Glycoscience: The art of making sugars of different kinds

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Demystifying the Glycosciences

- Glycobiology: Study of the function of sugars attached to proteins and membranes, including protein- and lipid- linked sugars.
- Glycoconjugates: Formed when mono-, oligo- or poly-saccharides attach to proteins and lipids. This occurs in ER and Golgi (mostly).
- Glycans: Carbohydrate entity attached to proteins and lipids. Found outside cells, in cytoplasm (complex) and nucleus decorating transcription factors (simple).
- *Lectins*: Glycan binding proteins

Function of glycans

- Structural component of cell wall and extracellular matrix proteins [Cancer and stem cell biomarkers]
- Intra- and extra-cellular trafficking of glycoconjugates [Protein therapeutics half-life]
- Cell adhesion: during cell-cell and cell-matrix interaction. [Inflammation, human-virus and human-microbiome interactions]
- Cell signaling: Intracellular and extracellular [transcription factor regulation. O-GlcNAc formation on Ser/Thr competes with phosphorylation]

Why is glycosylation so complicated?

- A. It is not part of the central dogma not part of regular course work.
- B. Because the biochemists made it look more complicated than it really is:
 - Database lists 700 different monosaccharides. In humans there are only 9!
 - They said that there are 10¹² possible carbohydrates.
 In reality it is closer to 10²-10³ classical structures.
 - The names are so complicated. Why doesn't everyone just use IUPAC nomenclature
- C. Because it is complicated

Common monosaccharides

- Most glycans are hexose sugars: 4 chiral carbons resulting in 16 different molecules (epimers and enantiomers).
- But many are of relative low abundance. Humans are made of 9 major monosaccharides.

All sugars are similar in structure



Different families of glycans



Of course there are more sugars in plants and the microbiome...

Hexose	Glc	Man	Gal	Gul	Alt	All	Tal	Ido	
0	•		0	•	0	•	0		
HexNAc	GlcNAc	ManNAc	GalNAc	GulNAc	AltNAc	AllNAc	TalNAc	IdoNAc	
Hexosamine	GlcN	ManN	GalN	GulN	AltN	AllN	TalN	IdoN	
Hexuronate	GlcA	ManA	GalA	GulA	AltA	AllA	TalA	IdoA	
\Leftrightarrow	♦	♦	\diamond		\Rightarrow	♦	\Diamond		
Deoxyhexose	Qui	Rha			6dAlt		6dTal		Fuc
\bigtriangleup	A								-
DeoxyhexNAc	QuiNAc	RhaNAc							FucNAc
\triangle	Δ	Δ							Δ
Di-deoxyhexose	Oli	Tyv		Abe	Par	Dig	Col		
Pentose		Ara	Lyx	Xyl	Rib				
		*		*					
Nonulosonate		Kdn				Neu5Ac	Neu5Gc	Neu	
\diamond						٠	\diamond		
Unknown	Bac	LDManHep	Kdo	Dha	DDManHep	MurNAc	MurNGc	Mur	
\bigcirc	•		\bigcirc			•			
Assigned	Api	Fruc	Tag	Sor	Psi				
\bigcirc									

http://www.ncbi.nlm.nih.gov/books/NBK310273/

... and more on bacteria that regulate immune function



A. TEM of *T. forsythia* showing glycans. **B.** Schematic *O*-glycan core to protein. Terminal trisaccharide is circled. **C.** Immune signaling by C-type lectin-like receptor (CLR) and TLR2 activated by *O*-glycans and TLR2 ligands (e.g., BspA) orchestrates.

Front. Microbiol., 17 October 2013

Relevance to human diseases

- Human glycans bind bacterial lectin-like adhesins
- Bacterial carbohydrates bind mammalian lectins
- Bacterial carbohydrates mimic human glycans, and condition the microbiome

Fusobacterium nucleatum

- Plays a role in periodontal disease.
- Associated with colon cancer



wikipedia

Glycocalyx – Physically big



Roseman, S. J. Biol. Chem. 2001;276:41527-41542





Neelamegham and Mahal, Current Opinion of Structural Biology, 2016



<u>Cell.</u> 2000 Oct 27;103(3):467-79.



TABLE 1. Human siglecs.



Nature Reviews | Microbiology



http://sourceforge.net/projects/gnatmatlab/

Which α(2,3)sialyltransferase, ST3Gal-3, -4 or -6, contributes to human selectin-ligand biosynthesis?



Alexander Buffone Nandini Mondal

Mondal et al. Blood. 125:687-96, 2015.



Buffone et al. J Biol Chem. 288(3):1620-33, 2013.

HL60 cell rolling on E-Selectin



Genome Editing with CRISPR-Cas9



The Scientist, 2014

HL-60 ST3Gal-4 knock out generated using CRISPR/Cas9



Abrogation of leukocyte rolling on all selectins



Profiling glycans



N-glycans: ST3Gal-4 controls sLe^X biosynthesis



O-glycans: ST3Gal-4 deletion abrogates sLe^x biosynthesis



Human neutrophils derived from hematopoietic stem cells (HSCs)





Human neutrophil rolling on selectins



The multistep cell adhesion cascade





Rapid glycan profiling and chemical 120 WT HL-60 cells synthesis 0 390.3 100 0 0---955.4 1316.5 80 Intensity 60 33.1 40 294.1 000 578.6 20 594.3 1939.6 00 1404.6 П Amplified 600 400 800 1000 1200 1400 1600 1800 2000 O-glycome m/z MS in media Intensity 120 [O] HL-60 cells α3 B3 Isolation O-glycan precursor: 100 390.3 Bn-α-GalNAc. peracetylated m/z 80 Intensity 60 Esterases HNAC 40 Golgi 20 ER CH3 п 400 600 800 1000 1200 1400 1600 1800 2000 m/z GalNAc Cytosol O Gal Nucleus 120 [N] HL-60 cells GlcNAc ▲ Fuc 1390.3 100 Neuraminic acid Plasma membrane 80 Intensity 955.4 60 1316.5 40 933.1 294.1 20 417.1 594 3 1404.6 1578.6 1939.6 п 400 600 800 1000 1200 1400 1600 1800 2000 m/z

Nature Methods 13, 81–86 (2016)



GlycoPAT: High-throughput glycoproteomics analysis





GlycoPAT: High-throughput glycoproteomics analysis

	GlycoPeptide Digestion	
🛿 GlycoProteomics Analysis Toolbox 🛛 💷 🔤 💌	To create a list of peptide fragments by enzymatic	digestion, please follow a six-step procedure as shown below:
Main Menu	- 1. Peptide Sequence Input-	6. Digest
	Sequence File: Select file	Digest
	File loaded is:	
1. GlycoPeptide Digestion	C:\Users\gangliu\Dropbox\glycopat\toolbox\d 🔶	Glycopeptide fragments are:
		Variable ptm: N {n{n{h{hn}}} } 0
		Variable ptm: N {n{n{h{hn}}} 0
	- 2. Enzyme Input	Variable ptm: N {n{n{h{h}{h{h}}}} 0
	Direction	Variable ptm: N {n{n{h{h}{h}}}} 0
2 Tandem MS Analysis	Enzyme: Trypsin v	Variable ptm: N {n{n{h}{h}{h}}} 0
2. Tandem no Analysis	Enzyme.	minPTM : 0
	Enzyme Name:	maxPTM : 2
	Trypsin	minPepLen : 4
		maxPepLen : 30
		MissedMax: 0
3. Browse Results	3. Fixed Modification	>fetuin
	Upload	AHYDLR
	Load from local file Select file	ALGGEDVR
		AQFVPLPVSVSVEFAVAATDC <i>IAK</i>
	File loaded is:	C <i>DSSPDSAEDVR</i>
	C:\Users\gangliu\Dropbox\glycopat\toolbox\de _	C <i>NLLAEK</i>
4. GlycoPeptide Fragmentation (optional)	I ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓	EPAC <i>DDPDTEQAALAAVDYINK</i>
		EVVDPTK
	4. Variable Modification	GSVIQK
	Upload	HLPR
	Load from local file Select file	HTFSGVASVESSSGEAFHVGK
E Cincle Spectra (apotation (optional)		HILNQIDSVK
3. Single Spectra Annotation (optional)	File loaded is:	
	C:\Users\gangliu\Dropbox\glycopat\toolbox\d	
	5 Digestion Parameter	
	3. Digestion Parameter	L CeisPDCeisPLL APL N{n{n{n{n}n{n}n{n}n{n}n{n{n}n{n{n}
	Max missing cleavages 0	I CeisPDCeisPI I API N/n/n/n/n/n/n/n/n/n/n/n/n/n/n/n/n/n/n/n
	max. missing cleavages	I C <i>PDC<i>PI I API N{n{n{h{n{h{s}}}}}n{h{s}}}n{h{s}}}n{h{s}}}n{h{s}}}</i></i>
	Min. length of peptide 4	L C <i>PDC<i>PL L APL N{n{n{h{n{h{s}}}}}</i></i>
		LC <i>PDC<i>PLLAPLN{n{n{h{n{h{s}}}}}</i></i>
	Max. length of peptide 12	LC <i>PDC<i>PLLAPLN{n{n{h{h{n{h{s}}}}}}h{n{h{s}}}}}f}DSR</i></i>
		LC <i>PDC<i>PLLAPLN{n{n{h{n{h{s}}}}}h{n{h{s}}}}DSR</i></i>
	Max. # of modifications 2	
	Min. # of modifications 0	Sava an
		Save as

GlycoProteomics Analysis Toolbo

Overall algorithm



GlycoPAT: High-throughput glycoproteomics analysis

	GlycoProteomics Analysis Toolbox					
GlycoProteomics Analysis Toolbox	MS/MS Analysis Parameter Input 1. Load a peptide file (output of Digestion Program) Select a File Loaded file: C:\Users\gangliu\Dropbox\glycopat\u00eque collows\glycopat\u00eque collows\u00eque collows\glycopat\u00eque collows\u00eque collows\u0					
2. Tandem MS Analysis	3. MS2 tolerance 1 Da					
3. Browse Results	6. Cut-off value (% of max peak, CID/HCD only) 0.02 Number =0 <4					
4. GlycoPeptide Fragmentation (optional) C:\Users\gangliu\Dropbox\glycopat\toolbox\demo\test C:\Users\gangliu\Dropbox\glycopat\toolbox\demo\test C:\Users\gangliu\Dropbox\glycopat\toolbox\demo\test Score Status Report: Score All Files						
5. Single Spectra Annotation (optional)	Start to read the inputs Please wait Start to calculate the scores Please wait					

Scoring parameters

- Xcorr
- P-value



- Top10
- % ion-match



Characterization of:

- Simple standard proteins
- Mixtures of standards
- Plasma cryoprecipitate from 5cc of blood

Cell Adhesion GlycoEngineering



Strauer B E, and Kornowski R Circulation. 2003;107:929-934

- MSCs (Mesenchymal stem cells) and CDCs (Cardiosphere derived stem cells) are promising cellular therapuetics.
- However, promising results from animal studies are not translating to clinical benefits
- Local infusion to damaged tissue is not beneficial
- Systemic infusion proximal to the therapeutic site
 - minimally invasive
 - allows repeated treatment

Goals

- Make stem cells home to sites of inflammation, much like white blood cells
- Create methods that can be used in a clinical setting with minimal effort
- Move studies to clinically relevant large animals



Chi Lo



Recombinant PSGL-1



Characterization of 19Fc



Lo, C.Y., et al. Biomaterials, 2013. 34(33): p. 8213-22.



19Fc coupling with PPG increases interactions with P-selectin







FUT7 increases CDC interactions with stimulated HUVECs



CDC FUT7 + Esel blocking

CDC

CDC FUT7



Large animal studies: Swine



Pig experiments: 30 min. brief ischemiareperfusion of LAD







Catheter placement for cell injection



echocardiogram

Pig experiments: 30 min. brief ischemia-reperfusion of LAD



Lo, C.Y. et al. Biomaterials (2016), 74: 19-30

Conclusion

- Glycosylation is a poorly communicated field-its easier than it looks
- There are tremendous opportunities for exploration:
 - New basic science
 - New applications
 - New drugs



The final frontier--- boldly go where no (wo)man has gone before

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NEW YORK STATE STEM CELL SCIENCE