the variability to the mannose structure, leading to different tissue tropism.¹²⁸ A series of C1-modified α -mannosides have been rationally designed as FimH antagonists and tested in animal models as a potential UTI therapeutic.¹²⁹ The Gram-negative bacterium *Heliobacter pylori* attaches to the heavily glycosylated human gastric mucosa and epithelial lining using various adhesins that specifically recognize Lewis B, sLe^X, and Lewis A, and di-LacNAc structures, which are expressed in gastric epithelial cells as mucins within the mucosa.^{130–132} These adhesins may have a role in persistent H. pylori infection with a majority of hosts being asymptomatic; however, 1-3% of those infected develop gastric cancer.¹³³ Alternatively, pathogenic bacteria can also interact with host lectins such as the C-type lectin, dendritic cell-specific ICAM-3-grabbing nonintegrin 1 (DC-SIGN), and the mannose-binding lectin that enable bacteria to adhere and enter host cells.^{134,135} For example, the Neisseria gonorrheae strain 1291 LOS expresses a terminal lacto-N-neotetraose structure on surface and binds to ASGPRs to mediate invasion of male primary urethral epithelial cells.¹³⁶

Bacteria utilize a range of GTs and GHs to modify host glycoconjugates and to enable cell adhesion. Neuraminidases are the most widely studied enzymes regarding their varying specificities.¹³⁷ Following influenza A virus infection, the viral neuraminidase acts on the sialylated viral receptors on host cells to cleave the terminal sialic acid residue and promote subsequent coinfection by *Streptococcus pneumoniae*.¹³⁸ Glycoconjugates on host cells are also targeted by bacterial toxins. For example, *Vibrio cholerae* (cholera toxin) targets complex *N*-linked glycoproteins; *Shigella dysenteriae* and Shiga toxigenic *E. coli* (Shiga toxin) specifically binds to the trisaccharide motif of the Gb3 receptor, which is mainly present on endothelial cells in the brain, intestine, and B lymphocytes; the neurotoxin from *Clostridium botulinum* (botulinum toxin) binds to both the peptide and the *N*-linked glycan on the neural receptor SV2; and high affinity binding of *Clostridium tetani* (tetanus toxin) to neurons is mediated solely by gangliosides.^{139–143}

1.2.4. Glycoconjugates in Cancers.—Glycosylation is utilized by cancer cells to evade immune clearance and move to metastatic sites such as lung, liver, and brain, *etc.*⁹⁹ Altered glycosylation with increase in sialylation, core fucosylation, *N*-glycan branching, or mucin-type *O*-glycosylation, is the most common phenomenon observed in cancer cells.¹⁴⁴

During cancer progression, the glycosylation pattern changes to truncated structures, such as the Tn antigen in O-glycans, or to abnormal structures, such as sLe^X (Figure 4).¹⁴⁵ Formation of such neoantigens in cancers facilitates their metastasis to other tissues or organs.¹⁴⁶ The abnormal glycosylation pattern arises from the availability of GTs during the biosynthesis of glycoconjugates inside the cancer cell that catalyze the addition of extra sugar residues in the core or at the termini of N-linked and O-linked glycans.¹⁴⁷ In addition, altered glycosylations are also associated with malignancy. GTs such as SiaT and FucT involved in the terminal glycosylation are often overexpressed in tumors to produce certain unusual glycans.¹⁴⁸ Several tumor-associated carbohydrate antigens (TACAs) have been reported to have a high correlation with cancers, including sLe^X, sialyl Lewis A(sLe^A), Tn, sialyl-Tn (sTn), GM2, GD2, GD3, and Globo-H (Figure 5).¹⁴⁹ sLe^X is overexpressed in colorectal, breast, lung, and gastrointestinal carcinomas, sLeA in colorectal and pancreatic cancer, and Tn in breast and other cancers.¹⁵⁰ Elevation of serum STn was found to correlate strongly with poor survival of patient with ovarian cancer.¹⁵¹ In human melanoma and neuroblastoma, gangliosides GD2, GM2, and GD3 are highly expressed.¹⁵² Globo-H was found in breast carcinoma cell line MCF-7, embryonal carcinoma 2102 cells, and breast, ovarian, stomach, oral, and prostate cancers.¹⁵³ Taken together, TACAs are commonly found on cancer cells but absent on normal cells and have received more and more attention in the development of anticancer immunotherapies.¹⁵⁴

Another major characteristic of cancer cells is the overexpression of abnormal glycoproteins and glycolipids. For example, *O*-glycosylated mucins are often overproduced by epithelial tumors and therefore can be used as cancer markers for diagnosis and development of therapeutics.¹⁵⁵ Increased levels of complex gangliosides including GD2, GD3, and fucosyl GM1 are also found on small-cell lung carcinomas, neuroblastomas, and melanomas.¹⁵⁶

Recently, the globo-series GSLs, including Globo H, SSEA3, and SSEA4, are found exclusively on the cell surface of many cancers and correlate with tumor metastasis and progression.^{157,158} The enzyme β 1,3-galactosyltransferase V (β 3GalT5) is essential for the biosynthesis of globo-series GSLs, as it catalyzes the galactosylation of Gb4 to SSEA3, which is further modified to GloboH and SSEA4. Overexpression of β 3GalT5 increases the expression level of surface SSEA-3 in breast cancer cells (Figure 6a).¹⁵⁹ Globo H is synthesized from SSEA3 by fucosyltransferases 1 and 2 (FUT1 and FUT2)¹⁶⁰ whereas SSEA4 is synthesized by β -galactoside a 2,3-sialyltransferase 2 (ST3Gal2).¹⁶¹ In breast cancer cells, the lipid moiety of globo-series GSLs interacts with caveolin-1 (CAV1) and focal adhesion kinase (FAK) to form a complex, which then interacts with AKT (protein kinase B) and receptor-interacting protein kinase (RIP), respectively (Figure 6b). The interaction between FAK and RIP prevents apoptosis triggered by the interaction between RIP and the Fas death domain (FADD) through the Fas-dependent pathway.¹⁵⁸ Knockdown of β 3GalT5 suppressed cell growth and induced cell apoptosis. However, knockdown of the enzymes for the synthesis of GH from SSEA3 (FUT1 and FUT2), or the enzyme for the synthesis of SSEA4 from SSEA3 (ST3Gal2) does not induce apoptosis in MDA-MB-231 cells.¹⁵⁹ These studies indicated that β 3GalT5 is the key enzyme to sustain survival of cancer cells, and this enzyme and all the three globo-series glycans could be the targets of cancer immunotherapy.

2. NATURALLY OCCURRING GLYCOCONJUGATES

2.1. Proteoglycans

2.1.1. Structure and Classification of Proteoglycans.—Proteoglycans (PGs) are a class of highly complex biomolecules composed of long linear chains of GAGs such as CS, DS, KS, heparin, and HS linked to a protein backbone at serine residues.³⁹ Hyaluronan is the only GAG which is present as a noncovalently linked complex with protein. GAGs are linear, negatively charged complex polysaccharides composed of repeating disaccharide (GalNAc or GlcNH₂ linked to D-glucuronic acid or L-iduronic acid) units with varying degrees of sulfation, and KS has the GlcNAc residue linked to the Gal–Gal unit (Figure 7).

Depending on the cellular and subcellular localization, PGs are classified into extracellular and intracellular proteoglycans. Each type is again divided into subtypes based on composition, sequence homology, structure of core protein, and size.¹⁶² The only known intracellular PG is Serglycin, which contains heparin side chains. Mast cells use Serglycin to store mast cell specific proteases that are released upon inflammation.¹⁶³ Out of 13 cell surface proteoglycans, seven have transmembrane domains and six are GPI-anchored proteoglycans. Syndecans and glypicans are two main families of extracellular PGs.¹⁶⁴ Syndecans are hybrid PGs because their ectodomain are generally attached to HS and in some cases to CS. Glypicans are found on the cell surface or in the pericellular matrix. Glypicans attached to cell surface *via* protein core or a GPI anchor.¹⁶⁵ Some examples of pericellular PGs include perlecan and agrin.¹⁶²

2.1.2. Functions of Oroteoglycans.—The microheterogeneity of PGs forms the basis of their diverse cellular activities.¹⁶² In addition to their role as a structural element in tissue organization, PGs are also involved in cell signaling by interactions with cell surface signaling molecules.¹⁶⁶ The catalogue of biological phenomenon in which PGs are involved is growing rapidly.

2.1.2.1. Cellular Gunctions.: PGs are implicated in a wide variety of biological events ranging from cell–cell, cell–extracellular matrix (ECM), to ligand–receptor interactions.¹⁶⁷ Chondroitin sulfate PGs, a key element of the extracellular matrix in the central nervous system (CNS) involved in the development of CNS and prevention of neural damage.¹⁶⁸ Chondroitin sulfates also promote or inhibit the neural growth by interactions with growth factors or transmembrane receptors, respectively.¹⁶⁹ The interactions between CS and specific proteins are greatly affected by the degree of sulfation with CS GAG chains. Interestingly, the sulfation pattern of CS GAG chains changes during development of nervous system and in response to CNS injury.¹⁷⁰ The role of HSPGs during the development of the mammalian CNS has also been documented.^{171,172}

2.1.2.2. Signal Transduction.: Cell surface HSPGs such as syndecans and glypicans bind to several growth factors and other matrix associated molecules that are implicated in various signal transduction pathways and are important for cell proliferation. Syndecans, through their HS chains bind to numerous growth factors to dictate morphogen gradients during development. Along with their role as an endocytosis receptor for the uptake of exosomes, syndecans also act as coreceptors for many receptor tyrosine kinases and

lipoproteins.¹⁷³ Syndecan-1 has been shown to drive the clearance of triglyceride-rich lipoproteins from the liver or intestine.¹⁷⁴ Glypicans, such as glypican-3 are critical for tumor growth and angiogenesis.¹⁷⁵

2.2. Glycoproteins

2.2.1. *N*-Linked and *O*-Linked Glycoproteins.—Post-translational proteins glycosylation is important for the proper folding, stability, and intracellular trafficking of proteins. In addition, the carbohydrate domains of glycoproteins can directly interfere with a wide variety of physiological processes. Compared to other post-translational modifications like protein phosphorylation and methylation, the post-translational glycosylation is highly diverse and complex. The *N*-linked and *O*-linked glycans are the two types of most studied glycoforms in protein glycosylation.⁶

N-Glycans contain a common core pentasaccharide structure, Man₃GlcNAc₂, that linked to the Asn residue in the protein backbone through amide bond formation (Figure 8). There are three types of N-glycans, namely, high-mannose, hybrid-type, and complex-type glycans. High-mannose glycans (HMGs) have additional mannose sugars residues at both the α -3 and α -6 mannose sites, known as the "D1 and D2 arms". HMGs are named according to number of mannose residues attached to the chitobiose core, for example, Man₉GlcNAc₂ contains nine mannoses attached to GlcNAc₂. In complex glycans, the terminal mannose residues of the core pentasaccharide are substituted with differently linked GlcNAc residues to form "antennae." Complex type glycans exist as bi-, tri-, and tetra-antennary forms depending on the number of antennae present on the core. Hybrid-type glycans are characterized as containing both high mannose type and complex type antennae on the core. The complex type antennae present in both hybrid and complex type glycans are extended with $\beta(1\rightarrow 4)$ Gal linkage. Additional modifications such as repeating LacNAc (GlcNAc- β (1 \rightarrow 4)Gal) units linked to terminal Gal *via* β (1 \rightarrow 3) linkage, addition of a bisecting GlcNAc at the mannosyl core, and fucosyl residue on the innermost as well as outer GlcNAc or Gal residues are also possible. Complex glycans commonly terminate with sialic acid residues linked via either a2,3- or a2,6-linkages.¹⁷⁶

O-Glycans are mostly linked to the side chains hydroxyl of Ser or Thr residue of proteins without any necessity of a consensus sequence. Other than Ser and Thr, Tyr, hydroxylysine, or hydroxyproline may also be the sites for *O*-linked glycosylation (Figure 9). The most commonly occurring *O*-linked glycans are the mucin-type, which contains a GalNAc residue at the reducing end that is linked to proteins. There are eight mucin-type core structures, however, further modifications to the core, such as sialylation, fucosylation, *etc.*, make them highly heterogeneous.¹⁷⁷ In general, *O*-linked glycans are comparatively less complex than *N*-glycans. The highly dense *O*-linked glycans on mucin resulted in cross-linked structures to form mucus.

2.2.2. Biosynthetic Pathway of *N***-Linked and** *O***-Linked Glycoproteins.**—The biosynthesis of *N*-linked glycoprotein begins with the synthesis of a dolichol-linked Glc₃Man₉GlcNAc₂ precursor, the glycan of which is then transferred to the side chain of Asn in a consensus glycosylation sequen of Asn-X-Ser/Thr, catalyzed by

oligosaccharyltransferase (OST).¹⁷⁸ The terminal glucose residues of the oligosaccharide precursor are then digested by *a*-glucosidase-I and -II to form a monoglucosylated glycoform (Glc₁Man₉GlcNAc₂), which is passed through the gate keeper calnexin/ calreticulin chaperone and folded properly. The glycan on the properly folded glycoprotein is trimmed further to Man₈GlcNAc₂, which then exits the ER and enters the Golgi apparatus for further processing by Golgi-resident GHs and GTs to form hybrid-type or complex type glycoforms (Figure 10a).

The medial-Golgi mannosidase removes the terminal mannose residues of Man₈GlcNAc₂ to form Man₅GlcNAc₂, which is further acted upon by an GlcNAc transferase called GnTI (MGAT1) to add a GlcNAc residue via β -1,2 linkage to the C-2 position of the mannose residue at the a-1,3 arm of Man₅GlcNAc₂. Subsequently, the terminal a1-3Man, and a1-6Man residues from GlcNAcMan₅GlcNAc₂ are trimmed by a-mannosidase II to form GlcNAcMan₃GlcNAc₂. Upon removal of both mannose residues, GnTII (MGAT2) catalyzes addition of a second GlcNAc residue to the C-2 of the mannose at the a1-6arm to give the main precursor for all biantennary complex-type N-glycans. Hybrid-type N-glycans are formed if the GlcNAcMan₅GlcNAc₂ glycan is not trimmed by *a*-mannosidase II and the intermediate GlcNAcMan₅GlcNAc₂ is further extended by β 1,4-galactosyl and/or a2,3/2,6-sialyl transferase. Additional branches on biantennary complex glycans can be formed by addition of β -1,4 bisecting GlcNAc at C-4 of the core Man with GnTIII or by addition of β -1,4 GlcNAc at C-4 of α 1-3Man with GnTIV or at C-6 of α 1,6Man with GnTV to give tri- and tetra-antennary N-glycans.¹⁷⁹ Further glycosylations with galactosyltransferases, sialyltransferases, and fucosyltransfersases change the N-glycans into highly diverse complex-type N-glycans, including glycans with core fucose and extended glycans with poly-LacNAc motifs.¹⁸⁰

The *O*-linked glycoproteins are formed by addition of GlcNAc residue to the hydroxyl of Ser/Thr side chain (Figure 10b).¹⁷⁷ At least 12 GalNAc transferases (ppGalNAcT) isozymes have been identified that initiate *O*-glycosylation of mucin glycoprotein. The synthesis of mucin-type glycans involves ppGalNAcT-catalyzed glycosylation in the presence of UDP-GalNAc as donor. Subsequent elongation and termination of *O*-linked glycans is conducted by several GTs.¹⁸¹ The expression and subcellular distribution of the various GTs determine the outcome of *O*-glycans which are often terminated with Gal, GlcNAc, GalNAc, Fuc, or Neu5Ac.

2.2.3. Glycoprotein Therapeutics.—It is well documented that glycosylation profile of therapeutic proteins significantly modulates production yield, stability, biological activity, immunogenicity, pharmacokinetics, and pharmacodynamics. Advances in the area of glycobiology has expedited the development of glycoprotein therapeutics including glycoconjugate vaccines, glyco-engineered monoclonal antibodies, antibody–drug conjugates(ADC), and other recombinant proteins for the treatment of life threatening diseases, including cancer, autoimmune diseases, *etc.*¹⁸²

Erythropoietin (EPO) is a glycoprotein best known for its binding to the erythropoietin receptor to promote the maturation of erythroid progenitor cells to erythrocytes and initiate hemoglobin synthesis.¹⁸³ Natural and recombinant forms of EPO were developed

for the treatment of anemia caused after chemotherapy or for those with deficiency of erythropoietin. EPO contains 3–5 *N*-glycosylation sites which accommodate tri- and tetraantennary complex type glycans terminating with galactose or sialic acid residues.¹⁸⁴ Although the in vitro activity of the deglycosylated form of EPO is not significantly affected compared to native form, the in vivo activity is greatly reduced due to rapid clearance of poorly glycosylated EPO by filtration in the kidney.¹⁸⁵ Galactose-terminated EPO is also rapidly up taken by ASGPR in hepatocytes and macrophages. Various approaches have been developed to incorporate fully sialylated tetra-antennary glycans to boost circulatory half-life and in vivo activity.¹⁸⁶

Glyconjugate vaccines are another important class of glycoprotein therapeutics that are part of routine vaccination schedules for protection against pathogenic infections.¹⁸⁷ The semisynthetic Hib glycoconjugate vaccine, that is marketed in Cuba, has been very successful at preventing *Haemophilus influenzae* type b (Hib) infection.¹⁸⁸ Pneumococcal conjugate vaccines have been formulated to cover more serotypes. The best-selling vaccine, Prevnar13 (Pfizer), is effective against the serotypes that are responsible for >70% of the invasive pneumococcal infections worldwide.¹⁸⁹ Glycoconjugate vaccines against *Neisseria meningitidis* are also successful. Several conjugated CPS vaccines are available, for example, Menactra, Menveo, and Nimenrix against serogroups A, C, W, and Y, Meningitec, Menjugate, NeisVac-C against serogroup C, MenHibrix against serogroups C/Y, and MenAfriVac against serogroup A.¹⁹⁰ At present several synthetic carbohydrate based vaccine are being developed against varieties of bacterial and viral infections.⁵³

Vaccines containing the glycan of cancer associated gangliosides including GM2, GD2, and globoH have been advanced to late stage clinical trials.¹⁹¹ However, the progress of vaccines targeting mucin type sialyl-Tn (sialyl*a*2–6GalNAc*a*-) antigen has seen slow in 20 years.¹⁹² A synthetic Globo H-KLH conjugate combined with QS-21 adjuvant is in phase 3 clinical trials for the treatment of triple negative breast cancer (NCT03562637) and a Globo H-DT conjugate with C34 adjuvant designed to induce a class switch and improve the IgG titer is in phase 2 trials for the treatment of multiple cancers (NCT02310464).

2.3. Glycolipids and Lipopolysaccharides

2.3.1. Structure of Lipopolysaccharides.—The glycolipid molecules commonly present on the surface of Gram-negative bacteria are lipopolysaccharides that are comprised of O-antigen, core oligosaccharide, and lipid A.¹⁹³ LPSs are endotoxins that cause severe symptoms, such as high fever, diarrhea, blood pressure decrease, or septic shock and sometimes could result in death.¹⁹⁴

Lipid A, the hydrophobic part of the LPS consists of GlcNH₂ β -1 \rightarrow 6GlcNH₂ disaccharide with a phosphate group at the 1 and 4' positions.¹⁹⁵ The 2-amino and 3-hydroxyl groups of both glucosamine residues are linked to fatty acid chains (Figure 11). The number of lipid chains and their length depend on species but generally remained conserved. The fatty acids of lipid A on the LPS molecule are embedded in the cell membrane while the rest of the LPS molecule projects from the bacterial outer membrane. Upon lysis of the bacterial cell wall by the immune system, the infection may result in fever, diarrhea, and septic shock.¹⁹⁶

The core oligosaccharide consists of inner core and outer core that connect lipid A to the O-antigen.¹⁹⁷ The inner core typically contains 3-deoxy-*a*-D-manno-octulosonic acid, also known as KDO, that attached directly to the 6-O position of the GlcNAc of lipid A. LPS typically contains one to four molecules of KDO, however, bacteria need at least one molecule of KDO for survival.¹⁹⁸ The inner core KDO residue is modified with 2-amino ethyl phosphate or heptose monosaccharide. The outer core oligosaccharide is structurally more diverse, consisting of glucose, galactose, and GlcNAc.¹⁹⁹ The O-antigen is the outermost part of LPS attached to the end of core oligosaccharide, and the structure varies among different strains but typically contains repeating chains of glycans with four to five sugar residues.²⁰⁰ The O-antigen component of LPS is much longer and highly complex and contains at least 20 different types of glycans residues which are not commonly found in nature.²⁰¹ Among different domains of LPS, the O-antigen has high structural diversity compared to lipid A and core oligosaccharide.²⁰²

2.3.2. Functions of Lipopolysaccharides.—The LPS in the bacterial cell is strongly amphipathic in nature due to the hydrophobic lipid chain and the hydrophilic core oligosaccharide and O-antigen that set a permeability barrier for toxic molecules.²⁰³ The effectiveness of the barrier depends on how densely the LPS is packed within the cell membrane. The LPS of Gram-negative bacteria is termed as "endotoxin" because the immune response raised against LPS can be toxic to the host. The immune system has evolved to target the most conserved component of LPS, the lipid A. Because of the considerable structural diversity of lipid A among bacterial species, different LPS structures trigger different host immune responses.^{204,205} For example, hexa-acylated, bisphosphorylated lipid A of E. coli and Salmonella is highly immunogenic, compared to other forms of lipid A.²⁰⁶ Synthesis of the less immunogenic lipid A structures is used by some pathogens to evade the immune attack. Alternatively, some pathogens mask the most conserved domain of LPS with highly variable sugar chains in the O-antigen domain to escape from host immune response. In addition, the presence of the O-antigen not only protects bacteria from lysis but also contributes to pathogen evasion of immune cell-mediated phagocytosis.207

2.3.3. Biosynthesis of Lipopolysaccharides.—LPS on the bacterial outer membrane is essential for the pathogen to survive. Although the biosynthesis of LPS is well-defined and common in most of the Gram-negative bacteria, some pathogens possess variability in the core domain of LPS. The biosynthesis of LPS is initiated in the cytoplasm and periplasm and then moved to the plasma membranes.¹⁹⁷ Biosynthesis of Kdo-Lipid A begins with the small building block, UDP-GlcNAc. During assembly of LPS, multiple enzymes work together sequentially to convert UDP-GlcNAc to disaccharide-1-P, Kdo2-lipid A, core oligosaccharide-lipid A, and O-antigen (Scheme 1).^{208,209}

The synthesis of lipid A takes place in the cytoplasm catalyzed by nine enzymes. The sugar nucleotide donor, UDP-GlcNAc, is processed to add fatty acid chains by three soluble enzymes, LpxA, LpxC, and LpxD. First, LpxA catalyzes addition of a lipid chain to the 3-O position of UDP-GlcNAc, followed by deacetylation of the 2-acetamino group of UDP-3-*O*-acyl-GlcNAc by LpxC. Next, LpxD introduces another lipid chain to the 2-amino group

of glucosamine to form UDP-2,3-diacyl-GlcN. Next, LpXH cleaves the pyrophosphate bond of UDP-2,3-diacyl-GlcN to form the intermediate lipid X. Then, LpxB, an inverting glycosyltransferase, catalyzes the transfer of 2,3-diacyl-GlcN from UDP-2,3-diacyl-GlcN to lipid X, and releases UDP. In the subsequent steps of the pathway, LpxK catalyzes the ATP-dependent phosphorylation of the disaccharide-1-P intermediate to form lipid IVa.²⁰⁸

The core oligosaccharides are successively constructed on lipid A through the action of several membrane-associated glycosyltransferases, using sugar nucleotide donors. For the inner core, the enzyme KdtA catalyzes the incorporation of Kdo residues at the 6'-O positions of the distal GlcNAc of lipid A, using the sugar nucleotide CMP-Kdo as the donor.²¹⁰ The resulting Kdo-lipid A is further acylated with fatty acids at the distal GlcNAc, catalyzed by LpxL and LpxM to form the hexa-acylated Kdo-lipid A.²¹¹

The assembly of the O-antigen takes place in the cytoplasm by GTs on membrane bound undecaprenyl phosphate. The O-antigen synthesis is not a stepwise addition of monosaccharides to the growing LPS,²⁰⁰ it is synthesized separately on a lipid carrier by the enzymes encoded by the *rfb* gene cluster and then transferred to the growing lipid A on the periplasmic face of the plasma membrane. The structural complexity of the Oantigens stems from variations in sugars, the sequences and linkages, and the substitution of monomers with either sugar or nonsugar residues. The structure of O-antigen may be linear or branched.²¹² During transportation from periplasm to inner membrane, the O-antigen is polymerized and connected to the core lipid A to form LPS²¹³

2.3.4. Structural Modification of Lipopolysaccharides and Bacterial

Virulence.—Gram-negative bacteria contain numerous genes to synthesize the various components of LPS and transport the whole complex to the cell surface.²¹⁴ In addition, they also contain genes to change the composition of LPS, the O-antigen, the core oligosaccharide, and even the most conserved lipid A.²⁰⁶ Structural modifications in lipid A, which usually occur in the fatty acid chain as well as in the hydrophilic sugar head, help the pathogen evade the recognition by host innate immune responses. The two phosphate groups in lipid A impart a net negative charge that helps to bind positively charged cationic antimicrobial peptides (CAMPs); however, some pathogens have evolved to contain a less negative charge to evade the immune attack. Some bacteria either remove the phosphate groups at the 1- and 4'-positions or modify them with phosphoethanolamine, which helps increase resistance to CAMPs.²⁰⁰

LPSs are key activators of immune responses during pathogenic infections. In milder infections, immune activation helps the host clear the pathogen; however, in more severe infections, induction of a cytokine storm might result in septic shock.²⁰⁰ Lipid A is responsible for immune activation, however, some Gram-negative pathogens modify lipid A structure to evade human TLR 4.¹⁹⁶ Some structural elements of Lipid A, particularly the phosphate group and fatty acyl chains, regulate TLR4 activation. For example, the *E. coli* lipid A, which is a potent immune activator consisting of two phosphate groups and six acyl chains with 12 or 14 carbons. In contrast, the highly infectious *Francisella tularensis* can produce LPS without the core-oligosaccharide and O-antigens.^{206,208}

3. SYNTHETIC GLYCOCONJUGATES

3.1. Synthetic Glycoconjugates and Their Clinical Significance

In nature, glycoproteins are highly heterogeneous, *i.e.*, various glycoforms are present at a given glycosylation site of the same peptide sequence. Therefore, to elucidate the underlying functions of carbohydrate in the context of glycoconjugates, a plethora of strategies and methods have been developed to prepare fully defined glycan structures and their conjugation to protein or lipid core. The synthesis of *O*- and *N*-glycoproteins was carried out through combined use of glycan and peptide synthesis or through ligation of synthetic glycopeptides or expressed proteins.²¹⁵ Neoglycoproteins are often considered as the best starting point to study the effects of glycan composition on protein function.

Pathogen-associated carbohydrate activates host immune responses during infection to induce cytokines and the production of antiglycan antibodies.²¹⁶ However, carbohydrates are weak immunogens, therefore their conjugation to a carrier protein is often necessary to enhance the immunogenicity. Some commonly used modifications on glycans includes introduction of alkenes, thiols, or activated esters at the reducing end for attachment of glycan to protein surface. The conjugation reaction usually takes place between an activated glycan and the primary amine of lysine residues, carboxylates, or the thiol group of cysteine on proteins, or with unnatural modifications that are site specifically inserted into the protein.²¹⁷ Alternatively, some cross-linkers have been developed that contain a difunctionalized spacer which is reactive against two different nucleophiles; for example, an amine from the glycan part and a thiol from the protein and vice versa.²¹⁸ Carbohydratebased vaccines using the carrier protein such as keyhole limpet hemocyanin (KLH), tetanus toxoid, or its nontoxic variant CRM¹⁹⁷ to facilitate multivalent glycan presentation for glycan specific immune responses are under development for cancers and infectious diseases.^{53,191} Other than carrier proteins, several other platforms have been explored for synthesis of glycoconjugates such as ferritin, dendrimers, polymers, nanoparticles, and carbon nanotubes etc. Gold nanoparticles have been used for glycan conjugation to study carbohydrate-protein interactions and to enhance the binding affinity through multivalent glycan presentation on the nanoparticle surface.²¹⁹

Conjugation of carbohydrate to lipids transforms glycans from being poorly immunogenic to being strong immune activators. Glycolipids play a dual role by interacting both with carbohydrate-binding and lipid-binding receptors, such as TLRs on immune cells, to induce an immune response.²²⁰ These interactions of glycolipids with immune cells could stimulate the immune system to exhibit adjuvant or modulation activities. The adjuvant activity of glycolipids has been demonstrated in synthetic vaccines through conjugation of immuno-active lipids to carbohydrate antigens.²²¹

3.2. Methods of Glycoconjugate Synthesis

3.2.1 Proteoglycan Conjugates.—The therapeutic potential of proteoglycans and their GAGs for new treatments remain unexploited because of their complex structural organization and association with various biophysical processes. Because of sulfation, most of the GAGs exist as anionic molecules linked to a protein backbone. Being

part of proteoglycans, GAGs also interact with other biomolecules through electrostatic, hydrophobic, and/or hydrogen bond interactions. Recently, GAGs grafted onto synthetic polymers, peptides, and nanoparticles have been explored for their therapeutic applications.

3.2.1.1. Glycosaminoglycan-Polymer Conjugates.: The proteoglycan, aggrecan, is composed of negatively charged CS linked to the core protein in a bottlebrush manner. Aggrecan is essential for connective tissue hydration; however, with age, enzymatic degradation of aggrecans affects its cellular synthesis and deficiency of this important biomolecule results in loss of tissue water retention. Recently, the Marcolongo group incorporated CS into a stable synthetic poly(acryloyl) backbone to mimic the naturally occurring aggrecan and serve as a tool for drug delivery and tissue enginering.²²² In another study, CS and heparin were grafted onto a hyaluronan backbone that is functionalized with a hydrazide linker.²²³ The construct prepared through reductive amination chemistry allows insertion of different ratios of CS and heparin side chains on the hyaluronic acid (HA) core.²²⁴ These copolymers were used for delivery of fibroblast growth factor (FGF-2) to mesenchymal stem cells (MSCs). The synthetic GAG copolymers has been used to fine-tune the graft density of PG mimetics for developing biomaterials with desired biochemical properties. The potential of embryonic stem cells (ESCs) for the treatment of neurodegenerative diseases, such as Alzheimer's disease (AD), multiple sclerosis (MS), and Parkinson's disease (PD), sparked a great interest in developing strategies for the efficient differentiation of ESCs into neural cells.²²⁵ Because GAGs have been implicated in the regulation of ESCs differentiation,²²⁶ treatment with exogenous GAG-grafted biomolecules for specific differentiation of ESCs into neural cells, emerged as a promising strategy.²²⁷ Interactions of growth factors with their receptors are often facilitated by PGs side chains. Heparin and HS can form ternary complexes with FGF2 and the corresponding FGF receptors presented on mouse ESC membranes.^{228,229} Recently, Liu et al. used lipidanchored synthetic GAG-mimicking glycopolymers (lipo-pSGF) for incorporation into the surface of ESCs to promote FGF signaling and ESC differentiation. The lipo-pSGF was found to bind efficiently to FGF-2 and enhanced the phosphorylation of ERK1/2, thereby promoting neural differentiation (Scheme 2a).²³⁰ In another related study, the Godula group reported fluorescently labeled synthetic neoproteoglycan conjugates to assess their affinity for FGF-2 using a microarray and the activation of ERK1/2. The synthetic neoproteoglycans were introduced into the plasma membrane of ESCs with deficient HS biosynthesis to study the possible mechanism involved in glycopolymer-mediated neural differentiation (Scheme 2b).²³¹

3.2.1.2. Glycosaminoglycan–Peptide Conjugates.: Conjugation of polyethylene glycol (PEG) to a protein or peptide drug has been proven to be beneficial for improving the pharmacokinetics.²³² PEGylation of peptides reduces renal extraction and degradation by proteolytic enzymes.²³³ However, PEG is not biodegradable, therefore, repeated administration resulted in cellular accumulation.²³⁴ In addition, PEGylated proteins or peptides often cause the production of anti-PEG antibodies.²³⁵ As an alternative to PEG, highly hydrophilic and biodegradable GAGs such as hyaluronan and heparosan (HPN) have been explored to improve the pharmacokinetics of protein or peptide drugs (Scheme 3).²³⁶ Recently, GAG conjugates of two antidiabetic peptide drugs, glucagon-like peptide-1

(GLP-1) and insulin, were shown to have much better half-life and blood-glucose lowering efficacy than unconjugated peptides after subcutaneous injection in mice.^{237,238} Various GAGs including chondroitin (CH) and heparosan (HPN) were conjugated to GLP-1 (at engineered Cys35) and insulin (at GlyA1, LysB29, or both) using a hydroxy succinimide-maleimide heterobifunctional linker and various arm lengths. Among the GAGs tested, conjugates containing CH and HPN provided the best-balanced profile of in vitro activity and circulation period in mice, suggesting that conjugation with GAGs is a promising strategy for improving the duration of peptide drugs.^{237,238}

3.2.1.3. Glycosaminoglycan–Nanoparticle Conjugates for Targeted

Delivery.: Functionalized nanoparticles have generated considerable attention in biomedical uses such as targeted drug delivery for cancer therapy and bioimaging.²³⁹ In particular, mesoporous silica nanoparticles (MSNPs) have been widely used as a carriers for anticancer drugs because of their biocompatibility, efficient surface functionalization, and chemical stability, *etc.*²⁴⁰ Several approaches have been explored for the targeted delivery of anticancer drugs to certain cancer cells. These strategies are relied on functionalization with specific ligands which can bind to the tumor-associated receptors to promote internalization *via* receptor-mediated endocytosis.²⁴¹ In this context, HA has been used to target CD44 on solid tumors, on metastatic cancers, and cancer stem cells.^{242,243}

HA-functionalized MSNPs incorporating doxorubicin (DOX) and a photosensitizer Chlorin e6 (Ce6) was used in photodynamic therapy (PDT) and chemotherapy to treat squamous cell carcinoma 7 (SCC7).²⁴⁴ The nanoconjugate (DOX/Ce6/HA-MSNP) binds CD44 ligand, and the whole complex undergoes endocytosis to exhibit photoinduced toxicity by forming highly reactive singlet oxygen (SO) in SCC7 cells. In other related studies, (i) doxorubicin loaded on HA-MSNPs functionalized with polyethyleneimine (PEI) has been used for targeted delivery with increased endosomal escape efficiency and controlled drug release;²⁴⁵ (ii) CD44-targeted HA nanoparticles were used to deliver siRNA into tumor cells;²⁴⁶ and (iii) HA-PEI/HA-PEG-based nanoparticles were also used to target CD44 on ovarian cancer for delivery of MDR1 siRNA *in vivo* to enhance drug potency and overcome MDRI-related multidrug resistance.(Figure 12).²⁴⁷

Lipid nanoparticles (LNPs) have gained tremendous momentum as a versatile nanocarrier platform to deliver many hydrophobic or hydrophilic therapeutic agents. A variety of drug liposome formulation have been developed and clinically approved for therapeutic use, indicating the success of this delivery platform from concept to clinic.^{248,249} For example, doxorubicin formulated with LNP was approved for ovarian cancer.²⁵⁰ Epaxal is another early example that used a LNP as the protein antigen in a hepatitis vaccine.²⁵¹ Many other liposome formulations have been approved, while numerous clinical trials are ongoing using liposomes for targeted delivery of anticancer, anti-inflammatory, antibiotic, antifungal, anesthetic, and other drugs and gene therapies.²⁵²

Liposomes consist of one or several lipid bilayers of phospholipids such as phosphatidylcholines, phosphatidyl ethanolamines, phosphatidylserines, and phosphatidylglycerols, and stabilizers such as cholesterol, ranging in size between 20 and $\sim 1000 \text{ nm}.^{253}$ Hydrophilic drugs can be enclosed in the aqueous interior of liposomes, while

hydrophobic drugs can be entrapped in the hydrophobic environment, making liposomes a versatile drug delivery system. The structure of liposome is dependent on the preparation method and liposome size is a critical parameter in determining the efficiency of drug encapsulation and half-life in circulation. The charge on the surface of lipid nanoparticle may be either positive or negative or zwitterionic based on the lipid headgroup that regulates the overall stability of the nanoparticles. Particles with neutral charge or low charge densities tend to aggregate over the time, whereas highly charged particles prevent aggregation.²⁵⁴

The important milestone in LNP-based drug delivery is evidenced by the recent development of COVID-19 mRNA vaccines by Pfizer/BioNTech and Moderna, which have shown notable effectiveness in disease prevention.²⁵⁵ The LNP formulation of mRNA encoding spike protein is delivered into host cells to produce spike protein as a foreign antigen and to elicits immune responses to the virus.^{252,256} The lipid nanoparticles of the two mRNA vaccines contain an ionizable lipid that is positively charged at low pH and is neutral at physiological pH to reduce toxicity and facilitate payload release.^{257,258} The LNPs also contain a PEGylated lipid to reduce the possibility of antibody association (opsonization) by serum proteins and clearance by phagocytes, thus conferring longer systemic circulation.²⁵⁹

3.2.2. Glycoprotein and Glycopeptide Synthesis.—Synthesis of glycopeptide or glycoprotein includes covalent attachment of a sugar residue or a glycan to an oligopeptide or protein. Glycopeptides and glycoproteins with precise glycan composition have been made by a variety of methods. Using the conventional solid-phase peptide synthesis (SPPS), the glycosylated amino acids can be coupled to the growing polypeptide chain; however, larger peptides are difficult to prepare because of accumulation of side products from incomplete reactions and epimerization that results in poor yield.²⁶⁰ As an alternative, the convergent coupling of a partially protected glycopeptide building unit to another short peptide has been used to overcome the issues with linear SPPS, but the stability of glycosidic bond remains a major problem in deprotection or release of the peptide from the solid support. Another straightforward strategy is direct coupling of the sugar residue to the aspartic acid side chain of polypeptide through amide linkage. Nevertheless, a key concern of this method is the low coupling efficiency of large oligosaccharides due to steric hindrance between glycans and peptide side chains.^{260–262}

Nowadays, chemoselective ligation has become an incredibly attractive approach to make homogeneous glycopeptides or glycoproteins. This technique allows the efficient conjugation of reactive glycosyl donors with unprotected peptides, avoiding protecting group manipulations. So far, the most efficient chemical method for the synthesis of glycopeptides and glycoproteins is native chemical ligation (NCL).²⁶² An alternative strategy is to combine the flexibility of chemical synthesis and the regio- and stereoselectivity of enzymatic synthesis. This chemoenzymatic method allows a convergent ligation of a preformed oligosaccharide to a polypeptide moiety, without the need for any protecting groups.²⁶⁰ Glycosyltransferases have been explored for stepwise addition of sugar residues on preformed glycopeptides using respective sugar nucleotide donors. In contrast, endoglycosidases, whose intrinsic activity is to cleave the β -1,4 linkage between two adjacent GlcNAc residues to release large intact oligosaccharide moieties from glycoproteins, were also shown to catalyze the transfer of various oligosaccharide

building blocks in the form of oxazolines to the GlcNAc acceptor in a single step.²⁶¹ A major disadvantage of this method is the nonselective reaction of oxazoline with protein, hydrolysis of the tranglycosylated product, and some of glycosidic linkages cannot be formed due to the lack of respective enzymes and the nucleotide sugars are expensive.

3.2.2.1. Native Chemical Ligation.: The concept of amide bond formation in the context of oligopeptide synthesis was first introduced by Kemp and co-workers *via* intramolecular aminoacyl transfer. In this strategy, a dibenzofuran scaffold was utilized to ligate a peptide bearing an electrophilic C-terminal activated ester with another peptide bearing a nucleophilic amino group at the *N*-terminal.²⁶³ Dibenzofuran moiety served as an auxiliary that facilitates the temporary formation of a disulfide linkage to bring the two peptides close enough for coupling with subsequent promotion of the O to N acyl transfer. Lastly, the auxiliary can be cleaved to afford the native peptide. Inspired by this strategy, several other scaffolds have been prepared for efficient peptide ligation to obtain large peptides or glycoproteins (Scheme 4a).²⁶⁴

In 1994, the Kent group introduced NCL that allows the chemoselective ligation of an unprotected peptide component with formation of an amide bond at the ligation site.²⁶⁵ In this approach, a peptide with a preinstalled C-terminal thioester couples with an *N*-terminal cysteine residue of another peptide to undergo thiol/thioester exchange to form a thioester intermediate with the cysteine thiol (Scheme 4b). This thioester intermediate promotes nucleophilic attack of the *a*-amino group of cysteine on the ester carbonyl that results in highly favored intramolecular S to N acyl rearrangement, leading to an irreversible formation of the native peptide bond. The introduction of *N*-terminal cysteine and thioester functionalities during the synthesis of polypeptides by SPPS provided additional flexibilities for insertion of unnatural amino acids. However, synthesis of peptide precursors on large scale for peptides large than 50 residues become a tedious and costlier endeavor that limits the use of NCL to smaller proteins or peptides.

NCL has been used as a powerful method for the preparation of biologically significant glycoconjugates. The Bertozzi group reported the NCL-based total chemical synthesis of antibacterial glycopeptide, diptericin *e*. Due to the lack of Cys residue in the primary sequence of diptericin, a G25C mutation was introduced at the connection site.²⁶⁶ In another early report, the same group employed NCL for the synthesis of a glycoprotein called lymphotactin (Lptn).²⁶⁷ Lymphotactin is an effective chemoattractant for T- and NK-cells, consisting of 93 amino acids and eight O-linked glycosites. In 2005, Unverzagt reported the first synthesis of an N-linked RNase B glycopeptide fragment having a complex-type glycan by NCL.²⁶⁸ The total synthesis of chemokine monocyte chemotactic protein-3 (MCP-3) containing 76 amino acid residues carrying a complex type N-glycan was first reported by Kajihara and co-workers, using a double NCL of three peptides with or without glycan.²⁶⁹ Later in 2012, the Danishefsky group reported the synthesis of two glycoforms of the *a*-subunit of human glycoprotein hormone (*a*-hGPH) bearing simple chitobiose units, as well as core-fucosylated, sialylated biantennary complex type N-linked dodecasaccharides.²⁷⁰ Following it, the total synthesis of homogeneous full-length β -hCG containing two chitobiose residues and four GalNAc moieties at the N- and O-glycosylation sites was reported by the same group in 2014 (Figure 13).²⁷¹

Despite its potential, the use of NCL in protein synthesis is limited by the necessity of having a *N*-termini Cys residue of one of the coupling partners. Therefore, to find an alternative to the use of *N*-terminal Cys residue, highly innovative methodologies have emerged involving the use of *N*-terminal auxiliaries.^{272,273} Although auxiliary-mediated ligations improved ligation efficiencies in peptide couplings, these methods suffer from longer reaction time, side reactions such as hydrolysis and epimerization, and tedious auxiliary removal steps. This limits their application in the preparation of large proteins.²⁷⁴

3.2.2.2. Expressed Protein Ligation.: The power of NCL combined with expressed protein ligation (EPL) allows synthesis of larger targets where one of the two coupling partners is often produced by recombinant DNA technology. Several methodologies for the synthesis of coupling fragments have been reported.²⁷⁵ For example, the peptide fragment with *N*-terminal cysteine was produced in bacteria by inserting a protease cleavage site adjacent to cysteine residue, which can be cleaved by proteases such as factor Xa and tobacco etch virus protease (TEV protease) to form the peptide fragment with *N*-terminal cysteine for coupling with the peptide containing a C-terminal thioester.^{276–278} The thioester containing coupling partner can be prepared as an intein fusion protein, which upon inteinmediated acyl transfer generates the fragment with C-terminal thioester for coupling with the cysteine containing fragment (Scheme 5).

The synthesis of a T-cell growth factor, interleukin-2 (IL-2), was reported by Tolbert et al.²⁷⁷ In this method, the C-terminal fragment containing the TEV protease recognition sequence (ENLYFQ) and a long C-terminal fragment of IL-2 (7-133) was expressed as a fusion protein. TEV protease mediated cleavage followed by NCL with a synthetic glycopeptide provided the homogeneous glycoform of full-length IL-2.²⁷⁷ The power of EPL was applied to the synthesis of maltose-binding protein (MBP) having homogeneous glycosylation.²⁷⁹ First, MBP was expressed in *E. coli* an intein fusion protein. Next. the thioester exchange reaction cleaves the intein from the protein, and the resulting thioester intermediate was then reacted *in situ* with a glycopeptide bearing an N-terminal cysteine, e.g., H-Cys-Asn(\beta-GlcNAc)-OH to give the thioester, which then went through an S-N acyl shift to furnish homogeneous MBP 26 bearing C-terminal glycosylation.²⁷⁹ Macmillan and Bertozzi reported a EPL-based synthesis of GlyCAM-1 containing two glycosvlated mucin subunits at both termini.²⁸⁰ The two consecutive ligations of glycosylated N- and C-terminal fragments with internal nonglycosylated fragment afforded the full-length multi-GalNAc containing glycoprotein.²⁸¹ EPL has also been utilized for preparation of full-length ribonuclease C and erythropoietin containing two complex type sialylated glycans (Figure 14).282-284

Entry of SARS-CoV-2 is initiated by interaction with host ACE2 receptor *via* the receptor binding domain (RBD) of the spike protein, which is an important target for vaccine design.^{285–287} However, the heterogeneous glycan compositions of the RBD may affect the neutralization and evasion of immune response generated by RBD-based vaccines.^{127,288} To understand the impact of RBD glycosylation on infection and antibody neutralization is of great interest; however, the size, physical properties, high structural diversity, and complexity of the RBD glycoproteins represent a significant synthetic challenge. Recently, EPL was used for construction of glycosylated RBDs containing homogeneous *N*-linked

glycans at N331, N343, and *O*-linked glycan at T323 (Scheme 6).²⁸⁹ The synthesis of homogeneous glycosylated RBDs was divided into two fragments: a synthetic glycopeptide RBD (319–360) fragment **1** with *N*-/*O*-glycans, which was functionalized with a C-terminal hydrazide; and a recombinant RBD fragment **2** (361–537) possessing an *N*-terminal Cys residue facilitating NCL. The glycopeptide fragment **1** (319–360) was prepared by NCL of fragment 3 (R319-L335) having desired glycosylation at sites T323 and N331 and fragment **4** (C336-N360) having biantennary complex type glycan at N343.

3.2.2.3. Sugar-Assisted Ligation.: To eliminate the necessity for Cys-bearing peptides, the Wong group developed a sugar-assisted ligation (SAL) strategy for synthesis of cysteine-free β -O-linked and N-linked glycopeptides.^{290,291} SAL utilized the acetamido group at the 2-position of sugar to introduce a sulfhydryl group for transthioesterification with peptide thioester that favors S \rightarrow N rearrangement at the ligation site. At last, the sugar can be regenerated by removal of the sulfhydryl group using hydrogenation (Scheme 7). This strategy was further extended with modified sugar analogues containing labels.²⁹²

3.2.2.4. Enzymatic Glycoremodeling for Synthesis of Homogeneous

Glycoproteins.: Glycosyltransferases have been used extensively for construction of a glycosidic bond.²⁹³ However, the use of GTs for large-scale production of glycoproteins is limited by their availability, strict substrate specificity, and use of expensive sugar nucleotide substrates such as UDP-Glc, UDP-GlcNAc, UDP-Gal, GDP-Man, GDP-Fuc, and CMP-sialic acid.²⁹⁴ However, one-pot in situ sugar nucleotide regeneration has been developed to overcome these limitations. Endoglycosidase catalyzed glycosylation of heterogeneous natural or recombinant glycoproteins is emerging as a powerful methodology for the production of proteins with homogeneous glycoforms.²⁹⁵ In a typical mechanism, endoglycosidase cleaves the β 1.4-linkage between the two adjacent GlcNAc residues at the N-linked glycosylation site to form mono-GlcNAc containing peptide or protein. Next, the predefined N-glycan oxazoline can be transferred en bloc to the GlcNAc protein via glycosynthase-catalyzed transglycosylation (Scheme 8).²⁹⁶ The transglycosylation based glycoprotein synthesis is enabled by exploitation of donor substrates and the discovery of glycosynthases, mutant of endoglycosidases without product hydrolyzing activities. Notable examples that include Endo-M, Endo-A, Endo-D, Endo-S, Endo-S2, and Endo-F3 with broader acceptor substrate specificity have been transformed into glycosynthases through site-directed mutagenesis.²⁶¹ Among those, EndoSN322A,²⁹⁷ EndoS2D184M,²⁹⁸ and EndoS2T138Q²⁹⁹ have been extensively used in the synthesis of complex glycoproteins, and glycopeptides such as glycosylated CD52, CMV, and pramlintide antigens and the homogeneous form of anticancer antibodies.

The synthesis of sperm-associated CD52 antigen carrying both *N*- and *O*-glycan at the predefined sites was accomplished by the Wang group.³⁰⁰ The GlcNAc-Asn and GalNAc-Thr building blocks were used to introduce GlcNAc and GalNAc residues at the desired sites using SPPS followed by transglycosylation of complex type glycan at the *N*-glycosite and glycosyl transferase mediated extension of GalNAc at the *O*-glycosite.³⁰⁰ In another related study, they also reported core-fucosylated bi- and triantennary complex glycoforms of CD52 (Figure 15).^{301,302} Several high-mannose glycopeptides derived from the human

cytomegalovirus (CMV) tegument protein pp65 and incorporated with T-cell epitope have been prepared by chemo-enzymatic synthesis to target human antigen presenting cells (APCs).³⁰³ In addition, a Man3 and sialylated complex type *N*-glycan variant of the antidiabetic drug, pramlintide were generated by using the EndoA-E173H and EndoM-N175Q mutants for transglycosylation, and the resultant glycopeptides showed both *in vitro* and *in vivo* activity as amylin receptor agonists with blood glucose lowering activity.³⁰⁴

3.2.2.5. Pathway Engineering.: In recent years, various methods of cell line engineering have been developed to produce proteins with desired glycosylation patterns in diverse species such as mammals, plants, insect, yeast, and bacteria.³⁰⁵ Among the techniques used, knockin, knockout, and knockdown of certain genes of the enzymes involved in glycan biosynthesis, overexpression of enzymes of interest, and small molecule inhibitors that change the activities of glycosidases and GTs inside cells, have been used to remodel glycosylation of expressed proteins. Advances in gene editing, like the CRISPR technology, facilitated the process of cell glycoengineering.^{306,307} Chinese hamster ovary (CHO) cells, for example, have been used widely to produce proteins with altered glycosylation pattern.³⁰⁸

The highly conserved N297 glycosite in the IgG Fc region is heterogeneously glycosylated with biantennary complex type glycans, containing core fuc, terminal GlcNAc, Gal, Neu5Ac, and bisecting GlcNAc.³⁰⁹ The composition of the IgG Fc domain glycan regulates the differential engagement of FcRs. It has been demonstrated that the a-1,6 linked Fuc residue on the core GlcNAc at N297 is the major determinant of antibody-dependent cellular cytotoxicity (ADCC), and therefore removal of Fuc residue considerably improved the ADCC activity.³¹⁰ Fucosyl transferase 8 (FUT8) catalyzes the a-1,6 linkage of Fuc to the core GlcNAc in the presence of GDP-fucose as substrate. Knocking out the FUT8 gene is an ideal strategy for recombinant production of IgGs with a low fucose content and improved ADCC. Yamane-Ohnuki *et al.* successfully demonstrated the production of anti-CD20 antibody from FUT8^{-/-} CHO/DG44 cell lines, which showed enhanced binding to the Fc γ RIIIA and 100-fold improvement in the ADCC activity compared to the antibody from normal CHO/DG44 cells (Figure 16).³¹¹

During glycan biosynthesis, *N*-acetylglucosaminyltransferase III (GnTIII) adds GlcNAc to Man residue through a β 1,4-linkage.³¹² Addition of bisecting GlcNAc to the *N*-glycan attached to Asn297 of IgG could also regulate ADCC. Umana *et al.* constructed a GnTIII cDNA transfected CHO cell line to produce antibodies with increased bisecting GlcNAc content and ADCC activity,³¹³ suggesting that bisecting GlcNAc has a positive impact on ADCC.

In addition to CHO cells, other mammalian cell lines such as NS0 and SP2/0 have been utilized for glycoengineering due to their easy handling and high-yield expression.³¹⁴ Apart from these, plant, insect, yeast, and bacteria cells have also been used for protein engineering.³¹⁵ Compared to mammalian cells, yeast expression systems are highly productive and cost-effective.³¹⁶ The utility of methylotrophic yeast *Pichia pastoris* facilitated the production of proteins with high mannose-type glycans.³¹⁷ Recently, bacterial expression systems emerged as a simple, quick, and cost-effective means for

glycoengineering.^{318,319} To lower the risk of an immunogenic response to nonhuman glycans, various strategies used to humanize yeast and to modulate bacterial glycosylation have been explored. Hamilton *et al.* developed a humanized *P. pastoris* strain through knockout of four yeast genes and knock-in of 14 heterologous glycosylation genes to produce human like erythropoietin with increased sialylation.³²⁰ The Wong group developed a glycoengineered yeast strain to produce antibodies of high-mannose glycoforms followed by endoglycosidase mediated cleavage and transglycosylation *in vitro* to generate homogeneous antibodies.³²¹ However, although there is a wide selection of nonmammalian expression systems available for glycoprotein production, none of them has been used routinely due to their complexity.

The N-glycan composition of IgG Fc domain contains mainly the G0F and G1F glycoforms with less amount of sialylation, wherein the Gal residues are critical for complementdependent cytotoxicity (CDC) and sialic acid is associated with anti-inflammatory properties.^{322,323} Therefore, various strategies have been developed to remodel or to enrich the desired glycosylation pattern. The Jeffery's lab attempted amino acid mutations in the Fc region of an antibody, including F241A, F243A, V264A, D265A, and R301A mutations, that were designed to provide access for GalT and SiaT to the glycosylation site, leading to more processed glycoforms.³²⁴ In another approach, hypergalactosylated antibodies were produced by knocking out genes ST3GAL4 and ST3GAL6 responsible for a 2.3-sialvl transferases.³²⁵ A single point mutation, F241A, in IgG-Fc resulted in production of IgG with 80% G2F and when further combined with a FUT8 knockout system, provides IgGs with 65% G2 glycoform (Figure 16).³²⁵ In addition to the point mutation F241A, overexpression of a2,6-SiaT and β 1,4-GalT produced IgG with 80% sialylation, the majority of which is a2.6-sialylation.³²⁶ Further work by Betenbaugh and co-workers showed that antibodies with 77% a2,6-sialyation could be achieved by overexpressing a2,6-SiaT and knocking out ST3GAL4 and ST3GAL6 with CRISPR/Cas9 in combination with four-point mutations (F241A, F243A, V262E, V264E) (Figure 16).³²⁷

3.2.2.6. Glycan-Mediated Antibody–Drug Conjugation.: Antibody–drug conjugates (ADCs) are one of the fastest growing biopharmaceuticals which are produced by conjugation of cancer cell-specific monoclonal antibodies with highly potent cytotoxic drugs.^{328,329} To date, a total of 11 ADCs have been approved by the FDA as a targeted therapy for cancer treatment. One of the key components of ADCs is the linker, which is responsible for coupling the cytotoxic drug to the antibody to maintain ADC stability during the systemic circulation.³³⁰ The conjugation site on the antibody along with the chemical properties of the linker play important roles in the stability and PK/PD properties of the ADC and the therapeutic window. In early development, cytotoxic drugs were nonselectively conjugated to the exposed lysine or cysteine, from interchain disulfides after partial reduction, on the antibody, leading to formation of a heterogeneous mixture with a varied number of drugs attached to several possible sites.^{331,332} This methodology resulted in reduction in potency and safety and made optimization of the process and pharmacological properties significantly challenging. Moreover, nonspecific conjugation near the complementarity-determining region may reduce binding affinity and specificity.³³³ To develop ADCs with controlled conjugation with a higher therapeutic

index, various methodologies have been explored to overcome the limitations of nonspecific conjugation.^{334,335} Some of the major strategies developed for site-specific conjugation include insertion of a specific amino acid, unnatural amino acid, short peptide, and glycan-based conjugation. The insertion of an unnatural amino acid in the antibody sequence allows site-specific conjugation of payload with a controlled drug–antibody ratio (DAR) for production of homogeneous ADCs.³³⁶

Glycan-based conjugation offers the unique advantage to couple the payload to the glycan N297 site in the CH2 domain rather than conjugation through amino acid residues. All IgGs have at least one conserved glycosylation site in the Fc domain.³³⁷ The biantennary complex type glycan present in the Fc domain can be used to generate the attachment site. For example, nonreducing end glycan residues, such as sialic acid, galactose, GlcNAc, mannose, and core fucose, have been explored to generate the conjugation site. The two major approaches to glycan-based conjugation include: (1) enzymatic deglycosylation of *N*-glycan to generate the acceptor, followed by enzymatic transfer of an unnatural sugar moiety containing a tag for conjugation, using a respective sugar nucleotide donor, and (2) endoglycosidase-mediated deglycosylation of IgG glycan leaving behind the innermost GlcNAc, followed by trans glycosylation with predefined oligosaccharide in the form of oxazoline, bearing the desired tag.

The fucose analogue 6-thiofucose was metabolically incorporated into anti-CD30 or anti-CD70 antibody for conjugation with maleimide containing monomethyl auristatin E (MMAE).³³⁸ The ADCs generated through thiofucose conjugation showed improved potency and homogeneity compared to the drug conjugate through hinge disulfides (Figure 17a). Qasba *et al.* discovered a mutant of galactosyltransferase, GalT(Y289L) that can transfer a modified GalNAc to GlcNAc acceptor.^{339,340} ADC generated using C-2 keto galactose conjugated to auristatin F showed excellent in vitro anticancer activity (Figure 17b).³⁴¹ In another study, GlcNAc-IgG obtained by endoglycosidase-mediated trimming of Fc *N*-glycan was used to introduce azido-GalNAc to the core GlcNAc using GalT(Y289L).³⁴² Payloads including MMAE, monomethyl auristatin F (MMAF), maytansine, or doxorubicin were efficiently conjugated to the azido-GalNAc with copperfree click chemistry to obtain homogeneous ADCs on gram scales (Figure 17c).³⁴² The anti-HER2 ADCs generated by this method showed a better in vivo antitumor activity compared to the ADC prepared by conventional lysine conjugation.³⁴²

Recently, terminal sialic acid gathered considerable attention for site-specific conjugation to obtained highly defined ADCs and glycoproteins. The native glycan on the N297 site of Fc domain lacks terminal sialic acid residues, therefore, in vitro sialylation has been performed to transfer either azido-modified or natural sialic acid using CMP-Neu5Ac as a donor and a mixture of β 1,4-Gal T and *a*2,6-Sial T to transfer Gal and Neu5Ac residues on to the native glycans of an antibody.³⁴³ The sialic acid residues could be oxidized under mild condition using periodates to yield aldehyde functionalized antibodies. The aldehyde or azido group on the sialic acid on IgG Fc glycan serves as a handle for conjugation *via* oxime ligation and copper-free click chemistry, respectively. Pan *et al.* reported a strategy in which an aldehyde group was introduced at the terminal Neu5Ac of the Fc glycan *via* periodate oxidation for conjugation to aminooxy functionalized cytotoxic drugs to achieve DAR ~

1.6 (Figure 17d).³⁴³ These glycoconjugated ADCs exhibited target-dependent anticancer activity and greater antitumor efficacy than the native antibody in a Her2-positive tumor xenograft model.³⁴³ In an alternative strategy, Haung *et al.* reported an Endo-S mutant that catalyzed the transglycosylation of Fuc- α 1,6 GlcNAc-IgG with a sialylated complex type *N*-glycan oxazoline to obtain a homogeneous Fc-sialylated antibody. The oxidation of terminal Neu5Ac residues formed an aldehyde, which was then treated with a cytotoxin bearing aminooxy or hydrazide nucleophiles to generate an oxime or hydrazone-linked conjugate, respectively (Figure 17f).³⁴⁴ The Boons group introduced a C-9 azido group on the terminal sialic acid of anti-CD22 monoclonal antibody Fc glycan. The azido moieties were then selectively conjugated using strain promoted alkyne–azide cycloaddition chemistry (SPAAC) to biotin, FITC, and the cytotoxic drug, doxorubicin (Figure 17e).³⁴⁵

4. GLYCOCONJUGATE THERAPEUTICS

4.1. Glycoconjugate Vaccines

4.1.1. Antimicrobial Vaccines.—The capsular polysaccharides (CPS) on the surface of pathogens served as an immunogen for development of vaccines against a variety of infectious diseases, including meningitis and pneumonia.^{346,347} After the first pneumococcal capsular polysaccharide vaccine was developed in 1917,³⁴⁸ several other vaccines, such as the tetravalent meningococcal, the *Haemophilus influenza* type b and *Samonella typhi* Vi *etc.*, were developed and routinely used in an immunization schedule.³⁴⁹ In polysaccharide vaccines, the APC are not involved in presenting the CPS to the B cells, therefore the CD4⁺ T-cells are not stimulated, resulting in a weak proliferation of B cells and production of IgM antibodies without affinity maturation.^{350,351} These limitations led to development of protein conjugate–polysaccharide vaccines.^{352,353}

The first pneumococcal glycoconjugate vaccine, Prevnar (PCV7), consisting of seven serogroups, 4, 6B, 9V, 14, 18C, 19F, and 23F, and conjugated to the carrier protein, CRM197, was used against infections caused by *S. pneumoniae* for children younger than 2 years.³⁵⁴ To cover additional serotypes, six more serotypes were included in PCV7 (PCV7 + 1, 3, 5, 6B, 7F, and 19A) to develop PCV13, which was approved in the USA in 2010 for use in children.³⁵⁵ The pneumococcal and meningococcal infections are controllable by the existing vaccines; however, continuous monitoring of the vaccine serotype coverage is required to combat emerging lethal serotypes. A typical example, PCV13 has been broaden with additional *S. pneumoniae* serogroups to develop PCV15 and PCV20 vaccines, both of which are in phase 3 clinical trials.³⁵⁶

The majority of the licensed glycoconjugate antibacterial vaccines were developed by conjugation of polysaccharides isolated from microbial culture to immunogenic carrier protein.⁵²

The main issues associated with manufacturing include glycan structural heterogeneity, complex purification, contamination with cell-based debris, and inconsistent protein conjugation steps.³⁵⁷ Synthetic glycoconjugate vaccines offer an attractive strategy to address the issues with traditional vaccine development and provide a safer and more effective alternative vaccine design. One of the significant discoveries in glycoconjugate

vaccine research is the development of the first synthetic glycoconjugate Hib vaccine, Quimi-Hib, which is composed of synthetically produced antigen comprising seven repeating units of poly-3- β -D-ribosyl-(1 \rightarrow 1)-D-ribitol-5-phosphate (PRP), conjugated to thiolated TT through thiol-maleimide coupling chemistry, was approved in Cuba for immunization of children against *Haemophilus influenzae* type b (Scheme 9).¹⁸⁸ However, the approved Quimi-Hib vaccine contains a mixture of various length polysaccharides; therefore, to identify the minimum glyco-epitope length for effective vaccine design, the Seeberger group assessed various lengths of well-defined Hib oligosaccharides conjugated to DT-CRM₁₉₇ in immunization studies. All of the vaccines were found to be immunogenic in a rabbit model, and it was revealed that the tetrameric conjugate is an excellent starting point for design of next generation Hib vaccines (Scheme 9).³⁵⁸

Neisseria meningitidis (N. meningitidis) is one of the causative agents of bacterial meningitidis worldwide among the population under the age of five years and in adolescents.³⁵⁹ Most of the lethal strains are surrounded by a polysaccharide capsule, which is used to differentiate 12 N. meningitidis serogroups. Six of them, A, B, C, W, X, and Y, cause the vast majority of infections in humans.³⁶⁰ Currently, there are three quadrivalent glycoconjugate vaccines available against serotypes A, C, Y, and W135.¹⁹⁰ For example, Menveo (GSK), consisting of polysaccharide of serotypes A, C, W135, and Y conjugated to CRM197, Menectra (Sanofi), consisting of polysaccharide of serotypes A, C, W135, abd Y conjugated to DT, and Nimenirix (Pfizer), consisting of polysaccharide of serotypes A, C, W135, and Y conjugated to TT. Furthermore, there are three monovalent serogroup C (Menjugate (GSK), and Meningtec and NeisVac-C (Pfizer)) and one serogroup A (MenAfriVac from the Serum Institute of India) vaccines available for all age groups. Glycoconjugate vaccines against serogroup B are limited by the concern of autoimmunity caused by self-antigen, the vaccine generated from the outer membrane vesicle (OMV) without any glycan antigen was developed and approved in Cuba against serogroup B.361 Various strategies have also been developed to prepare homogeneous glycoconjugate vaccines against N. meningitidis based on the serotype-specific repeating units of meningococcal capsular polysaccharide (Figure 18).³⁶¹

Pozsgay *et al.* reported the synthesis of MenA CPS fragments and their conjugation to human serum albumin (HSA) *via* Diels alder cycloaddition to evaluate their antigenicity by reaction with meningococcal A antiserum (Scheme 10a).^{362,363} The glycoconjugate vaccine against MenA CPS that suffers from poor hydrolytic stability is a CPS consisting of repeating units of $(1\rightarrow 6)$ -linked 2-acetamido-2-deoxy- α -D-mannopyranosyl phosphate.³⁶⁴ Therefore, replacement of the ring oxygen with a methylene group tends to be attractive strategy to enhance its stability. Accordingly, Gao *et al.* reported the carbocylic analogues of MenA CPS from monosaccharide to trisaccharide and their conjugation to CRM197 and HSA (Scheme 10b).^{365,366} Immunization of these glycoconjugates induced anti-MenA CPS specific IgG with in vitro antibacterial activity, although to a lesser extent than the isolated LPS conjugates to same carrier protein.³⁶⁶ In another study by Fallarini *et al.*, HSA conjugates of MenA CPS were able to induce both in vitro T-cell proliferation and in vivo antigen specific IgG production (Scheme 10c).³⁶⁷

The MenC polysaccharide a-(2,9)-linked polysialic acid with random acetylation at 7/8positions has been used for vaccine development. Despite having the O-acetylated (OAc1) polysaccharides in the licensed MenC vaccine, some MenC strains contain di-O-acetylated (OAc2) polysaccharide which may interfere with immune responce.³⁶⁸ Liao et al. reported a series of nonacetylated a-(2,9)-oligosialic acids of various lengths ranging from a dimer to a pentamer,³⁶⁹ synthesized using methodology originally developed by the Wu group (Scheme 11a).³⁷⁰ The synthetic polysialic acid was conjugated to a carrier protein such as KLH or HSA for immunization in mice.³⁶⁹ The vaccine elicited robust T cell response in mice and the trimeric form was shown promising as an integral part of vaccines against MenC. Later in 2016, the same group reported a new type of fully synthetic vaccine conjugate composed of α 2,9-linked di-, tri-, tetra-, and pentasialic acids as epitopes and the glycolipid monophosphoryl lipid A (MPLA) as adjuvant (Scheme 11b).³⁷¹ Evaluation of vaccination in C57BL/6J mice showed robust immune responses comparable to the corresponding polysialic acid conjugates and adjuvant. The MenW CPS consists of a glycan repeating unit of $[\rightarrow 6)$ -*a*-D-Gal*p*-(1 \rightarrow 4)-*a*-D-Neu*p*5Ac(7/9*O*Ac)-(2 \rightarrow]. Wang *et al.* disclosed the first iterative glycosylation and deprotection synthetic strategy for making MenW CPS oligosaccharides in various lengths from di- to decasaccharides to form the glycoconjugate with CRM197 (Scheme 11c).³⁷² The immunological evaluation suggests that the tetra saccharide is the minimum saccharide length required to induce bactericidal antibodies.372

N. meningitidis serotype X is considered to be a big health threat because currently available antimeningococcal vaccines do not cover the MenX capsular antigen. The CPS of MenX is a homopolymer of $(1\rightarrow 4)$ -linked 2-acetamido-2-deoxy-*a*-D-glucopyranosyl phosphate residues. A synthetic glycoconjugate consisting of MenX CPS fragments conjugated to CRM197 was used to determine minimal length for immunogenic activity.³⁷³ Upon immunization, it was revealed that oligomers longer than three repeating units are essential to mimic the native CPS.³⁷³ In another similar study, a tetrameric unit of MenX CPS conjugated to tetanus toxoid were immunologically evaluated for the development of a potential MenX vaccine candidate (Scheme 12b).³⁷⁴ Recently, a longer length MenX CPS fragment was prepared by an enzyme-catalyzed on-column elongation procedure using UDP-GlcNAc as a nucleotide donor and conjugated to CRM197 for immunological study in a mouse model.³⁷⁵ The functional antibodies generated from the vaccine are similar to those generated from immunization with naturally occurring or enzymatically prepared MenX CPS conjugates (Scheme 12c).³⁷⁵

Pneumococcal infection is caused by the bacteria *Streptococcus pneumoniae* (*S. pneumoniae*). Depending on the structures of their polysaccharide capsules, 97 serotypes (ST) of *S. pneumoniae* were characterized, and 20 of them caused 90% of pneumococcal disease.³⁷⁶ Currently, there are two types of vaccine available; a pneumococcal polysaccharide vaccine, PPSV23 (Pneumovax23), and pneumococcal conjugate vaccines such as PCV10 (Synflorix) and PCV13 (Prevnar13).¹⁸⁷ A 15-valent vaccine developed by Merck has lately finished late stage clinical trials and may be available in near future.³⁷⁷ The Seeberger group reported a synthetic glycoconjugate containing fragments of *S. pneumoniae* serotype 2 (ST2), 3 (ST3), and 8 (ST8) capsular polysaccharides (Scheme 13).^{189,378}

Vaccination with neoglycoconjugates consisting of polysaccharide fragments conjugated to CRM₁₉₇ elicited a robust T-cell-dependent B-cell response in mice.³⁷⁹

Some of the synthetic antibacterial and antifungal glycoconjugate vaccine candidates are summarized in Table $3.3^{380,381}$

The surface glycoproteins hemagglutinin and neuraminidase are the major determinants of immune response against influenza viruses,³⁹⁰ which are largely responsible for the outbreak of the influenza epidemic and pandemic.³⁹¹ Currently, immunization with chicken egg-derived inactivated virus is the common method to control influenza infections. However, current vaccines are only effective against circulating strains that closely match the inoculating strain and must be updated yearly. Our group studied the effect of glycosylation on the structure, folding, and function of influenza hemagglutinin from different strains and subtypes and identified two (N27 and N142) from six N-glycosites on each hemagglutinin monomer which are essential for hemagglutinin folding and viral infection.³⁹² The innermost GlcNAc residues were also found to be essential for folding and trimerization, and the epitopes covered by glycans are highly conserved. Using these findings, hemagglutinin-based universal influenza vaccines were developed with broadly protective immune responses, including the monoglycosylated hemagglutinin of consensus sequence.^{393,394} the egg-based virus with such monoglycosylated hemagglutinin on the surface,³⁹⁵ a chimeric hemagglutinin with consensus H5 as the head and consensus H1 as the stem, and the neuraminidase-defective attenuated virus.³⁹⁶ Immunization studies showed that the antibodies generated from hemagglutinin bearing only a GlcNAc residue at each glycosite showed better hemagglutinin stem selectivity, higher hemagglutinin inhibition, and broader neutralization activity against influenza subtypes than the antibodies elicited by fully glycosylated hemagglutinins. In addition, the highly conserved stem region of hemagglutinin was expressed in yeast and used as an immunogen for universal vaccine design.³⁹⁷ Upon immunization with C34 adjuvant, the monoglycosylated hemagglutinin stem protein induced cross-reactive antibody neutralization activities, strong ADCCmediated protection as well as T-cell responses against various strains, and a broad protection in challenge studies. Recently, a chimeric vaccine with consensus avian influenza H5 sequence as globular head and consensus human influenza H1 sequence as stem was shown to elicit highly effective and broadly protective antibody, CD⁴⁺ and CD⁸⁺ T cell responses against influenza variants.³⁹⁸ Interestingly, the mono-GlcNAc chimeric vaccine induced a high titer of stem-specific antibodies with improved ADCC, better neutralizing potency and cross reactivity against H1, H3, H5, and H7 strains and subtypes, as compared to the fully glycosylated chimeric vaccine. Immunization studies of the chimeric vaccine adjuvanted with glycolipid C34, showed higher levels of IFN- γ and IL-4 secretion and production of more CD8+ T cells.

The SARS-CoV-2 S protein exists as a trimer and contains 22 *N*-linked and at least 2 *O*-linked glycosites per monomer.²⁸⁸ The S protein glycosylation is critical for protein folding and for evasion of the host immune attack, and thus affecting the vaccine efficacy. Recently, the impact of site-specific S protein glycosylation on viral infectivity was studied, and the result showed that lung epithelial cells derived S protein is more infective than from other cell lines.³⁹⁹ The work has led to the development of mono-GlcNAc-containing

S protein (SMG) with better exposure of the conserved epitopes shielded by glycans as a candidate vaccine. The mice immunization studies with SMG suggested that glycodeletion is a simple and effective approach for development of a broadly protective COVID-19 vaccine. In another relevant study, the Wong group showed that the glycosite-deleted mRNA vaccine of S protein elicited robust antibody and CD8⁺ T cell responses with broader protection against diverse COVID-19 variants compared to the unmodified mRNA vaccine⁴⁰⁰

4.1.2. Anticancer Vaccines.—Glycan biosynthesis is a well-controlled phenomenon through the action of various enzymes involved in the pathway. Aberrant or unusual protein glycosylations, such as a change in glycosylation and carbohydrate composition is typically regulated by glycan processing enzymes, correlate with the development of diseases, most commonly cancer.^{149,401} Carbohydrates in the context of cancer, regulate tumor development, such as invasion, proliferation, and metastasis.⁴⁰² Accordingly, changes in the glycosylation patterns were recognized as a biomarker in the progression of human cancers. Cancer immunotherapy recently emerged as a potential treatment because of its excellent target specificity and lesser side effects. 403 However, most of the immunotherapeutic agents target tumor-specific surface proteins such as programmed death ligand-1 (PDL-1), cytotoxic T-lymphocyte-associated protein 4 (CTLA-4) etc. Targeting the tumor-associated carbohydrate antigens (TACAs) presents an alternative way to develop immunotherapeutic agents and therapeutic vaccines.¹⁹¹ Depending on their structures, TACAs are subcategorized into globo series glycolipids, such as Globo H, SSEA4, and SSEA3; the gangliosides, such as GD2, GD3, GM2, GM3, and fucosyl GM1; the blood group antigens, such as Lewis^x, Lewis^y, sialyl Lewis^x, and sialyl Lewis^y; and the glycoproteins including Thomsennouveau (Tn), Thomsen-Friendreich (TF), and sialyl-Tn (STn).^{157,404–407} TACAs are distinctly overexpressed in a large number of tumors such as breast, prostate, colon, ovary, and lung cancer, melanoma, neuroblastoma, B-cell lymphoma, etc., but not on normal cells.^{404,406} TACAs on tumor cells are immunogenic, rendering them a potential target for vaccine development.¹⁹¹ However, isolation of these tumor antigens from natural sources is extremely challenging due to their structural heterogeneity. Therefore, advanced methodologies in the field of glycan synthesis such as one-pot synthesis, chemoenzymatic synthesis, and automated glycan synthesis have been utilized to produce well-defined cancer antigens for anticancer vaccines development.

In many instances, carbohydrates are not immunogenic. However, a large majority of anticancer vaccines are composed of TACAs covalently conjugated to an immunogenic protein or lipo (peptide) carrier to induce a T-cell response, which leads to the production of high affinity IgG antibodies against the tumor expressing the antigen and to induce the activation of long-lasting memory B-cell and cytotoxic T-cells.^{192,408,409} Until now, various linker strategies and conjugation chemistries have been explored and a series of glycoconjugate tumor vaccines have been generated using TACAs such as gangliosides, Lewis structure series, *O*-glycans and Globo series, and carrier proteins including bovine serum albumin (BSA), keyhole limpet hemocyanin (KLH), diphtheria toxoid (DT), tetanus toxoid (TT), ovalbumin (OVA), and MUC1 peptides.^{53,192,408,410–414}

Depending on the type of glycan antigen and the components of immune activation, the glycoconjugate cancer vaccines are classified into monoepitope monocomponent, clustered

monoepitope monocomponent, clustered monoepitope multicomponent, and multiepitope multicomponent vaccines. The monoepitope vaccines containing a single glycan epitope conjugated to a carrier protein are most extensively explored,⁴¹⁵ and some of them, for example GM2-KLH⁴¹⁶ and sTn-KLH⁴¹⁷ vaccines, failed to achieve the desired end point and overall survival in phase 3 clinical trials.⁴¹⁷ The immune response generated by monoepitope vaccines did not react well with carbohydrate antigen,^{418,419} particularly the mucin-type glycan antigen which often present in clusters on the tumor surface.⁴²⁰ These limitations opened the opportunities for design of vaccines presenting clusters of tumor antigens. Accordingly, a Tn(c)-KLH conjugate adjuvanted with QS-21 (Scheme 14) was evaluated in phase 1 clinical studies to show that the level of prostate specific antigen (PSA) in treated population was either reduced or remained stable.⁴²¹ In another phase 1 clinical trial, a KLH conjugate of TF(c) in combination with QS-21 showed anticancer effects in patients with relapsed prostate cancer.⁴²² Zhu *et al.* designed and synthesized a vaccine construct consisting of three alternating repeats of Gb3 and MUC5AC peptide marker to target ovarian carcinoma (Scheme 14).⁴²³

Tumor cells usually express a mixture of carbohydrate antigens in different proportions at each stage during progression of the disease.⁴²⁴ Therefore, design of a multiantigen vaccine is a promising way to target a transformed tumor population. Danishefsky's group addressed this issue by mixing several mono-epitopes to form a single vaccine for administration. In the phase II clinical study, the patients were coinjected with monovalent KLH conjugates of GM2, Globo H, Lewis^y, TF(c), Tn(c), STn(c), and Tn-MUC1 mixed with adjuvant QS21 as a heptavalent vaccine.⁴²⁵ A strong immune response was elicited in the vaccinated patients against at least three antigens. The overall antibody titer against each of the antigens in the mixture was lower than administration of each vaccine individually, probably due to the overdose of highly immunogenic carrier protein and impaired the response against the TACAs.⁴²⁵ The similar findings were reported during coadministration of a mixture of GM2-KLH, Globo H-KLH, Le^y-KLH, TF(c)-KLH, Tn(c)-KLH, sTn(c)-KLH, and glycosylated MUC1-KLH.⁴²⁶ Therefore, a multi-epitope monocomponent pentavalent vaccine consisting of prostate and breast cancer specific TACAs was prepared and studied.⁴²⁷ In earlier attempts, three different TACAs, such as Tn, Le^y, and Globo H, were conjugated to KLH for immunization and the antigen specific IgM and IgG response was reported.^{427,428} Later, a highly elaborative multiepitope vaccine was prepared using Globo-H, STn, Tn, TF, and Le^y antigens as amino acid building blocks and coupled together via peptide bonds (Figure 19).⁴²⁸ The glycopeptide cargo was then conjugated to KLH for immunological evaluation to demonstrate that the vaccine induced strong IgG responses against each of the antigens except Le^{y, 429} Therefore, in the second generation vaccine, Le^y was replaced with a clinically proven TACA, GM2.^{428,429} In preclinical evaluation, antigen specific antibodies were elicited that recognized the cancer cells overexpressing the respective antigens. The vaccine was safe in a phase I clinical study and elicited a strong IgG and IgM titer against at least three or more antigens in the study population.⁴²⁹

Despite promising and encouraging preclinical results, most of the conjugate anticancer vaccines failed to enter advanced phase clinical studies.⁴³⁰ The major limitations include complicated conjugation steps, inconsistency in conjugation numbers, ambiguous nature of the glycoconjugate, and finally the strong immunogenicity of the carrier protein and

immunodominant functional groups in the linkers that ultimately affect vaccine efficacy and reduce the desired antibody response.^{191,431} Fully synthetic homogeneous vaccines were pursued, containing a TACA conjugated to an adjuvant or other immunological epitope without the use of carrier protein. The first synthetic vaccine of such kind was developed by Toyokuni *et al.*, in which a dimeric Tn antigen was conjugated to a TLR agonist such as the immunoactive lipopeptide, tripalmitoyl-*S*-glyceryl-cysteinyl serine (Pam3Cys) (Figure 20a).⁴³² The vaccine, di-Tn-Pam3Cys, induced an antigen-specific IgG response without the carrier protein. In another study, a series of Pam3Cys-based conjugates of Le^y antigens were prepared and studied for the impact of multivalent antigen presentation, conjugate structure, and adjuvant effect (Figure 20b).⁴³³

To induce antibody class switch and long-term memory B cells, the involvement of T cells is required for antibody affinity maturation in B cells. Accordingly, the two-component glycopeptide vaccines containing both B- and a T-cell epitopes were prepared and evaluated for their immune response. Lo-Man *et al.* reported a dendrimeric multiple antigenic glycopeptide (MAG) consisting of Tn antigen linked to a poliovirus (PV) CD4⁺ T cell epitope (Figure 21a).^{434,435} The elicited antibody cross reacted with murine and human tumor cell lines expressing the Tn antigen with antibody-dependent cell cytotoxicity.⁴³⁶

Dumy *et al.* designed regioselectively addressable functionalized templates (RAFTs) as new scaffolds to exhibit clustered Tn antigen (B-cell epitope) and the CD4+ helper T-cell peptide from the type 1 poliovirus (Figure 21b).⁴³⁷ The RAFT-Tn4–1PV and RAFT-Tn4– 2PV vaccines upon mice immunization, elicited antibodies that recognize the native form of the Tn epitope expressed on human tumor cells. In another study, a universal T-helper epitope, nonnatural pan HLA DR-binding epitope (PADRE) peptide, was used to prepare a glycopeptide construct composed of PADRE and three tumor-related epitopes from the human mucin MUC1, a nonglycosylated repeat unit and two units glycosylated with the Tn and TF epitopes, respectively (Figure 21c).⁴³⁸ A robust antigen specific response was generated upon immunization.⁴³⁹ Kunz's and co-workers conjugated sialyl-Tn glycopeptide antigen from the tandem repeat region of MUC1 to a TH-cell peptide epitope from ovalbumin (OVA_{323–339}) *via* nonimmunogenic linker (Figure 21d).⁴⁴⁰ It has been proposed that after this vaccine is taken up by antigen-presenting cells (APCs) to present the ovalbumin T-cell epitope to the T-cell receptor (TCR), it would lead to the activation and differentiation of naive T cells followed by stimulation of B cells.^{440,441}

Toll-like receptor ligands, for example tripalmitoyl-*S*-glyceryl cysteine peptides like Pam₃CysSer(Lys)₄, were used as immunostimulators by the Kunz group to construct a vaccine consisting of Pam₃CSKKKK lipopeptide conjugated to tumor-associated MUC1 glycopeptides containing Tn, STn, and TF antigens (Figure 22a).⁴⁴² Mice immunized with Pam₃Cys–icosaglycopeptide conjugates in combination with complete Freund's adjuvant (CFA) led to a specific humoral immune response; however, the antiserum titers were not as high as those from the corresponding MUC1 tetanus toxoid vaccine.⁴⁴² A monophosphorylated derivative of *Neisseria meningitidis* lipid A was also used as a built-in adjuvant for the construction of structurally defined glycoconjugate vaccines (Figure 22b). The Guo group reported MPLA conjugates of modified GM3,²²¹ STn,⁴⁴³ or Globo H⁴⁴⁴ and showed that MPLA derivatives with Globo H elicited high titers of antigen-specific

IgG antibodies compared to the use of modified sTn and GM3 antigens without an external adjuvant. $^{\rm 445}$

The first examples of anticancer vaccines without the use of a carrier protein or another immune stimulant epitope were developed by the Andreana group by conjugation of Tn or STn antigen to zwitterionic polysaccharides (ZPSs) that can induce MHCII-mediated immune responses (Figure 23).^{446,447} The immunization of the vaccine with commercially available MPL-based adjuvant elicited a strong immune response and high titers of IgM/IgG antibodies that not only recognized STn-expressing cancer cells (MCF-7 and OVCAR-5) but also showed complement-dependent cellular cytotoxicity.⁴⁴⁷

The presence of a B-cell epitope (TACA), a Th cell epitope, and a built-in adjuvant in a single construct led to development of three- and four-component synthetic vaccines to induce strong and long-lasting IgG responses. Accordingly, Boon's group developed a novel three-component vaccine consisting of a B cell epitope (tumor associated MUC1 glycopeptide), an adjuvant (Pam₂CysSK₄ or Pam₃CysSK₄), and a Th epitope (a mouse MHC class II restricted PV) (Figure 24a).⁴⁴⁸ The vaccine induced a highly robust IgG response that reacts with MUC1-expressing cancer cells without coadministration of external adjuvant.⁴⁴⁸ Later, Renaudet *et al.* prepared a four-component vaccine consisting of Tn antigen, PADRE, a CD8⁺ CTL peptide epitope (OVA_{257–264}), and a built-in adjuvant (Pam₃Cys) (Figure 24b).⁴⁴⁹ This vaccine elicited robust IgG/IgM, CD⁴⁺, and CD⁸⁺ T-cell responses against Tn antigen, PADRE, and OVA_{257–264}, respectively, probably due to proper antigen processing and presentation. Immunization of the resultant vaccine reduced the tumor size in the challenge study.⁴⁵⁰ These studies demonstrate the potential of cancer vaccines with B cell, CD4⁺, and CD8⁺ T cell epitopes as self-adjuvants.

Globo H, one of the most thoroughly studied TACAs, was originally isolated in the form of glycolipid from the breast cancer cell line, MCF-7.¹⁴⁹ In addition to its abundance on ovarian, gastric, lung, prostate, pancreatic, endometrial, and liver cancers, GloboH is an important regulator in the tumor microenvironment, promoting tumor progression through several mechanisms, therefore representing an ideal target in cancer immunotherapy.^{149,451} Adagloxad simolenin (OBI-822), originated in the Danishfsky lab, is a vaccine developed by the Taiwanese biotech company, OBI Pharma, consisting of the Globo H epitope covalently linked to the immunostimulatory carrier protein KLH (Figure 25). Adjuvanted by the potent saponin-based adjuvant OS-21, the Globo H-KLH vaccine was well tolerated in two phase I studies in patients with metastatic breast or prostate cancer.^{452,453} OBI-822 is currently in a phase 3 clinical trial (GLORIA) for the treatment of patients with Globo H-positive, triple-negative breast cancer. The second-generation GloboH vaccine was developed in our lab by using a different combination of carrier proteins and adjuvants. Globo H conjugated to DT-CRM₁₉₇ in combination with glycolipid adjuvant showed improved an immunological profile compared to the first-generation Globo H-KLH vaccine (Figure 25).⁴⁵⁴ Glycolipid C34 is a well-known ligand of the CD1d receptor present on DCs. Upon presentation of glycolipid by CD1d to the T-cell receptors on NK cells, activation of the NKT cells generated a selective Th1 response rather than Th2, and resulted in significant class switching to produce a robust IgG response against three globo-series epitopes: Globo H, SSEA4, and SSEA3.454

Because of the expression of TACAs on normal tissues or cells, some of the TACA-based vaccines faced major setbacks due to the self-tolerance by the immune system that resulted in poor immunogenicity. Unnatural modifications of TACAs have been used as a potential strategy to generate robust antibody responses that can cross react with native antigens on tumor cells (Figure 26). The Ye group introduced modifications on GM3 and STn antigens and then conjugated the modified antigens to protein carriers for vaccination.455,456 Mice immunization studies showed that the modified antigen-KLH conjugates elicited higher titers of anti-GM3/STn antibodies than the unmodified GM3/STn-KLH conjugates (Figure 26).^{455,456} More recently, the same group also reported several Globo H analogues with modification on the N-acyl group and conjugated to CRM₁₉₇. The immunological studies of modified GloboH-CRM₁₉₇ adjuvanted with glycolipid C34 showed that the fluorine-modified N-acyl Globo H conjugates induced higher titers of IgG antibodies that recognize and eliminate the cancer cells expressing the Globo H antigen (Figure 26).⁴⁵⁷ Another vaccine with azido modifications at the reducing and non-reducing ends of Globo H conjugated to CRM₁₉₇ elicited stronger IgG response than the native Globo H vaccine that can cross react with Globo H⁺ cancer cells.⁴⁵⁸

4.1.3. Anti-HIV Vaccines.—The HIV-1 envelope glycoprotein is a trimer of the heterodimer consisting of receptor-binding gp120 and transmembrane gp41 subunits. The gp120 spike is heavily glycosylated by the host derived glycosylation machinery, where half of the gp120 mass comes from the glycan coat.⁴⁵⁹ There are approximately 25 glycosylation sites, of which \sim 7–8 glycosites are in the V1/V2 and V3 variable loops, \sim 4 are in inner domain and the others in the rest of outer domain of gp120.⁴⁶⁰ Glycosylation on gp120 is essential for proper folding, viral infectivity, and to help the virus escape from host immune attack.⁴⁶¹ The outer domain of gp120 is the primary viral component first exposed to the immune system. However, dense glycosylation covers the large protein surface shielding the neutralization sensitive peptide epitopes from immune recognition. 462,463 Nevertheless, the discovery of broadly neutralizing antibodies (bNAbs) that penetrate the glycan shield and bind to the epitope consisting of both protein and carbohvdrate components offer exciting opportunities for development of glycoconjugate-based HIV-1 vaccine (Figure 27).^{464–468} First-generation bNAbs, such as 2G12 and b12, were reported to target a high mannose glycan patch on the gp120 outer domain and the CD4-binding site, respectively.^{469–471} Despite relatively weak coverage and potency, passive transfer of these antibodies provided protection against simian-HIV in rhesus macaques.^{469,472,473} Secondgeneration antibodies, including PG9, PG16, and PGT series antibodies, VRCO1, 35O22, VRC-PG05, and VRC-34.01, etc., were obtained by cloning antigen-specific antibodies from B-cells of HIV-1 positive donors.^{463,468} Structural and biophysical epitope mapping studies of these antibodies led to identification of several vulnerable targets on the viral spike protein. Most of these antibodies are in various phases of development for HIV-1 prevention and treatment.⁴⁷⁴ Synthetic carbohydrate-based immunogens, consisting of a glycan or glycopeptide mimic of epitopes recognized by the bNAbs conjugated to a protein carrier, are capable of inducing bNAbs.475

The bNAb, 2G12, was the first anticarbohydrate antibody to target the high mannose oligosaccharide patch on gp120, particularly at glycosylation sites N295, N332, N386, and

N392.⁴⁷⁶ The antibody was shown to bind Man₉ and Man₄ glycans where the terminal Man- α 1,2-Man disaccharide was involved in binding.⁴⁷⁰ In an attempt to mimic the 2G12 epitope, the Wang group reported a cholic acid scaffold conjugated to three high-mannose type Man₉GlcNAc₂ glycans regioselectively (Figure 28a).⁴⁷⁷ The cluster was found to be 46-fold more effective than monovalent glycan in competition assays. In another study, the same group used galactose as a scaffold to attach Man₉GlcNAc₂ glycan, which was identified as the best 2G12 ligand, using thiol–maleimide coupling methods. The 2G12 antibody showed 70-fold higher affinity toward the tetravalent Man9 cluster than Man₉GlcNAc₂Asn (Figure 28b).⁴⁷⁸ The oligocluster was then conjugated to either a carrier protein (KLH) or a universal T-helper peptide for vaccination. The rabbit immunization studies showed a modest antiglycan IgG response, weak cross reactivity with gp120, and lack of neutralization activity.⁴⁷⁹

The Wang group prepared another tetravalent cluster of Man₄GlcNAc₂, a D1 arm of Man₉GlcNAc₂, mounted on a cyclic peptide scaffold through Cu(I)-catalyzed Huisgen 1,3dipolar cycloaddition reaction (Figure 29a). Additionally, a fluoride was also introduced at 6-O position of the terminal mannose residue. The synthetic constructs were then coupled to T-helper peptide epitopes for 2G12 binding studies.⁴⁸⁰ In a similar study, the Danishfsky group designed a Man₉GlcNAc₂ cluster on a cyclic peptide scaffold containing 0-3 oligomannose units. The bivalent construct was then attached to outer membrane protein complex (OMPC), yielding almost 2000 glycopeptide copies per conjugate (Figure 29b).^{481,482} Immunological evaluation of the glycoconjugate in the presence of QS-21 adjuvant elicited a higher titer of antiglycan antibodies in guinea pigs and rhesus macaques. However, the antisera failed to cross-react with HIV gp160 and did not neutralize the different viral isolates.⁴⁸³ Our lab developed an AB3 type of dendrimeric scaffold to attach 3, 9, and 27 copies of synthetic Man₄ and Man₉ glycans and achieved an affinity for 2G12 that is comparable to that of gp120 for 2G12, suggesting that the synthetic glycodendrimer might be an ideal vaccine candidate.⁴⁸⁴ Constantino et al. exploited a flexible polyamidoamine (PAMAM) scaffold to attach four and eight copies of high mannose antigens such as Man₄, Man₆, and Man₉ to improve avidity toward 2G12 (Figure 29c). Conjugates of synthetic glycodendrons with DT-CRM₁₉₇ were prepared and formulated with MF59 adjuvant for immunization in mice and rabbits to elicit a strong antigen specific response; however, the antisera failed to recognize recombinant gp120.485 Burton and colleagues designed neoglycoconjugates consisting of a variable number of Man4 glycans on bovine serum albumin (BSA) (Figure 29d). Immunization of rabbits with BSA-(Man₄)₁₄ elicited Man₄ specific antibodies but again failed to bind gp120.486

The icosahedral capsids of bacteriophage $Q\beta$ has also been utilized because of its safety, immunogenicity, and ability to create multivalently on its surface.⁴⁸⁷ The $Q\beta$ is recombinantly expressed in *E. coli* and self-assembles into virus-like particles. Finn *et al.* prepared $Q\beta$ -Man₄ and $Q\beta$ -Man₉ to better mimic the oligomannose clustering on gp120 (Figure 30a).⁴⁸⁸ Later, Davis reported unnatural analogues of mannose residues and incorporated them at the termini of Man₄ glycan, which was then conjugated to bacteriophage $Q\beta$. The nonself D1 arm mimics are better inhibitors of 2G12/gp120 binding than the natural form both as unconjugated and protein-conjugated forms.⁴⁸⁹ In both studies, immunization of rabbits with both $Q\beta$ -Man₄/Man₉ and $Q\beta$ -nonself D1 arm generated
glycan-specific antibodies (Figure 30b).^{488,489} Nonetheless, these antibodies were not crossreactive to native gp120 and did not show any HIV-1 neutralizing activity. Recently, Nguyen *et al.* designed highly antigenic 2G12-binding glycopeptides through in vitro selection.⁴⁹⁰ The trivalent Man₉-glycopeptide conjugated to CRM₁₉₇ was used for immunization of mice in combination with Adjuplex as an adjuvant (Figure 30c).⁴⁹¹ Glycopeptide-specific antibodies were elicited with no detectable HIV-1 neutralizing activity. Interestingly, the immune response was raised against the core mannose residue.⁴⁹¹

Since the discovery of new bNAbs from HIV positive patients, including for example, PG9, PG16, and PGT series antibodies, research in glycan-based vaccines has shifted the focus to identify the real ligands of such antibodies that recognize the glycan epitopes on gp120. Kwong et al. reported the structure of PG9 cocrystallized with a scaffolded HIV-1 V1/V2 loop to demonstrate that PG9 interacts with gp120 through the N-linked glycans at N160 and N156/N173 and a peptide strand.⁴⁶⁶ Based on this information, the Wang group reported a series of V1/V2 glycopeptides from two different HIV-1 strains (CAP45 and ZM109).⁴⁹² The peptides were glycosylated with Man₅GlcNAc₂ and sialylated complex type glycans (SCT) at N160 and N156/N173 sites using transglycosylation of GlcNAc peptides with respective glycan oxazolines (Scheme 15a). Binding analysis studies of synthetic glycopeptides with PG9 suggest the necessity for Man₅GlcNAc₂ at N160 and additional SCT glycans at N156/N173 for high affinity PG9 recognition.⁴⁹² Later, the Danishfsky group generated V1/V2 loop peptides from HIV-1 A244 strains containing Man₅GlcNAc₂, and a core chitobiose at the N160 and N156 sites.⁴⁹³ The glycosyl amine building blocks were coupled to peptide fragments through a Lansbury aspartylation followed by NCL of two peptide fragments to construct the glycosylated V1/V2 peptide (Scheme 15b). The surface plasmon resonance (SPR) binding analysis suggests the binding of PG9 to only Man₅- and Man₃-containing peptides.⁴⁹³

The PGT series antibodies, such as PGT128 and PGT121, are highly potent and neutralize over 70% of globally circulating strains.^{464,494} Structural and biophysical studies showed that these antibodies recognize specific high mannose *N*-glycans (at N322 and N301) around the V3 loop and the conserved peptide domain in the V3 loop of gp120.464,495 To mimic the PGT antibodies epitopes, Wang et al. prepared V3 glycopeptide derived from the HIV-1 JR-FL strain containing Man₉GlcNAc₂ at the N332 site.⁴⁹⁶ In another related study, they also prepared V3 glycopeptide derived from the HIV-1 A224 strain, where the Man₉GlcNAc₂ glycan is located at the N334 site (Figure 31a,b).⁴⁹⁷ Synthetic glycopeptides were tested for their antigenicity by binding with bNAbs and showed that PGT128 is highly specific for high mannose glycan at N301/N332, antibody 10-1074 for high mannose glycan at N332, and PGT121 for sialylated complex type glycan at N301.⁴⁹⁸ Based on promising preliminary results, they prepared a three components vaccine by conjugation of V3 glycopeptides from both the HIV-1 strains (JR-FL and A224) to the T-helper epitope and the TLR2 agonist adjuvant. Immunization of rabbits with these synthetic immunogens elicited glycan-specific antibodies that were cross-reactive to various gp120s but failed to neutralize HIV-1 virions.497 Haynes et al. reported an HIV-1 JR-FL V3 glycopeptide fragment with two Man₉GlcNAc₂ glycans at N301 and N332 (Figure 31c) installed via Lansbury aspartylation.⁴⁷⁵ This HIV-1 JR-FL glycopeptide fragment containing two Man₉GlcNAc₂ glycans at N301 and N332 was used for immunization in

rhesus macaques to report that the glycopeptide induced antibodies bound specifically to envelope glycoprotein but did not neutralize HIV-1.⁴⁹⁹

Recently, the Wang group prepared another three-component vaccine wherein the V3 glycopeptide derived from the HIV-1 JR-FL strain was linked together to create a trivalent presentation followed by conjugation to T-helper epitope and the Pam3CysSK4 (Figure 32).⁵⁰⁰ A stronger glycopeptide-specific antibody response was generated that cross-reacted with heterologous HIV-1 gp120s and gp140 trimers, but the antisera did not show HIV-1 neutralizing activity.⁵⁰⁰

Design of the optimal immunogen for induction of bNAbs is the principal challenge in the development of HIV-1 vaccine. The discovery of bNAbs that recognize glycan-dependent regions on the HIV-1 Env protein, such as the high-mannose cluster centered at N332 (2G12) and the variable loops V1, V2 (PG9, PG16), and V3 (PGT-series) offered valuable information to the immunogen design. Among the synthetic glycoconjugate constructs studied to date, some can elicit an antigen-specific immune response and can cross react with HIV-1 gp120, but the induction of an effective HIV-1 protective response remains elusive.

4.1.4. Processing of Carbohydrate Antigen in Glycoconjugate Vaccines.—

APCs such as B cells, macrophages, and DCs, process and present antigens by major histocompatibility complex (MHC) molecules to T cells. As professional APCs, DCs are expert in the activation of naive CD8⁺ and CD4⁺ T cells by presenting antigens through MHCI and MHCII, respectively, and by providing cytokines and costimulatory stimuli.⁵⁰¹ DCs can uptake antigen through endocytic mechanisms, including phagocytosis, macropinocytosis, clathrin-mediated endocytosis, and trogocytosis. After uptake, protein antigens will be transported through early endosomes to proteosome, where it is processed into peptides by cathepsins. The processed peptides will be loaded on MHCII and presented to CD4⁺ T cells.⁵⁰² Meanwhile, through cross-presentation, exogenous protein antigens can be transported into the cytosol, where they are processed into peptides by the proteasome. Synthetic glycopeptides or glycopeptides from glycoprotein processed by DCs can bind to MHCI or MHCII molecules, and the complexes are presented to CD8⁺ or CD4⁺ T cells, respectively.⁵⁰³ Under normal conditions, resting DCs present endogenous peptide to maintain peripheral tolerance.⁵⁰⁴ DCs are activated upon receiving invaded signals through innate pattern-recognition receptors (PRRs). Mature DCs present foreign antigens, increase surface levels of costimulatory molecules, and secrete cytokines to stimulate adaptive immune responses.505

4.2. Glyco-engineered Therapeutic Antibodies

With over 60 antibody drugs available for use, monoclonal antibodies (mAbs) are one of the most successful class of biopharmaceuticals that are being used for treatment of life-threatening diseases such as cancers and autoimmune disorders.⁵⁰⁶ Certain types of mAbs, for example anticancer antibodies (rituximab, trastuzumab, and alemtuzumab), act by immune mediated effector functions such as ADCC and CDC. ADCC is a mechanism by which antibodies recruit immune cells to kill target cells through interaction of their Fc-domain with Fc γ receptors (Fc γ Rs) on immune cells such as dendritic

cells and macrophages.^{507,508} CDC is triggered when the IgG Fc domain interacts with complement component 1q (C1q), resulting in activation of complement cascade and lysis of target cells.⁵⁰⁹ Typically, the N297 glycosite in the IgG Fc domain is heterogeneously glycosylated,⁵¹⁰ with more than 30 different glycoforms, usually the biantennary complex type glycans bearing O-2 terminal galactose and mostly core fucosylated, being characterized.^{511,512} Recent studies demonstrated that the glycan structure on the IgG Fc-domain can differentially affect the biological activity and efficacy of therapeutic antibodies.^{513,514} For example, core Fucose at Fc-glycan significantly lowered the binding affinity to Fc γ IIIA receptor that led to reduction in ADCC.^{315,337} Moreover, the glycans bearing terminal *a*2,6-sialic acid has been implicated in anti-inflammatory activities of IVIG in animal models.⁵¹⁵ The high mannose glycan at N394 of the human IgE Fc domain is essential for initiation of anaphylaxis.⁵¹⁶ Therefore, the Fc-mediated effector functions of mAbs could be controlled by modulating Fc–Fc γ Rs interactions through optimizing the structure of the *N*-glycan present on the IgG Fc-domain.

4.2.1. In Vivo Glycoengineering.—Recombinantly produced therapeutic antibodies are highly heterogeneous in their Fc-glycosylation.⁵¹⁷ Thus, different strategies have been developed to produce highly defined homogeneous glycoforms or to enrich specific glycoforms for functional studies and improvement of therapeutic efficacy. In vivo alteration of the glycosylation pathway in host expression systems has been used to produce antibodies, with lack of core fucose, increase in galactose, and sialic acid content, etc.⁵¹⁸ Although glycan processing enzymes are well organized in the biosynthetic pathway, competition of the enzymes for acceptor substrates is the main factor causing the glycan microheterogeneity on expressed proteins. The addition of bisecting GlcNAc on core mannose residues of Fc N-glycan via overexpression of GnTIII to restrict the downstream action of α 1,6-fucosyl transferases to reduce core fucosylation³¹³ formed the basis of GlycoMab technology originally developed by Glycart Biotechnology (acquired by Roche).⁵¹⁹ This platform is used for development of the anti-CD20 antibody, Obinutuzumab, which was approved for the treatment of patients with previously untreatable chronic lymphocytic leukemia.⁵²⁰ Although bisecting GlcNAc inhibits core fucosylation, it is unable to block the glycosylation completely. Therefore, disabling the a1.6-fucosyl transferases activity encoded by the FUT8 gene has emerged as a powerful strategy.^{311,521} Potelligent Technology developed by Kyowa Hakko Kirin is one of the most successful platforms for production of 100% nonfucosylated antibodies using FUT8-/- CHO cells.⁵²² The anti-CCR4 antibody, Mogamulizumab, developed using this technology is the first glycoengineered antibody approved for treatment of relapsed/refractory cutaneous T-cell lymphoma.^{523,524} This platform has been used to produce several glycoengineered antibodies for clinical trials (Table 4). In fucosylation, the GDP-fucose is an essential substrate for $a_{1,6}$ -fucosyl transferases to transfer the fucose residue. GDP mannose 4,6dehydratase (GMD) is involved in the biosynthesis of GDP-fucose from GDP-glucose. Therefore, targeting GMD to interfere with GDP-fucose biosynthesis using GMD knock out CHO cells produced 100% nonfucosylated antibodies.^{525,526} In addition, introduction of heterologous GDP-6-deoxy-D-xylo-4-hexulose reductase (RMD), an enzyme that essential for biosynthesis of GDP-D-rhamnose could also inhibit GMD activity to reduce the GDP-

fucose level and ultimately lower the core fucosylation.⁵²⁷ This technology termed as GlymaxX was developed by ProBiogen.

The recombinant glycoproteins produced from mammalian cell lines such as CHO, BHK, or SP2/O can be heterogeneous and sometimes contain nonhuman glycans. For example, the glycoproteins from CHO cells contain nonhuman N-glycolylneuraminic acid (Neu5Gc). In addition, CHO cells produce glycoprotein with a2,3-linked instead of a2,6-linked Neu5Ac. Moreover, NS0 and SP2/0 mouse myeloma or baby hamster kidney (BHK) cells generate glycoproteins with Gal-a1,3-Gal (a-Gal epitope) that are recognized as antigenic epitopes by humans.^{528,529} To overcome these limitations, Glycotope developed GlycoExpress technology that offers a toolbox of glycoengineered human cell lines optimized for production of antibodies with the desired glycosylation to improve therapeutic potency.^{530,531} The GlycoExpress technology allows efficient control of production of glycoproteins with or without core fucose, $a_{2,3/2,6}$ sialylated or nonsialylated, digalactosylated (G2), or nongalactosylated (G0) glycans. For therapeutic efficacy, glycoproteins require a homogeneous and humanized glycosylation profile which may not be achievable using commonly used expression systems due to complex glycan biosynthetic pathway. To produce homogeneous glycoproteins, Meuris and co-workers developed the GlycoDelete technique, in which the GnT-I^{-/-} mutant of human embryonic kidney 293S cells [293SGnTI (-) cells] was produced to convert the N-glycans into hybrid and complex types. 532, 533

Other than mammalian expression systems, eukaryotic systems have been used for glycoengineering to produce nonfucosylated antibodies. Yeast-based expression systems gained considerable attention as an alternative to mammalian expression systems due to their high expression yields, less contamination with human viruses, and low production costs.^{321,534} However, the recombinant proteins produced by yeast expression systems generally cause immunogenic reactions due to presence of hypermannosylated glycans.³¹⁷ Therefore, various technologies have been developed to humanize the yeast expression systems. For example, Jacobs and colleagues have successfully produced humanized glycoproteins by altering the N-glycosylation pathway of the methylotrophic yeast Pichia pastoris.^{535,536} In this GlycoSwitch Technology, they knocked out the a1,6mannosyltransferase OCH1 gene involved in hypermannosylation and introduced various glycosyl transferases genes such as GnT-I, mannosidase II, and GnT-II to produce humanized glycoproteins.^{536,537} In another similar attempt, GlycoFi Inc. (acquired by Merck) also used *P. pastoris*, knocking out four genes and introducing 14 genes to produce a glycoprotein with 90% homogeneous human-like glycans.^{320,538} EPO produced using GlycoFi technology showed a remarkable improvement in potency and serum half-life compared to EPO produced using a wild-type expression system.⁵³⁹

In contrast to gene manipulation techniques, modified sugar analogues have been used as inhibitors of certain glycan biosynthesis pathway. For example, kifunensine, an a1, 2-mannosidase inhibitor that prevents the trimming of a1,2-mannose residues from highmannose glycans before they are processed to complex types, resulted in the production of polymannosylated glycoproteins. Okeley *et al.* reported fucose analogues such as 2-fluorofucose and 5-alkynefucose for the production of nonfucosylated antibodies by

selectively blocking the GDP-fucose biosynthetic pathway responsible for endogenous synthesis of fucosylated glycans.⁵⁴⁰ An anti-CD40 antibody, SEA-CD40, produced in CHO cells fed with fucose analogues, exhibits enhanced ADCC activity and is currently in phase 1 clinical studies.^{541,542} Later, 6,6,6-trifluorofucose and its 1-phosphonate analogue were reported as potent GMD inhibitors for the production of low fucose content antibodies expressed in CHO cells⁵⁴³ and from murine hybridoma cell lines.⁵⁴⁴

4.2.2. In Vitro Glycoengineering.—In-vitro Fc-glycoengineering of IgGs is an emerging technology to produce homogeneous antibodies with improved effector functions and for site-specific ADCs.^{561,562} The in vitro glycan remodeling of antibodies, using glycosidase to trim the terminal sugars or GTs to attach the glycan residues at the nonreducing end, has been employed on an intact antibody.⁵⁶² This method is independent of the production cell line and, therefore, has been used for making glycovariants of therapeutic proteins in milligram to kilogram quantities with relatively minimal production effort. The glycan profile of mAbs produced by GnTIII overexpressing CHO cells has been shown to have an increase in terminal galactose and a decrease in core fucose, and as a result, a significant increase in ADCC activity was observed.³¹³ In vitro glycoengineering has been used for the addition of bisecting GlcNAc to the degalactosysted Fc N-glycan of Rituxan and Herceptin, using recombinant rat GnTIII to obtain the modified mAbs with 31–85% GlcNAc content (Scheme 16).⁵⁶³ The modified mAbs with >80% bisecting GlcNAc content showed a 10-fold enhancement in ADCC activity with minimal effect on CDC. However, degalactosylation resulted in a 50% reduction in CDC compared to variably galactosylated control antibodies. In another study, scientists at Roche used GTs, such as $a_{2,6}$ -SiaT and $\beta_{1,4}$ -GalT, and activated sugars (UDP-Gal, CMP-Neu₅Ac) to edit the terminal glycosylation of Fc glycan of an intact IgG1 against a receptor of the EGFR family, expressed in CHO cells.⁵⁶⁴ This method allows production of well-defined antibodies in adequate quantities in less amount of time than cell line engineering. Recently, Washburn et al. reported a robust and scalable enzymatic approach for in vitro sialylation of IVIG.⁵¹⁵ The tetra-Fc-sialylated IVIG showed a 10-fold enhancement in anti-inflammatory activity in animal models. Despite significant developments, the success of this strategy relies on the IgG Fc N-glycan composition, and the efficiencies of the respective glycosidases and GTs used in the reaction sequence.

Another highly convergent two-step in vitro glycoengineering strategy is based on endoglycosidase-mediated removal of the highly heterogeneous glycan mixture at the desired glycosylation site, leaving behind the core GlcNAc on protein backbone. The predefined *N*-glycan is then transferred *en bloc* to GlcNAc catalyzed by glycosynthase to produce a homogeneous glycoprotein.^{297,565} The field picked up momentum when the Wang group reported two novel mutants of endoglycosidase S (EndoS) from *Streptococcus pyogenes*, namely, EndoS D233A, and D233Q with better transglycosylation activity and lower hydrolyzing activity, for glycosylation of GlcNAc- or core-fucosylated GlcNAc-containing antibodies.²⁹⁷ The discovery of these glycosynthase mutants led to the preparation of antibodies with desired glycoforms for functional studies.^{322,566–568} Our group used this platform for glycoengineering the anticancer antibodies, Rituxan and Herceptin, to identify the α 2,6-sialylated biantennary complex type glycan as the optimized

glycoform for enhancement of ADCC and CDC.⁵⁶⁶ Kurogochi *et al.* used Herceptin, having nonfucosylated pauci-mannose, high-mannose, and complex type glycans produced in transgenic silkworm cocoons. Glycoengineering using ENG'ases and their mutants (such as EndoSD233Q) provided a library of glycovariants of Herceptin to study the effect of Fc glycosylation on antibody effector functions.⁵⁶⁷ The Davis group used in vitro glycoremodeling of Herceptin to incorporate modified Neu5Ac with a chemical reporter in the Fc glycan for fluorescent imaging and ADC development.⁵⁶⁸

The potential of EndoS and its glycosynthase mutants for protein engineering is limited by their strict substrate specificity typically toward biantennary complex type glycans.^{569,570} Later, EndoS2, a glycosidase from the same family of EndoS, was reported to show much broader specificity toward high mannose, hybrid, and complex type glycans.⁵⁷¹ The systematic site-directed mutagenesis studies on EndoS2 by the Wang group identified residue D184, which is homologous to the EndoS D233, to prepare a series of mutants with excellent transglycosylation and diminished hydrolytic activity.²⁹⁸ Wong and co-workers identified several novel sites on EndoS2, including T138, D182, D226, T227, *etc.*, to prepare the mutants that can transglycosylate all high mannose, hybrid, bi-, and triantennary complex type glycans (Scheme 17).²⁹⁹ Other novel glycosynthase mutants (D165A and D165Q) of EndoF3 from the bacterial GH18 family were capable of transferring triantennary complex type glycans onto core-fucosylated IgG.³⁰¹ Apart from sugar oxazolines, sialyglycopeptide has been used as a substrate for transglycosylation to prepare homogeneous IgG glycoform.⁵⁷²

In addition to glycosylation in the Fc region, some antibodies are also glycosylated in the Fab region, which may be critical for the recognition of target and the half-life of antibodies. Nearly 20% of IVIG are *N*-glycosylated in the Fab region. Recently, an interesting study published by Wang and co-workers used a chemoenzymatic approach to manipulate Fc and Fab glycosylation of the therapeutic anti-EGFR antibody, Cetuximab.⁵⁶⁵ Using three different endoglycosidases (Endo-S, Endo-S2, and Endo-F3), their glycosynthase mutants and *a*1,6-fucosidase, the authors remodeled immunogenic *N*-glycans to sialylated complex type *N*-glycans and fully nonfucosylated galactosylated *N*-glycan at the Fc domain. The modified Cetuximab showed better affinity for the Fc γ IIIa receptor and significantly improved ADCC.⁵⁶⁵

Success of the in vitro glycoengineering platforms led to the identification of clinical candidates for cancer immunotherapy (Table 4).^{308,573} The first glyco-engineered Rituxan (CHO-H01) developed from CHOptimax technology by the Taiwanese Biotech company, CHO Pharma Inc., is in phase 2a clinical trials in Taiwan for the treatment of refractory or relapsed follicular lymphoma (ClinicalTrials.gov Identifier: NCT03221348). Moreover, GlycoT Therapeutics, a University of Maryland spin-off, is developing chemo-enzymatic glyco-engineering technologies to produce therapeutic antibodies or glycoproteins with well-defined glycoforms with unique properties.

4.3. Glycan-Based Adjuvants

Advancement in vaccine development technologies provided insights into their immunological mechanism for prevention of infectious diseases and in cancer

immunotherapy. Vaccines contain both molecularly defined antigen and immune activators, called adjuvants, to induce antigen-specific immune response. Compared to traditional whole-pathogen vaccines, the synthetic subunit vaccines are precisely designed for their efficacy and safety. However, the subunit vaccines are less immunogenic and therefore required adjuvants to enhance antigen-specific B and T cell responses.¹⁹¹ Alum has been the most widely used adjuvant used in approved vaccines.^{574,575} Cervarix, a combination of alum with the TLR-4 ligand MPLA, was approved for use in a vaccine against human papillomavirus (HPV) infections^{576,577} Vaccines adjuvanted with aluminum are not very immunogenic and only elicit antibody-mediated Th2 immune responses. MF59 is a potent oil-in-water emulsion used in anti-influenza vaccine with an excellent safety profile. MF59 is composed of squalene mixed with surfactants Tween 80 and Span 85 to significantly enhance the potency and breadth against the viral strains that are not included in the vaccine.^{578,579} Despite its potency, MF59 may not be suitable for every vaccine because of its poor induction of Th1 responses. Nevertheless, another Th1 immunoactivator, CpG, has been added to the MF59 to boost the immune response and the Th2 to Th1 shift.^{580,581} The adjuvant system, AS01, is a liposome-based combination of 3-O-desacyl-4'-monophosphoryl lipid A (MPL) and the saponin QS-21. AS01 has been used in the vaccine formulations targeting malaria and herpes zoster, for enhancing antigenspecific immune responses.^{576,582}

4.3.1. Monophosphoryl Lipid A (MPLA).—Because of their excellent biocompatibility and great safety profile, carbohydrate-containing adjuvants have been preclinically and clinically evaluated in human vaccines.⁵⁸³ Lipid A is the most bioactive component of LPS from Gram-negative bacteria, and it is mainly responsible for triggering a strong immune response through interactions specifically with TLRs.¹⁹⁷ The discoveries of different TLRs and their role as signaling receptors for lipid A facilitated the thorough investigation of TLR recognition that led to a better understanding of immune response.^{584,585} The number, structure, and location of fatty acid chains and the degree of phosphorylation determine the immunological and endotoxic activity of lipid A.⁵⁸⁶

In the 1970, Edgar Ribi removed the 1-O phosphate group of lipid A disaccharide from *Samonella minnesota* R595 through selective hydrolysis to prepare MPLA, a mixture of hexa-acylated diglucosamines, without polysaccharide side chains, and one phosphoryl group (Scheme 18).⁵⁸⁷ Compared to parent LPS, MPLA was at most 0.1% toxic, which had no impact on its immunostimulatory activity.^{587–589} Ribi Immunochemicals, a commercial supplier of the MPLA adjuvant system (a formulation of MPLA, trehalose, and oil), was acquired by Corixa and then by GSK Biologicals. Later, Myers *et al.* reported that removal of the 3-*O*-position fatty acid chain further reduced the pyrogenic properties without substantially affecting the adjuvant properties.^{590,591} The resulting MPL, which is isolated and structurally derivatized from the LPS of *S. minnesota* R595, was shown to be a safe and potent adjuvant.⁵⁹² Currently, MPLA is actively used by GSK Biologicals in several vaccine formulations, such as AS01, AS02, and AS04. The AS04 adjuvant system has been used in clinically approved vaccines such as FENDrix against hepatitis B virus and Cervarix against HPV.^{576,577} Combinations of MPL adjuvant and QS21 (AS15, AS02, and AS01)

have been developed to generate effective immune response against infectious diseases and cancers. 582,593

The majority of studies have demonstrated that the adjuvant activity of MPL is its ability to activate antigen presenting cells, such as DCs and macrophages, leading to induction of cytokines.^{594,595} Upon activation, these cells phagocyte, process, and present the vaccine antigen to T lymphocytes. In addition, MPL either directly or indirectly stimulates the induction of Th1.⁵⁹⁶ This capacity of MPL to stimulate the cytokine cascades necessary for the induction of cellular immunity make it an effective adjuvant by itself.⁵⁸⁵

Despite their clinical success, the MPLAs isolated from bacteria are highly heterogeneous in their structural integrity due to incomplete and nonspecific hydrolysis, which affect their biological activity. Extensive SAR studies with modifications to the carbohydrate part, phosphorylation, and the number of fatty acid chains of various lengths provided insights into their structure, toxicity, and adjuvant activities.^{597–599} In 1999, Johnson *et al.* modified the side chain lipids of MPL with different lengths of fatty acid chains to show that the chain length of fatty acid is the main determinant for adjuvant activity in human peripheral monocytes (Figure 33a).⁶⁰⁰ Later, Jiang *et al.* reported the study of modifying the reducing end sugar of MPLA with 3-*O*-substituted analogues and showed that there was no effect on the adjuvant activity as compared to natural lipid A (Figure 33b).⁶⁰¹

Corsaro *et al.* reported novel analogues of *E. coli* MPLA, including those with introduction of methyl phosphate, modification of 6-OH to aldehyde or substituted amides, and alteration of lipid pattern in addition to 6-O modifications (Figure 34).⁶⁰² Preliminary in vitro immunostimulatory evaluation suggests that some of these novel derivatives, particularly those with modification at the 6-O position, induce stronger TNF-*a* secretion than MPL.

Because of its strong immunostimulatory activities and nontoxic nature, MPLA has been utilized as a built-in adjuvant in combination with synthetic vaccines against cancers and HIV-1 in preclinical studies.¹⁹¹ In this context, MPLA has been utilized as carrier and a built-in adjuvant for synthetic vaccines against cancers and HIV-1 in preclinical studies. The covalent attachment of MPLA to various TACAs, including GM3, GM3 derivative (GM3NPhAc), STnNPhAc, Globo H, and *a*2,9-sialylated di-, tri-, tetra-, and penta-sialic acid showed more robust immune response than conjugation with protein carriers.^{221,371,443,603,604}

4.3.2. Saponin-Based Adjuvant QS-21.—QS21 is a purified plant extract derived from the soapbark tree *Quillaja saponaria* Molina.⁶⁰⁵ Structurally, QS-21 consists of four domains: a central quillaic acid triterpene backbone (black), a branched trisaccharide domain (blue) that is linked to the triterpene through glucuronic acid, a tetra saccharide domain (pink), and an acyl chain domain (red) which is linked to the triterpene through a hydrolytic labile ester linkage (Figure 35). QS-21 is a 65:35% mixture of two isomers, namely QS-21-apiose and QS-21-xylose, based on the structure of terminal sugar of the linear tetrasaccharide.⁶⁰⁶

QS-21 stimulates both Th1 and Th2 immune responses and activate the production of antigen-specific cytotoxic CD8+ T-cells.^{607,608} The immune stimulatory activities of QS-21 led to the development of its use as adjuvant, either alone or in combination (AS01, AS02) in numerous clinical studies of vaccines against different cancers 607 and infectious diseases.^{580,609} Recently, QS-21 containing the AS01 adjuvant has been approved in the vaccines against malaria (Mosquirix)⁶¹⁰ and shingles (Shingrix)⁶¹¹ from GSK.

Despite promising adjuvant activity and extensive clinical studies, the use of QS-21 alone as an adjuvant is limited by inherent issues, such as availability, toxicity, and the spontaneous hydrolysis of the acyl chain ester linkage.⁶¹² In addition, the mechanism behind the mode of action of QS-21 is poorly understood, which further hinders the rational design of potent adjuvant. Therefore, to address the limitations and to identify the functional groups that are crucial for its immunostimulatory properties, diverse semisynthetic QS-21 analogues were synthesized to establish the structure-activity relationships (SAR).^{598,607,613} One of the strategies to modulate QS-21 efficacy is through the chemical derivatization of naturally derived saponin. For example, Kensil et al. prepared QS-21 derivatives through modifications at the carboxylic group on the glucuronic acid and the aldehyde on the triterpene.⁶¹⁴ Immunogenicity evaluation of the antigen, and ovalbumin (OVA) in C57BL16 mice in the presence of QS-21 derivatives suggests that the modifications at the -COOH retained adjuvant activity, however, the modifications at the aldehyde did not show adjuvant activity for antibody production, suggesting that aldehyde functionality is involved in immune stimulation.⁶¹⁴ In a separate study, Marciani *et al.* reported the synthesis of the saponin adjuvant, GPI-0100 from Quillaia saponaria bark extract, by hydrolysis of the acyl chain followed by conjugation of dodecyl amine to the carboxylic acid of glucuronic acid via amide bond formation (Scheme 19a). The deacylated QS-21 induced a Th2 response but not a Th1 or cytotoxic T lymphocyte response, whereas the amidated variant, GPI-0100, restored the Th1 immunity and induced CD⁸⁺ T-cell responses.⁶¹⁵ The Michalek group reported the chemical synthesis of structurally defined OS-21616 and OS-17/18617-based adjuvant candidates. Among the QS-21-based analogues, the xylose substituted derivatives showed effective adjuvant activity and maintain a robust antibody response.⁶¹⁶ The synthetic QS-17/18 analogue IV showed an adjuvant activity similar to GPI-0100, with enhanced Th-1/Th-2 immune responses (Scheme 19b).⁶¹⁷ The same group recently synthesized two analogues of QS-7, differing in the acetylation at the 3- and 4-O positions of the quillaic acid C28 fucose residue. The acetylated analogues potentiated a mixed Th1/Th2 antigen-specific immune response, whereas nonacetylated analogues only induced a Th2-biased immunity, suggesting that 3- and/or 4-O acetyl groups of the fucose are crucial for the adjuvant activity of the QS-7 analogues.⁶¹⁸

Gin and co-workers pioneered the development of novel glycosylation strategies for convergent synthesis of homogeneous and pure samples of saponin isomers including QS-21_{Api},^{619,620} QS-21_{Xyl},⁶²¹ and QS-7_{Api}.⁶²² Gin's group also reported the design, synthesis, and adjuvant evaluation of QS-21 with stable amide bearing acyl chains.⁶²³ These novel, non-natural analogues exhibited no impairment in adjuvant activity but differ in toxicity profile (Table 5). The simplified acyl chain analogue [SQS-0102] showed unacceptable toxicity, while the [SQS-0103] was found to be safe but lost aqueous solubility.⁶²³ The carboxyacyl variant [SQS-0–0-4–5] showed improved water solubility

and excellent adjuvant properties when combined with anti-MUC1 and anti-KLH. In addition, the low toxicity of this variant made it into a promising lead for further modification.⁶¹³ Accordingly, truncations in the linear tetrasaccharide domain of [SOS-0-0-4-5] provided respective tri-, di-, and monosaccharide variants. Immunoadjuvant activity evaluation revealed that the trisaccharide derivative [SQS-0–0-5–5] is equipotent to QS-21, whereas the di- [SQS-0-0-6-5] and monosaccharides variants [SQS-0-0-9-5] resulted in higher toxicity and reduced potency. These results demonstrated that the end sugar of linear tetrasaccharide is tolerable for modification.⁶¹³ Later, to evaluate the role of the central glycosyl linkage in adjuvant activity, analogues with variable linker lengths, and stereochemistry were prepared and evaluated. These derivatives showed conformational dependent *in vivo* adjuvant activity.⁶²⁴ Next, saponin variants which contain iodobenzoic acid⁶¹² and aldehyde tucaresol⁶²⁵ on the acyl chain, with or without a branched trisaccharide domain were prepared to understand the effect of branched trisaccharide in the adjuvant mechanism. The new analogues were safe, highly potent, and induced both Th1 and Th2 responses, suggesting that the entire branched trisaccharide may be dispensable for adjuvant activity. The aldehyde on the triterpene was proposed to be important for Th1 immunity, however, the Gin group showed that the adjuvant activity was affected by the C4-aldehyde when measured with IgG responses in mice.⁶¹² The extensive SAR established on QS-21 and its semisynthetic analogues by the Gin group that led to the discovery of QS variants with enhanced adjuvant properties were described recently.609,613

4.3.3. a-Galactosyl Ceramide-Derived Adjuvants.—Invariant natural killer T (iNKT) cells are a type of cytotoxic T cells that are activated to secrete Th1 and Th2 cytokines upon interaction of the T cell receptors with a glycolipid presented by CD1d on dendritic cells. Activation of NKT cells triggers regulation of immune responses against pathogens, autoantigens, and cancers.^{626,627} NKT cells are classified into invariant NKT cells (iNKT) and type II NKT cells based on phenotype and the types of secreted cytokines.⁶²⁸ Both subtypes get activated upon binding to the glycolipid antigen.^{629,630} Many glycolipids from bacterial or human origins have been identified as activators of NKT cells.⁶³¹ KRN7000, a synthetic analogue of *a*-galactosyl ceramide (*a*-GalCer) isolated from the marine sponge Agelas mauritianus, is a potent antitumor agent in a variety of experimental and spontaneous tumor metastasis models.^{630,632} KRN7000 was originally developed by Kirin as a potent stimulator of NKT cells.⁶³³ It consists of a galactose head which is linked to ceramide through an *a-O*-glycosidic linkage. The crystal structure of Cd1d–glycolipid complex suggested that the fatty acid chain occupied the CD1d binding groove, while the sugar head was exposed to the surface for interaction with receptors on iNKT cells (Figure 36).^{634–636} The formation of CD1d–glycolipid complex activates iNKT cells that led to a massive secretion of IL-4 and IFN- γ cytokines with increased cytotoxic activity (Figure 36).^{637,638} In addition to activating other cell types such as T-, B-, NK-, and DCs, the secreted cytokines would also induce the Th1 response with antitumor, antiviral, and adjuvant activities or the Th2 response, which is correlated with autoimmune diseases.639,640,649

The structure of *a*-GalCer-CD1d binary complex revealed the hydrophobic interactions between a region residing the A' and F' pockets of Cd1d and the lipid chain of *a*-

GalCer.^{634,636} Therefore, changes in the lipid chain length was thought to affect the affinity of TCR toward the glycolipid–CD1d complex and ultimately, iNKT cell activation.⁶⁴¹ Miyamoto *et al.* reported an *a*-GalCer analogue with a shorter Phyto sphingosine chain, known as OCH, that stimulates iNKT cells to secrete higher amounts of IL-4 than IFN- γ .^{642,643} Modifications in the acyl chain resulted in the discovery of 7DW8–5, a phenyl glycolipid having a fluorophenyl substituted C10 fatty acid chain,⁶⁴⁴ which exhibited potent adjuvant activity in vaccines against HIV, malaria, and influenza vaccines and induced a robust CD8⁺ T-cell response in nonhuman primates (Figure 37).^{644–646} In addition, several 4-(4-fluorophenoxy)phenyl undecanoyl analogues of *a*-GalCer with different sugar heads (Gal and Glc) were prepared^{647,648} and shown to stimulate both murine and human iNKT cells and provide antipathogen protection as well as potent adjuvant effect when combined with Globo-H based anticancer vaccines.^{454,649}

Modifications on the sugar head of *a*-GalCer revealed that the *a*-anomeric conformation of the galactose moiety is essential for adjuvant activity as activation with both a-GalCer and *a*-GlcCer resulted in stimulation of NTK cells, but β -GalCer showed no proliferative responses.⁶³⁰ The a-anomeric configuration of the inner sugar is also found to be important in disaccharide sugar heads. For example, *a*-linked ceramides of Gal-*a*1,6Gal, Gal-*a*1,6Glc, Gal-a1,3Gal, and Gal-a1,2Gal could stimulate NKT cells when the inner sugar is either Glc or Gal despite the configuration of the outer sugar moiety, whereas Gal- β 1,4Gal- β -Cer could not.^{630,650} There was no difference in the stimulatory activity of a-GalCer and *a*-GlcCer, indicating that the 4-OH configuration of sugar appears not to be essential; however, a-ManCer showed no stimulatory activity, suggesting the importance of the 2'-OH of inner sugar, probably for the TCR contact site of the glycolipid.^{626,630} The necessity of the 2'-OH position was further confirmed by the modifications such as H, azido, amino, NHAc, methoxy, etc., that led to reduction in adjuvant activity. 598,630,642 Because the 4'-OH is not as sensitive to substitution as the 2'-OH position, Zhang et al. reported novel aromatic 4'-O substituted analogues that induced comparable Th1/Th2 responses.⁶⁵¹ while benzylmodified 4-O variants by Janssen et al. promoted Th1-biased immunity (Figure 37).652 Sulfation at 3'-O positions have also been reported to stimulate Th1 immune responses.⁶⁵³

According to the crystal structure of TCR/*a*-GalCer/CD1d ternary complex, the 6'-O position of Gal is pointed toward solvent and therefore not affecting the binding between the other complexes⁶²⁶ Accordingly, modifications such as *a*1,6-Gal, *a*1,6-Glc,⁶³⁰ and a small fluorophore⁶⁵⁴ at the 6'-O position of Gal retained the activity to stimulate NKT cells. The carboxylic acid and methyl substitution at the 6-O-position of Gal resulted in induction of both Th1 and Th2 responses.⁶⁵⁵ In addition, the 6'-modified substituted phenyl amide analogues with an intact phytoceramide tail made by Trappeniers *et al.* activated the secretion of Th1 cytokines and showed potent immunogenicity.⁶⁵⁶ In another related study, Liang *et al.* reported the study of analogues where substituted phenyl acetamide was introduced at 6-position of Gal that resulted in higher IFN- γ /IL-4 secretion than *a*-GalCer in vitro (Figure 37).⁶⁵⁷ Recently, addition of an acyl chain at the 6'-position of Gal resulted in stimulation of iNKT cells to induce a Th2 response. Interestingly, *a*-GalCer-6'-(1-naphthyl) urea (NU-*a*-GalCer) and *a*-GalCer-6'-(pyridin-4-yl) carbamate analogues with modification at the 6'-O position of Gal elicited Th1 response and reduced lung metastasis in the B16 melanoma model.^{658,659}

The C-glycoside is an analogue of *a*-GalCer where the glycosidic oxygen is replaced with the methylene group to show enhanced Th1 responses.⁶⁶⁰ Thioglycosides⁶⁶¹ showed no adjuvant activity in mice but induced Th1 responses in humans.⁶⁶² Removal of the 3-OH and 4-OH on the Phyto sphingosine polar portion produced nonstimulatory analogues, revealing that both hydroxy groups are important for NKT cell activation.⁶⁴² Moreover, modification at the 4-OH, such as a 4-deoxy-4,4-difluoro analogue, induced CD1d-dependent TCR activation of NKT cells.⁶⁶³ X-ray crystallographic studies revealed that the amide NH of phytosphingosine chain interacts with the *a*2 loop of mouse Cd 1d through hydrogen bond.⁶⁶⁴ The *a*-GalCer derivatives with inverted NH stereochemistry showed a reduced stimulation of mouse iNKT but not human iNKT.⁶⁶⁵ Replacement of the amide group with a cyclic ring system such as azetidine (RCAI-18) or pyrrolidine (RCAI-51) resulted in the induction of a slightly lower level of cytokines for RCAI-18, whereas RCAI-51 was not active to stimulate murine iNKT cells.⁶⁶⁶ Other modifications, such as replacement of the amide with an ester and methyl substitution at the amide nitrogen of *a*-GalCer, reduced cytokine secretion by iNKT cells.^{598,641}

4.4. Glycan-Mediated Targeted Delivery of Oligonucleotide Therapeutics

With 14 approved products in the markets and over 100 in the clinical pipeline, oligonucleotides are emerging as a class of therapeutics with extraordinary potential for treating a wide range of rare diseases.^{667,668} Oligonucleotide drugs are designed based on Watson-Crick base pairing and the sequence of the RNA associated with the disease. Representative oligonucleotide-based therapeutics include small interfering RNA (siRNA) that targets and degrades disease-causing mRNA through RNA-induced silencing complex (RISC) mediated RNA interference and antisense oligonucleotide (ASO) that binds complementary mRNA and induces sequence-specific cleavage of the RNA by endonuclease RNase H. Approval of several oligonucleotide-based drugs generated tremendous involvement by major pharmaceuticals as well academic laboratories; however, wide acceptance of oligonucleotides as a drug is limited by several properties such as large molecular weight and negatively charged phosphate backbone that restrict free uptakes of siRNA drugs by cells in the absence of any delivery agent. In addition, naked siRNAs are instantly cleaved by RNases, rapidly eliminated from circulation by kidneys and absorbed by liver, contributed to the poor drug-like properties of siRNAs..⁶⁶⁹ Although chemical modifications to the internucleotide linkages and the ribose sugar were introduced to improve serum stability, protein binding, and potency, and to lower immunogenicity, these modifications were still not enough to pass the lipid bilayer.⁶⁷⁰ Lipid nanoparticles have been used extensively for delivery of siRNA drugs to limit enzymatic degradation and to enhance endosomal escape.668

ASGPR was discovered by Gilbert Ashwell and Anatol Morell in 1965. They demonstrated that asialylated ceruloplasmin was rapidly cleared from the circulation and fully recovered in liver within 5–10 min, however degalactosylation of ceruloplasmin reduced the clearance, implicated the important of terminal galactose residues for recognition by ASGPR.^{671–673} The structure of carbohydrate ligand (GalNAc > Gal), ligand valency (4 = 3 > 2 > 1), and the spatial ligand arrangement play important roles in binding and, ultimately, clearance from the circulatory system.^{674,675}

Building on decades of work on ASGPR mediated delivery, scientists at Alnylam Pharmaceuticals conjugated a trimer of GalNAc to siRNA and showed that the conjugates had drastically improved RNAi activity in liver hepatocytes *in vivo*.^{676,677} Multivalent GalNAc moieties avidly bind to the ASGPR, therefore, the GalNAc–oligonucleotide conjugates were used for targeted liver delivery. Hepatocytes contains ~500 000 copies of ASGPR at surface of which 5–10% are present at a time during the recycling process.⁶⁷⁸ Cell surface ASGPR interacts with the GalNAc-siRNA in the presence of Ca²⁺ at pH > 6 in clathrin-coated pits on the plasma membrane, which then internalize the ligands *via* clathrin dependent receptor-mediated endocytosis.⁶⁷⁹ Following complete internalization, acidification during endosomal maturation dissociates the GalNAc-siRNA from the ASGPR, which then recycles back to the plasma membrane of the hepatocyte. At last, glycosidases in the endosome cleaves the tri-GalNAc ligands from siRNA and degrades the linker part within 4 h (Figure 38).⁶⁸⁰

The initial work on GalNAc-conjugated oligonucleotides focused on using a trivalent cluster with the presentation distance between sugars thought to be optimal at 15–20 Å between each GalNAc.⁶⁸¹ A trivalent cluster was linked to the oligonucleotide either by postsynthesis conjugation (*e.g.*, amide coupling, phosphonamidite coupling, or click chemistry) or by coupling the cluster to the solid support prior to the oligonucleotide synthesis. Great improvements in GalNAc-siRNA conjugates, including the siRNA sequence used, backbone modifications, and GalNAc presentation, facilitated the GalNAc-conjugated oligonucleotides-based drug development.^{681,682}

At the beginning, Alnylam Pharmaceuticals used the Tri-GalNAc ligands conjugated to the sense strand of siRNA *via* a (*3R*,5*S*)-3-hydroxy-5-hydroxymethylpyrrolidine moiety.^{676,677} The siRNA backbone was modified by introducing 2'-F or 2'-OMe substitutions on ribose sugar and with two phosphorothioate linkages at the 3' of the guide strand to enhance stability and binding affinity toward the target gene. Later, siRNAs are further modified, resulting in a significant enhancement in stability, pharmacokinetics, and higher potency than first-generation conjugates.⁶⁸³ This platform technology paves the way for Alnylam Pharmaceuticals to generate a promising pipeline of oligonucleotide medicines for cardiometabolic and liver diseases.^{679,684} Recently, the U.S. FDA has approved Vutrisiran (Amvuttra, Alnylam Pharmaceuticals) for the treatment of transthyretin-mediated (ATTR) amyloidosis.. Vutrisiran Sodium is a transthyretin (TTR) targeting siRNA conjugated to Tri-GalNAc.

Arrowhead Pharmaceuticals developed a dynamic polyconjugates (DPCs) platform using GalNAc as a targeting ligand. DPCs are composed of a polymer which is linked to a PEG to inhibit membrane interactions of polymer, a targeting ligand for delivery to specific cell type, and the siRNA, which is active pharmaceutical ingredient (API).⁶⁸⁵ Targeting ligand guides the cargo to the cell of interest and the DPC-siRNA complex is taken up into the endosome, where the low pH cause protonation of polymer that led to endosomal rupture and release of siRNA into cell cytoplasm. For the first-generation DPC technology, conjugation of siRNA to the polymer backbone was done though disulfide linkage. In the second-generation DPC.2 technology, the siRNA is not attached to the polymer but instead conjugated to targeting ligand and coinjected with DPC.⁶⁸⁶ By employing the

second-generation platform, Arrowhead Pharmaceuticals has established an attractive siRNA therapeutics pipeline.^{679,684,687} GalXC is another RNAi technology platform developed by Dicerna Pharmaceuticals.⁶⁸⁴ In this platform, GalNAc monomer is covalently attached to the four nucleotides in the extended region of dicer-substrate siRNAs. Data from clinical and preclinical studies suggested that GalXC platform offered higher potency, excellent targeting specificity, long duration of action, and high therapeutic index.^{679,684}

4.5. Targeted Protein Degradation *via* Carbohydrate-Specific Lysosomal Targeting Receptors

Recently, targeted protein degradation became a potential tool to eliminate disease causing proteins. In the past, many tools have been developed to degrade proteins by exploiting the natural protein homeostasis machinery available in our body.⁶⁸⁸ For example, PROTAC or the proteolysis-targeting chimera composed of a protein of interest (POI)-binding component attached to an E3 ligase-binding component using a suitable linker. PROTACs degrade proteins by catalyzing the K48 polyubiquitination of the POI, thereby marking it for degradation by the proteasome.⁶⁸⁹ While PROTACs have been around for a while, researchers have recently been digging into the possibilities of targeted protein degradation, and lysosome targeting chimeras (LYTACs), first reported by the Bertozzi group at Stanford University, was used to recruit proteins to lysosome-shuttling receptors located at the cell surface (Figure 39) for degradation.

The first-generation LYTAC consists of a POI-binding element attached to a synthetic glycopeptide ligand, an agonist of the cation-independent mannose-6-phosphate receptor (CI-M6PR). LYTACs employing antibodies as POI-binders have also been made, with one of them successfully degrading the neurodegenerative disease-causing protein: apolipoprotein E4 (ApoE4). LYTACS targeting membrane-associated proteins like EGFR, CD71, and PD-L1 has also been constructed.⁶⁹⁰ The second-generation LYTAC exploits liver-specific ASGPR using the tri-GalNAc-LYTAC conjugate to showcase the more efficient uptake than the M6Pn-LYTAC in an HCC cell line, owing to the surface abundance of ASGPR compared to CI-M6PR in hepatocytes.⁶⁹¹

Because of their high molecular weight compared to PROTACs, delivery of LYTACs is particularly challenging. In vivo studies of antibody-LYTACs showed a rapid clearance phase post injection, however, between 6 and 72 h, only a moderate decrease in serum concentration was observed.⁶⁹⁰ Nonetheless, LYTACs appear to be a promising new strategy for the targeted degradation of extracellular proteins and membrane-associated proteins. The liver-specific GalNAc-LYTAC has opened the possibility of synthesizing more cell type-specific LYTACs.⁶⁹²

SUMMARY

Carbohydrates are a fundamental part of human health and defects in glycosylation are a main contributor to human disease. Significant developments in glycobiology made this field more tractable and understandable. The implications of dysregulated glycosylation in disease progression, from immune evasion to cognition, led to considerable progress in

targeting glycans for therapeutic applications. In fact, glycobiology has already been started serving human health with several approved drugs, and some are currently in clinic studies.

Naturally isolated capsular polysaccharides as well as their conjugates with carrier proteins have been used in vaccine formulation for the treatment of various infectious diseases. However, naturally isolated polysaccharides are limited by their heterogeneous composition and difficulty in characterization. Consequently, vaccines with superior safety profile and clearly defined oligosaccharide structures with high manufacturing reproducibility are leading the carbohydrate-based vaccine research. The carbohydrates aberrantly expressed by malignant cells present a window of opportunity for development of glycoconjugate vaccines which can elicit T cell-dependent and long-term immune responses to eliminate tumor cells. Novel vaccine designs including multicomponent epitopes, vaccines with built-in adjuvants, and vaccines with highly immunogenic tumor antigens have fueled the clinical pipeline and increased the success of anticancer vaccine development.

For anticancer antibodies that work *via* ADCC, the fine structure of Fc glycans is crucial for safety and therapeutic potency. Different glycoforms have been shown to modulate the ADCC and CDC activities, and the pharmacodynamic and pharmacokinetic behaviors of the therapeutic antibodies, whereas other Fc glycan composition may become immunogenic. *In vitro* glycoengineering approaches using endoglycosidase-based glycosynthases facilitated the development of homogeneous IgG glycoforms with improved clinical outcome as next-generation therapeutic antibodies. In addition, the glycoengineering or synthetic glycobiology methods developed to produce humanized or human glycoconjugates from species ranging from bacteria to yeast and higher eukaryotes have opened new opportunities for discovery research and translational innovation.

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Biographies

Sachin S. Shivatare obtained his Ph.D. in Carbohydrate Chemistry (2013) from Academia Sinica, Taiwan, under the supervision of Prof. Chi-Huey Wong and Prof. Chung-Yi Wu. His doctoral thesis focused on development of chemoenzymatic synthesis of HIV-1 gp120 related complex carbohydrates, the development of glycan microarrays, and glycoconjugate vaccines. In 2013, he joined CHO Pharma Inc., Taiwan, as a senior scientist where he worked on the glycoengineering of therapeutic antibodies and the development of carbohydrate-based therapeutics. Later in 2019, he joined Prof. Wong's lab at The Scripps Research Institute, California, as a staff scientist. Currently, he is working at Amgen Inc., California, as a Senior Scientist. His research interest is development of biotherapeutic agents, such as antibody–drug conjugates, and glycoengineered antibodies with improved therapeutic potencies, development of technologies for oligonucleotide drug delivery.

Vidya S. Shivatare obtained her Ph.D. in Chemistry (2015) from Academia Sinica, Taiwan. In 2015, she joined Prof. Wong's lab at Genomics Research Center, Academia Sinica,

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ABBREVIATIONS

ACE2	angiotensin-converting enzyme 2
ADCC	antibody-dependent cellular cytotoxicity
ADCs	antibody drug conjugates
APCs	antigen presenting cells
ASGRs	asialoglycoprotein receptors
B3GNT5	N-acetylglucosaminyltransferase 5
B4GALNT1	β 1,4 GalNAc transferase
ВНК	baby hamster kidney
bNAbs	broadly neutralizing antibodies
BSA	bovine serum albumin
CAMPs	cationic antimicrobial peptides
CDC	complement-dependent cytotoxicity
CHO cells	Chinese hamster ovary cells
CPS	capsular polysaccharide
CRD	carbohydrate-recognition domain
DAR	drug–antibody ratio
DC-SIGN	dendritic cell-specific ICAM-3-grabbing non-integrin 1
DT	diphtheria toxoid
Endo	endoglycosidase
EPL	expressed protein ligation
ER	endoplasmic reticulum

Fc 7 Rs	$Fc \gamma$ receptors
FGF2	fibroblast growth factor 2
FITC	fluorescein isothiocyanate
FUT8	fucosyl transferase 8
GAGs	glycosaminoglycans
GBPs	glycan-binding proteins
G-M CSF	granulocyte-macrophage colony stimulating factor
GMD	GDP mannose 4,6 dehydratase
GnTIII	N-acetylglucosaminyltransferase III
GPI	glycosylphosphatidylinositols
GSLs	glycosphingolipids
GT	glycosyl transferase
H. influenza	Haemophilus influenza
HPI	host-pathogen interactions
HSA	human serum albumin
IFNg	interferon g
iNKT cells	invariant natural killer T cells
KdO	3-deoxy-D-manno-octulosonic acid
KLH	keyhole limpet hemocyanin
LPS	lipopolysaccharides
MAG	myelin-associated glycoprotein
MAG	multiple antigenic glycopeptide
MERS	Middle East respiratory syndrome
MPLA	monophosphoryl lipid A
MSCs	mesenchymal stem cells
MSNPs	mesoporous silica nanoparticles
NCL	native chemical ligation
Neu5Gc	glycolylneuraminic acid
NKT cells	natural killer T cells

OVA	ovalbumin
Pam3Cys	tripalmitoyl-S-glyceryl-cysteinyl serine
PAMAM	polyamidoamine
PEG	polyethylene glycol
PG	proteoglycans
RAFT	regioselectively addressable functionalized templates
RBD	receptor binding domain
SAL	sugar assisted ligation
SARS-CoV-2	severe acute respiratory syndrome coronavirus 2
Siglecs	sialic-acid-binding immunoglobulin-like lectins
SPPS	solid-phase peptide synthesis
ST3GAL5	a 2,3-sialyltransferase 5
TACA	tumor associated carbohydrate antigens
TCR	T-cell receptor
TLRs	Toll-like receptors
TNFa	tumor necrosis factor a
TT	tetanus toxoid
UDP	uridine diphosphate
ZPSs	zwitterionic polysaccharides
<i>a</i> -GalCer	<i>a</i> -galactosylceramide

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Figure 1:

Cell surface glycoconjugates in living systems. Membrane carbohydrates are linked to glycolipids and glycoproteins. Proteoglycans have part of their amino acid sequences inserted among lipid chains.



Figure 2:

Schematic presentation of diverse types of GSLs. Major GSLs expressed in immune cells and proposed GSL biosynthetic pathways.



Figure 3:

a) Role of glycoconjugates in biological processes. b) Schematic of overall structure of C-type, S-type, P-type, and I-type lectins. The number of domains accompanying the CRDs varies among family members.



Figure 4. Cell surface glycans in healthy and diseased states.



Figure 5:

Structures of representative cancer associated glycans.



Figure 6:

a) Biosynthetic pathway of SSEA3, GH, and SSEA4 involving B3GalT5. b) The key role of the B3GalT5 enzyme and the globo-series GSLs in the apoptosis and survival of breast carcinoma cells.



Figure 7: General structure of proteoglycans.



Figure 8: Representative structures of N-linked oligosaccharides.



Figure 9:

General structure of O-linked oligosaccharides.

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Figure 10:

Biosynthetic pathway for A) N-linked; and B) O-linked glycoprotein synthesis.



Figure 11.

A general structure for bacterial lipopolysaccharides (LPS).



Figure 12.

a) HA-functionalized MSNPs incorporating doxorubicin (DOX). b) CD44-targeted HA-PEI -based nanoparticle to deliver DOX, siRNA, and MDR1 siRNA.



Figure 13: Examples of glycoproteins prepared by NCL.





Structures of glycoproteins prepared by EPL-based methods.



Figure 15:

Synthesis of glycosylated peptides.





Strategies for cell line engineering to remodel protein glycosylation.





Strategies for glycan-based site-specific antibody-drug conjugation.


Figure 18:

Chemical structures of meningococcal capsular polysaccharide repeating units from different serogroups.



Figure 19:

Pentavalent vaccine containing Globo H, STn, Tn, LeY or GM2 and TF conjugated to KLH.



Figure 20.

Fully synthetic two-component vaccines linked to Pam3Cys adjuvant, a toll-like agonist.



Figure 21:

Two component synthetic vaccines. a) Th epitope PV conjugated Tn glycopeptides; b) Th epitope PV conjugated with RAFT cyclic peptide and tetravalent of Tn; c) Th epitope PADRE conjugated Tn and Tf-MUC1.



Figure 22.

Two component synthetic vaccines. a) TLR2 ligand Pam₃CSKKKK conjugated to MUC1 glycopeptides containing Tn, STn, and TF antigens. b) MPLA conjugates of modified GM3, STn, or Globo H.







Figure 24.

Examples of three- and four-component vaccines



Figure 25: Structures of Globo H-KHL and Globo H-DT vaccines.



Figure 26. Structures of TACA modified vaccines.



Figure 27:

a) Schematic diagram of HIV-1. b) Epitopes of bNAbs on trimeric HIV-1 envelope spike glycoprotein. Antibodies in green font (phase 3), red (phase 1), and blue (preclinical).



Figure 28:

a) Structure of a cholic acid-based oligomannose cluster to mimic the 2G12 epitope;

b) Tetravalent Man₉GlcnAc₂ scaffold conjugated to KLH and T-helper peptide for immunization.







Figure 30:

a) Bacteriophage $Q\beta$ conjugated to Man₈ and Man₉ glycans. b) Unnatural Man₄ cluster on bacteriophage $Q\beta$. c) Trivalent Man9-glycopeptide conjugated to the CRM₁₉₇.



Figure 31:

Synthetic V3-targeting bNAb epitope. a) glycopeptides from JR-FL (left) and A244 (right) strains. b) Structure of three-component vaccine bearing gp120 glycopeptide, T-helper epitope, and a TLR2 agonist adjuvant. c) JR-FL strain-derived V3 glycopeptide.



Figure 32:

The three-component vaccine containing A244 derived V3 glycopeptide, a T-cell epitope and a TLR2 agonist adjuvant.



Figure 33:

a) MPL derivatives with various length fatty acid side chains. b) MPLA derivatives bearing varied 3-*O*-substitution.



Figure 34:

Structure of *E. coli* MPLA and its semisynthetic modifications in lipid pattern, phosphate group, and at the 6-O hydroxy position.



Figure 35: Structures of QS-21 and its four domains.



Figure 36:

Structure of α-GalCer, a synthetic analogue of a glycolipid isolated from the marine sponge *Agelas mauritianus*. b) Mechanism of NKT cell activation.



Figure 37: Structural modifications of α -GalCer for SAR studies



Figure 38:

Targeting the ASGPR for delivery of GalNAc-siRNA to hepatocytes.



Figure 39:

LYTAC technology for targeted degradation of cell membrane and extracellular proteins.



Scheme 1: Biosynthetic pathway for the synthesis of bacterial LPS



Scheme 2:

a) Synthesis of lipid-anchored GAG biomimetics and their incorporation into mouse ESC cell membranes for neural differentiation. b) Microarray screening of a library of fluorescently labeled neoproteoglycan conjugates for those binding to FGF2 and promoting neural differentiation.



Scheme 3:

GAG conjugates of anti-diabetic peptide drugs, Glucagon-like peptide-1 (GLP-1) and Insulin, to improve pharmacokinetics



Scheme 4:

a) Dibenzofuran-Based Rigid Scaffold Mediated Ligation of Peptides. b) Mechanism of Native Chemical Ligation.



Scheme 5:

Mechanism of expressed protein ligation



Scheme 6:

Semisynthetic preparation of SARS-CoV-2 RBD glycoforms using EPL.



Scheme 7: Mechanism of SAL



Scheme 8:

Catalytic mechanism of glycosidase and glycosynthase during glycoprotein glycoremodeling.



Scheme 9:

Synthesis of commercially available *Haemophilus influenza* vaccines, a) Quimi-Hib; and b) Synthetic *Haemophilus influenza* vaccines by the Seeberger group.



Scheme 10:

a) Conjugation of MenA CPS fragment to albumin. b) Synthetic 1-C phosphono and carbocyclic analogue MenA CPS fragments conjugated to CRM₁₉₇. c) MenA CPS fragments conjugated to HSA.



Scheme 11:

a) Convergent synthesis of MenC CPS polysialic acid antigen and its bioconjugation to carrier protein; b) Synthetic self-adjuvanted MenC polysialic acid conjugate vaccine; (c) Synthetic MenW CPS glycoconjugate vaccines.



Scheme 12:

Synthesis of MenX CPS conjugate vaccines.



Scheme 13:

Synthesis of glycoconjugates based on S. pneumoniae serotype 2, 3, and 8 polysaccharides.



Scheme 14:

Structure of semisynthetic mono-epitope cnjugate vaccines.


Scheme 15:

Synthetic glycopeptide mimics of the gp120 V1/V2-loop. Cyclic glycopeptides derived from stains (a) CAP45 and ZM109, and (c) strain A224 containing different N-glycans

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Scheme 16:

Methods for in-vitro glycoengineering. a) Preparation of IgGs with bisecting GlcNAc G0F glycan; b) Preparation of different glycovariants of Herceptin on bulk scale by roche.



Scheme 17:

Endoglycosidase mediated in-vitro glycoengineering. Structures of various N-glycans used for SAR studies to identify α 2,6-sialylated biantennary complex type as an optimized glycan for effector functions.

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Scheme 18:

General structure of LPS. Structure of natural lipid A from *Salmonella minnesota*. Structures of chemically modified monophosphoryl lipid and 3-O-desacylmonophosphoryl from *S. minnesota R595 Lipid A*.





a) Synthesis of GPI-0100 from deacylated *Quillaja* saponins. b) Synthetic analogues of QS-21 and QS-17/18.

Table 1:

Subsets of galectins and siglecs, their cell type expression and preferred natural glycan ligands.

Name	Expression	Ligand	Name Expression		Ligand	
gal-1	T, Mac, N, Eo, B, Mc, Ba		Sig3	Mac, Myp, Mo, Mic	¢°•°	
			Sig5	N, Mo, B, MC		
			Sig6	B, MC, Troph		
gal-3	T, Mac, N, Eo, Mc, Ba	An Surfree	Sig7	NK, Mo, T, MC	♦ ^{aθ}	
			Sig8	Eo, Ba, MC	¢° ^u m	
gal-8	T, Mac, B	GD1a GM3 GM3 GM3 GM3 GM3 GM3 GM3 GM3 GM3 GM3	Sig9	MO, N, cDC, NK, T	\$*3 ⁶⁵	
gal-9	T, Eo	CMI CAS	Sig10	B, Mo, Eo	0 ⁰⁰ - ¹⁴	
			Sig11	Mac, Mic	♦ ^{ab} ^{ab}	
gal-13 (PP13)	T, Eo	Ain Ser Ser GB-D RG-A RG-B	Sig14	N, Mo		
			Sig16	Mac, Mic	\$ ^{a6} ^{a3}	

Abbreviations: B cells (B), basophils (Ba), dendritic cells (DC), eosinophils (Eo), macrophages (Mac), mast cells (MC), microglia (Mic), monocytes (Mo), natural killer cells (NK), neutrophils (N), and T cells (T).

Table 2.

Classification of major viruses targeting glycosylated receptors and their glycoepitopes.

Virus family/subfamily	Virus type	Glycoepitope		
	Influenza A virus	(a 2–3)-linked Neu5Ac: Avian virus; (a 2–6)-linked Neu5Ac: Human virus		
Orthomyxoviridae	Influenza B virus	(a 2–6)-linked Neu5Ac; (a 2–3)-linked Neu5Ac		
	Influenza C virus	9-O-acetyl Neu5Ac		
	Dengue virus			
Flavivirus	Japanese encephalitis virus.	Heparan sulfate		
	West Nile virus			
Hepacivirus	Hepatitis C virus	Heparan sulfate		
A	Adeno 37	(a 2–3)-linked Neu5Ac		
Adenoviridae	Adenovirus 2, 5	Heparan sulfate		
Papillomavirus	Human papillomavirus types 11, 16, 33	Heparan sulfate		
	MERS-CoV			
Coronavirus	SARS-CoV	Heparan sulfate		
	SARS-CoV-2			

Table 3:

Synthetic antibacterial and antifungal glycoconjugate vaccine

Pathogen	Serotype	Structure		
	ST5	HO OH HO OH	381	
S. pneumoniae	ST14	HO CH CH HO CH CH HO CH HO HO CH HO CH HO CH HO HO CH HO CH HO HO CH HO CH HO HO CH HO CH HO CH HO HO CH HO CH HO HO CH HO CH HO CH HO HO CH HO CH HO CH HO HO CH HO CH HO CH HO HO CH HO CH HO HO CH HO CH HO CH HO CH HO HO CH HO CH HO CH HO CH HO CH HO HO CH HO CH	189	
	6B		382	
	ST23F		383	
Shigella dysenteriae	Type- 1	HO CH HO TO HO	384	
Shigella flexneri	Type-2a	HO OH HO OH NHAC NH S N TT	385	

Pathogen	Serotype	Structure		
Bacillus anthracis		HO TOT HO TOT HO TOT HO TOT HO TOT HO TOT HO TOT HO TOT OH		
		HO HO OH HO HO OH HO OM	387	
	PSII	HO CR HO OH OH HO OH HO HO OH NHAC HO R = H or H ₂ PO ₃ OH OH HO HO HO OH NHAC OH HO HO HO OH NHAC ON HO CRM 197	388	
Ciostridium difficile	PSII	HOLOGIO HI OH HOLOGIO HI HO HOLOGIO HI HO HOLOGIO HI HOLOGIO HI HI HOLOGIO HI HI HOLOGIO HI HI HOLOGIO HI HI HOLOGIO HI HI HOLOGIO HI HI HOLOGIO HI HI HI HOLOGIO HI HI HI HOLOGIO HI HI HI HI HI HI HI HI HI HI HI HI HI H	389	

Table 4.

List of antibodies produced from cell line-based glycoengineering platforms.

Technology	Company	mAb	Target	Status	ref
		Mogamulizumab	CCR4	Approved in 2018	523,545
	Kyowa Hakko	BIW-8962	GM2	In clinical trials	546
		KHK-2823	CD123	In clinical trials	547
	Kırın (KHK)	MDX-1342	CD19	In clinical trials	548
Dettaligent Technology	KHK and Amgen	KHK-4083	OXO-40	In clinical trials	549
FUT8 ^{-/-} CHO Cells	KHK and	Benralizumab	Anti-IL-5Ra	Approved in 2017	550
	MedImmune	MEDI-551	CD19	In clinical trials	551
	KHK and Teva	KHK-2804	Anti-tumor specific Antigen	In clinical trials	552
	KHK and Life Science Pharma	Ecromeximab	GD3	In clinical trials	553
GlycoMab Technology	Clugart Dogho	Obinutuzumab	CD-20	Approved in 2013	313,554,555
GnTIII overexpressed CHO cells	Glycart-Roche	GA-201	EGFR	In clinical trials	556
		Lumretuzumab	Anti-HER3	In clinical trials	557
GlycoExpress Technology	Glycotope	PankoMab	Anti-TA- MUC1	In clinical trials	558
Glycoengineered human cell lines	2 1	TrasGEX	Anti-HER2	In clinical trials	559
		CetuGEX	Anti-EGFR	In clinical trials	560
CHOptimax Technology In-vitro glycoengineering	CHO Pharma Inc.	CHO-H01	Anti-CD20	In clinical trials	NCT03221348
SEA Technology Fucose analogues to inhibit core fucosylation	Seattle Genetics	SEA-CD40	Anti-CD40	In clinical trials	540,542

Table 5.

Structural modifications to the QS-21 by the Gin group.

