Final Report for ESF Research Network Programme Euroglycoforum Funded Meeting- Meeting 3298

"Glycan Microarray Technologies, Applications, and Future"

September 19-21, 2010 at the Emory Conference Center Hotel, Atlanta, USA

Summary
The meeting was organised by the National Institute of General Medical Sciences with support for European participants from the ESF Euroglycoforum RNP (EGSF). Following cancellation of the EGSF conference scheduled for April, 2010 in Groningen due to the Icelandic dust cloud, this meeting allowed more than 20 participants from Europe and Japan, and 42 participants from the U.S. and Canada to get together. The state of the art of glycochemistry and glycobiology research enabled by glycan microarrays was reviewed in presentations from all participants followed by in depth discussion.

The microarray portion of the workshop was followed by a bioinformatics workshop led by Will York, involving programmers and bioinformatics specialists to work cooperatively on database improvements and new capabilities in data handling and analysis.

The funding for the Consortium for Functional Glycomics will be ending next year so this was an opportunity to look at results and decide on future projects leading on from these. Due to the efforts of the CFG and groups in Europe, glycan microarrays are now a standard tool for the evaluation of glycan binding proteins and new or modified glycan motifs. The key role of glycan arrays was summarized by Rick Cummings in his keynote address to begin the meeting: “Glycan arrays *generate* hypotheses.” In it last year the CFG has formulated a set of paradigms by which glycan binding proteins mediate cell communication (see Appendix 1).

Many new results were presented during the workshop and vigorous discussions took place regarding the interpretation of glycan array results, the improvement of array design and construction, and the coordination of array resources in order to determine the scope and limitations of the technology as it currently stands.

Scientific Content and Discussion

I***. Activities of the Consortium for Functional Glycomics Year 10.***
A. **Paradigm Protein identification.**
Candidate paradigms for glycan binding and biological activity have now been formalized, and glycan-binding proteins (GBPs) identified. As a result of this programme the following has been accomplished:

- Participating Investigator (PI) experts were identified for each GBP family.
- Paradigms were selected for each family, with formal justification for these choices; the paradigm GBPs are listed in the Appendix 1.
- The selected paradigms were approved by the Steering Committee (SC).
- The CFG Paradigm Pages wiki-style web page was established (see http://www.functionalglycomics.org/CFGparadigms/index.php/Main_Page)
- The core PI experts performed initial annotation of these pages.

At present, the CFG community, including those in Europe, is invited to contribute further information and interpretation to these pages. It is envisioned that these will become a leading resource for investigators to set their results in a larger context, and to tap into the most current and complete information for these key systems.

B. Final-Year Bridging Grants. The availability of funds for bridging grant-type efforts to help complete the CFG mission in Year 10 was discussed. The following parameters for this funding have been identified. The key review criterion will be: will the work help fulfil the goal of the CFG. A focus on completing the specific aims for the selected paradigm proteins is therefore essential. Topics likely to be favourably reviewed include, but are not limited to:

- Enhancement of database capabilities to analyze data,
- Custom glycan synthesis to support studies of paradigm proteins,
- Studies of the binding behaviour of proteins, and additional cross-platform comparisons, including those with European colleagues.

C. Cross-Platform Comparisons. Prof. Mahal's proposal includes provisions for providing a core set of five GBPs to other array practitioners for comparison of binding results. The Mahal lab will also coordinate the collection and distribution of other GBPs provided by participating investigators, with special attention to the paradigm proteins. Thus, PI's are encouraged to contact Professors Paulson or Mahal if they are interested in contributing GBPs to this effort. Contributions from European Groups are welcomed and Professor Ten Feizi (Imperial College, London) is already involved in cross platform comparisons.

D. Review papers establishing the state of the art. An important part of completing the CFG mission is to communicate the lessons learned about GBP paradigms and the tools used to study them. In addition to the normal production of primary literature, interested members of the glycan array community are urged to write critical reviews that define the current state of the art and chart paths forward. It is anticipated that there will be substantial contributions from European based investigators of such review papers.

II. Computational Analytical Tools: What do participating investigators need to make better use of array data?
To both stimulate thinking over the long term, and to set some goals for the bioinformatics workshop participants, the following computational capabilities were identified as being of great potential value to scientists seeking to use glycan microarray data.

- Small component motifs (terminal units, disaccharides, trisaccharides, etc.)
- Identification of glycan motifs recognized by GBPs
- Largest common component motifs (under way in several groups)
- Larger "biological" units (sialyl Lewisx, blood group antigens, etc.)
- Comparisons between different proteins
- BLAST-type searching for GBPs: what are the "most similar" proteins with similar binding behaviour?
- Comparisons between different versions of the same protein (different linkers, presentation densities, etc.)
- Help in processing serum data
- Ability to test hypotheses: e.g.does a proposed motif fit the data?
- Incorporate concentration-dependent data
- Identification of binding "rules" (for example, protein A binds motif X, except when there is an adjacent a-linked motif Y, or especially well when motif X is terminal…)
- Analytical tools to help extract lessons from what doesn't bind
- Bring in three-dimensional structural information or calculations

III. Connecting Molecule Builders with Users: Can the glycan synthesis community be better connected to the array community, and other potential users of their compounds, beyond individual collaborations?
Some mention was made of an idea from Lara Mahal and Nikki Pohl to establish a virtual database of glycan structures that could be made by synthesis laboratories, based on their published capabilities. A common way to represent glycan structures would be needed to develop such a system. The NIH screening centers offer a precedent for the collection and distribution of glycan structures. It could be possible to convince glycan synthesis laboratories to donate molecules that are made in the course of methods development or other studies. There are a large variety of suitable structures which have been synthesised by groups throughout Europe who should be encouraged to donate such molecules. This would enhance the range and variety of structures available to the glycan array community .

IV. Key Issues in Glycan Array Development
Linda Baum provided the following "wish list" for glycan array capabilities:

(a) Control over array display characteristics
- multivalency, density modulation, "vertical" presentation of glycans from the surface, and the use of specific sites of presentation in peptides and lipids

(b) More effective mimicry of cell surfaces

- mobility on the planar surface, clustering into microdomains, use of bona fide membranes

It is clear from many of the presentations at this workshop that many of these issues are receiving attention from the developers of glycan microarrays, and that a great many different arrays are being developed as needed. A brief list of the glycan arrays described at this workshop are presented in Appendix 2

Recommendations

• ***Evergreening***. Vigorous efforts should be continued to make CFG array and database resources available to investigators after glue grant funding is over. Jim Paulson informed the group that applications for three year awards for this purpose will soon be submitted, headed by Rick Cummings and Rahul Raman, respectively. The resulting array facility, derived from Cores D and H, will continue the printing and use of the latest version of the CFG glycan array, but not the synthesis of glycan samples for distribution to investigators. Similarly, the application designed to support evergreening of the CFG databases will focus on the existing resource, and on ways to add new information to the database, but not on the addition of analytical capabilities to the database.

• ***Cross-platform comparison***. Excellent discussions took place regarding cross-platform comparisons between glycan arrays. Prof. Mahal's recently-funded bridging grant will provide a starting mechanism to distribute glycan binding proteins to interested facilities. However, it is anticipated that the key players – including Prof. Ten Feizi (Imperial College), Jeff Gildersleeve (NCI), Rick Cummings (Emory) and Core H will soon prepare a bridging grant application to address this issue more directly and with a larger number of paradigm proteins.

Future funding themes. Topics and capabilities that are strongly worthy of NIH support in the future include the following:

– Continued availability of glycan arrays to the glycochemistry and glycobiology communities, as discussed above.
– Increasing the number and types of glycans on "general" arrays, and the development of tissue-specific glycan arrays.
– Continued development of diverse platforms for arrays and understanding of the differences in presentation of glycans on the different arrays
– Development of software to interpret array results.
– Enhance capabilities to predict and determine the three-dimensional structures of array- and protein bound glycans, and improve the curation of arrays with the aid of such structural information.
– The loss of the central Core D resource to renew supplies of soluble glycan reagents and expand the glycan array library will be keenly felt. New mechanisms to make such molecules available should be developed.

Metadata. Discussions with those involved in GBP bioinformatics revealed a need for protein sequences to be submitted with samples. Trivial names are not adequate, as they lead to confusion and an inability to retrieve all of the data regarding a particular protein from the database.

Impact of the Event on European Glycan Array Development

The meeting provided an excellent opportunity for those working on all aspects of glycoarrays or in associated bioinformatics areas in both Europe and the US to meet together, to compare results, and to discuss future directions and plans. As the funding of the Consortium for Functional Glycomics, which includes the activities of the glycan array and synthesis cores, will end in 2011 it was especially useful to be able to see the progress in the identification of 'paradigm' carbohydrate proteins by the consortium and the plans for future work on these.

It is apparent that a substantial number of array providers are based in Europe. The platforms may differ from that employed by the CFG and they may be targeted to different purposes but they provide complementary information which will continue to contribute to any future work

It is significant that development of many of these platforms has proceeded along different routes to the CFG platform and the characteristics of some of these array platforms address the key issues in array development identified in the meeting.

Another benefit from the separate development of European platforms is that they can participate in cross platform comparison exercises and in analysis of core set GBPs from Prof. Mahal. This is already starting to take place with support of the bridging grant to Prof. Mahal but it may be anticipated that several other exercises will be set up in the future.

In another area investigators in Europe have, and can continue to, contribute GBPs especially in areas where they have special expertise and experience.

The list of GBP's selected as paradigm proteins by CFG identifies their area of interest allowing focus by European investigators on other proteins involved in interaction with glycans or other aspects relating to biological roles of glycosylation.

As there will continue to be development of various array platforms in Europe there are possibilities for specialised array development as CFG will focus on their existing glycan array (with addition of glycans when available)

It should be noted that there is considerable synthetic capability throughout Europe which will be able to help provide glycans for the virtual glycan library. Collaborations in this area could be significant since CFG will no longer have its own synthesis facility.

Complementary expertise and experience in glycan arrays is available in several European laboratories. Review papers can be produced by European investigators highlighting their areas of expertise and development plans.

An important future activity will be cross platform comparison analysis of core set GBPs which is currently organised by Prof. Mahal (New York University) funded by the CFG. Any researchers interested in taking part in this exercise should contact Prof Mahal. lkmahal@nyu.edu

This report contains material from the full report on the meeting compiled by MG Finn for the NIGMS and which is available online at;
http://glycomics.scripps.edu/SubgroupWorkshop/WorkshopSept2010Rpt.pdf

European Delegates funded by ESF

Julie Bouckaert, Belgium

Sabine Flitsch, UK

Carmen M.,Galan, UK

Jun Hirabayashi, Japan

Cornelis Hokke, Netherlands,

Yaroslav Katrilik , Slovakia

Emanuela Lonardi, Netherlands

Maksim Navakouski, Russia

Roland Pieters, Netherlands

Niels Reichardt, Spain

Jürgen Seibel, Germany

Valentin Wittmann, Germany

Manfred Wuhrer, Netherlands

Han Zuilhof, Netherlands

Meeting Programme

Workshop on Glycan Array / Bioinformatics

Dates: September 19 to 23, 2010

Location: Emory Conference Center Hotel, Atlanta, Georgia (USA)

The goals of this workshop are twofold: first, to assess the current state of glycan array design, construction, use, and interpretation, with a focus on how glycan arrays have contributed to the CFG's overall mission; and second, to create a roadmap for developing glycan array resources, including methods to compare cross-platform results, in the final year of glue grant funding.

GLYCAN MICROARRAY TECHNOLOGIES, APPLICATIONS, AND FUTURE

Sunday, September 19th from 8 p.m. to 9 p.m. at the Oak Amphitheater

6:00 p.m. to 6:30	Registration
6:30 p.m. to 8:00	Reception / Dinner (served in the Dining Room)
8:00 p.m. to 8:45	Glycan Microarrays - Promises and Challenges Keynote Lecture: **Richard D. Cummings** (Emory University)
8:45 p.m. to 9:00	Goals of the Workshop **M.G. Finn** & **Jim Paulson** (The Scripps Research Institute)

Monday, September 20th from 8:15 a.m. to 9:30 p.m. at the Oak Amphitheater

7:00 a.m. to 8:00	Breakfast (served in the Dining Room)

Session 1: CFG Arrays - What and Why

Chair: **Ron Schnaar** (The Johns Hopkins School of Medicine)

8:15 a.m. to 8:30	Making the Leap from Chip to Cell **Linda Baum** (University of California - Los Angeles)
8:35 a.m. to 8:55	Carbohydrates at the Interface **Daniel M. Ratner** (University of Washington)
9:00 a.m. to 9:15	Characteristics of the CFG Glycan Array version 5.0: Final Glue Grant Funded Glycan Array **Nahid Razi** (The Scripps Research Institute)

9:20 a.m. to 9:35	Updates on Glycan Array Data Management at the CFG **Rahul Raman** (Massachusetts Institute of Technology)
9:40 a.m. to 10:15	AM BREAK

Session 2: Array Technologies and Multivalency

Chair: **M.G.Finn** (The Scripps Research Institute)

10:15 a.m. to 10:30	Glycoarrays: New Methods for Preparation and Quantitative Analysis of Multivalent Interactions **Valentin Wittmann** (University Konstanz)
10:35 a.m. to 10:50	Rapid Screening of Lectins for Multivalency Effects with a Glycodendrimer Microarray **Roland Pieters** (Utrecht University)
10:55 a.m. to 11:10	Synthesis and Lectin Array Characterization of Novel N-glycan Clusters **Lai-Xi Wang** (University of Maryland)
11:15 a.m. to 11:30	Monitoring Enzymes Using Glycoarrays **Sabine Flitsch** (Manchester Interdisciplinary Biocentre)
11:35 a.m. to 11:50	Enhancing the Lectin Microarray: Advances in Technology **Lara Mahal** (New York University)
11:55 a.m. to 12:10	Analyses of Lectin Specificities Using Motif Segregation of Glycan Array Data **Brian B. Haab** (Van Andel Research Institute)
12:15 to 1:30	LUNCH (served in the Dining Room)

Session 3: Enzymatic Synthesis of Glycans

Chair: **Jim Paulson** (The Scripps Resarch Institute)

1:30 p.m. to 1:45	Efficient Sequential One-pot-multienzyme Synthesis of Complex Carbohydrates for Glycan Microarrays **Xi Chen** (University of California - Davis)
1:50 p.m. to 2:05	Preparation of an N-glycan Microarray by Combining Modular Synthesis of Core Structures with On-Chip Nanoscale Enzymatic Extension **Niels Reichardt** (CICbiomaGUNE)
2:10 p.m. to 2:25	Ionic Liquids in Carbohydrate Chemistry: Novel Chemo-enzymatic Approaches to Prepare Mucin Type Glycan Probes **M Carmen Galan** (University of Bristol)
2:30 p.m. to 2:45	Expanding Natures Diversity by Enzyme and Substrate Engineering for the Synthesis of Array-able Glucans **Juergen Seibel** (University of Wuerzburg)

2:50 p.m. to 3:05	New Strategies for Expeditious Oligosaccharide Synthesis **Alexei Demchenko** (University of Missouri - St. Louis)
3:10 p.m. to 3:30	PM BREAK

Session 4: Arrays Illuminating Glycobiology, Part I

Chair: **Ruben Donis** (Centers for Disease Control and Prevention)

3:30 p.m. to 3:45	Influenza viruses on the Glycan Array **Gillian M. Air** (University of Oklahoma Health Sciences Center)
3:50 p.m. to 4:05	Versatility of the Neoglycolipid (NGL)-based Carbohydrate Microarray System and Applications in Pandemic Influenza A (H1N1) 2009 Virus Studies **Ten Feizi** (Imperial College London)
4:10 p.m. to 4:25	Elements of Mucin Glycoprotein Recognition **David Live** (University of Georgia)
4:30 p.m. to 4:45	Sialoside Analog Arrays for Identifying High Affinity Ligands of Siglecs **James C. Paulson** (The Scripps Research Institute)
4:50 p.m. to 5:05	Glycan Microarray Analysis of Recombinant Hemagglutinin **James Stevens** (Centers for Disease Control and Prevention)
5:10 p.m. to 6:00	**POSTER SESSION** (Dogwood Room)
6:00 p.m. to 7:30	DINNER (served in the Dining Room)
7:45 p.m. to 9:30	**GROUP DISCUSSIONS: Glycan Arrays and the CFG**

Tuesday, September 21st from 8 a.m. to 8 p.m. at the Oak Amphitheater

7:00 a.m. to 8:00	Breakfast (served in the Dining Room)
8:00 a.m. to 8:15	Discussions of the Draft Report

Session 5: CSI: Glycan Arrays

Chair: **Ron Schnaar** (The Johns Hopkins School of Medicine)

8:20 a.m. to 8:35	High-Throughput Profiling of Glycosyltransferases using CarboArrays and SAMDI Mass Spectrometry

	Adam Eisenberg c/o Milan Mrksich (University of Chicago)
8:40 a.m. to 8:55	Glycoconjugate/Lectin Microarray Based on an Evanescent-field Activated Fluorescence Detection Principle **Jun Hirabayashi** (National Institute of Advanced Industrial Science and Technology)
9:00 a.m. to 9:15	Glycosylaminoglycan Arrays a Label Free Detection **Geert-Jan Boons** (University of Georgia)
9:20 a.m. to 9:35	Host-Microbial Interactions in the Gut and Glycan-Lectin Arrays **Lokesh Joshi** (National University of Ireland)
9:40 a.m. to 10:30	AM BREAK

Session 6: Arrays Illuminating Glycobiology, Part II

Chair: **Will York** (University of Georgia)

10:30 a.m. to 10:45	Glycan Arrays for Investigation of *Cryptosporidium*-host Cell Interactions: Analysis of Glycan Binding Proteins and Monoclonal Antibodies to Surface Glycans **Honorine Ward** (Tufts University)
10:50 a.m. to 11:05	Application of Natural Glycan Microarrays for the Analysis of Antibody Responses in Human Schistosomiasis **Cornelis Hokke** (Leiden University Medical Center)
11:10 a.m. to 11:25	Glycan Microarray for Autoantibody Detection in Colorectal Cancer **Manfred Wuhrer** (Leiden University Medical Center)
11:30 a.m. to 11:45	Identification by Glycan Microarray and Validation of a Fully Protective Vaccine Target for Chagas Disease **Igor C. Almeida** (University of Texas at El Paso)
11:50 a.m. to 1:00	LUNCH (served in the Dining Room)

Session 7: Arrays Illuminating Glycobiology, Part III

Chair: **Rick Cummings** (Emory University)

1:00 p.m. to 1:15	Glycan Arrays and Cancer Vaccines: Partners for Life **Jeff Gildersleeve** (National Cancer Institute-Frederick)
1:20 p.m. to 1:35	Probing Immunogenic Sugar Moieties of HIV-1 using Carbohydrate Cluster Microarrays **Denong Wang** (SRI International)
1:40 p.m. to 1:55	GM1 Derivatives for Glyco-arrays: Towards Rapid Detection of Various Neuropathies **Han Zuilhof** (Wageningen University)

2:00 p.m. to 2:15 Binding of Lectins and Toxins Using Multiple Glycan Platforms: A Comparative Study
Suri S. Iyer (University of Cincinnati)

2:20 p.m. to 2:35 Use of a Microarray to Develop New Labeling Molecules for the Study of Post-translational Glycosylation
Mary Cloninger (Montana State University)

2:40 p.m. to 3:30 PM BREAK

Session 8: Digging Deeper: Structure and Activity

Chair: **David Goldberg** (Palo Alto Research Center)

3:30 p.m. to 3:45 Synthetic GPI Conjugates for the Exploration of GPIomics
Zhongwu Guo (Wayne State University)

3:50 p.m. to 4:05 Structural Sampling of Glycan Interaction Profiles Pinpoints the Natural Receptors of Bacterial Fimbrial Adhesins
Julie Bouckaert (Vrije University Brussel)

4:10 p.m. to 4:25 Glycosylation Properties of the Kidney Filter
Harry Holthofer (Dublin CIty University)

4:30 p.m. to 4:45 Tools for Mining Motifs and Building Glycan Cartoon Structures
Sanjay Agravat (Emory University)

4:50 p.m. to 5:05 Mining Glycan Array Data: Methods and Tools
Kiyoko Aoki Kinoshita (Soka University)

5:10 p.m. to 5:25 Standarization of Glycan Array Data - a World Wide Effort
Rene Ranzinger (University of Gerogia)

6:00 p.m. to 7:30 DINNER (served in the Dining Room)

7:30 p.m. to 8:30 **GROUP DISCUSSIONS**

BIOINFORMATICS TO THE CFG WORKSHOP ON GLYCAN ARRAYS

Wednesday, September 22nd from 9 a.m. to 5:30 p.m. at the Azalea Room

8:00 a.m. to 9:00 Breakfast (served in the Dining Room)

9:00 a.m. to 9:10 Welcome and Objectives
Will York (University of Georgia)

9:10 a.m. to 9:20 Presentation of aim and plan for Group 1 : Development of a standard representation of glycan array data

	Rene Ranzinger (University of Georgia)
9:20 a.m. to 9:30	Presentation of aim and plan for Group 2 : Data exchange and access **Rahul Raman** (Massachusetts Institute of Technology)
9:30 a.m. to 9:40	Presentation of aim and plan for Group 3 : Data analysis and data mining of glycan array data **David Goldberg** (Palo Alto Research Center)
9:40 a.m. to 12 noon	Hacking in the working groups
12 noon to 1:00	LUNCH (served in the Dining Room)
1:00 p.m. to 4:30	Hacking in the working groups
4:30 p.m. to 5:30	Day one summary and day two plans for each group
6:00 p.m. to 7:30	DINNER (served in the Club Room)
7:30 p.m. to 8:30	Free time for hacking or exploring

Thursday, September 23rd from 9 a.m. to 4:30 p.m. at the Maple Room

8:00 a.m. to 9:00	Breakfast (served in the Dining Room)
9:00 a.m. to 12 noon	Hacking in the working groups
12 noon to 1:00	LUNCH (served in the Dining Room)
1:00 p.m. to 3:00	Hacking in the working groups
3:00 p.m. to 3:30	Preparation of summary presentation
3:30 p.m. to 3:45	Summary for Group 1
3:45 p.m. to 4:00	Summary for Group 2
4:00 p.m. to 4:15	Summary for Group 3
4:15 p.m. to 4:30	Summary and action items of the Hackathon

Appendix 1 Paradigms for carbohydrate-protein recognition formulated by CFG

Paradigm Type	Paradigm Protein	Glycan Array Data based on searches in the CFG website	Comments
C-type lectins	DC-SIGN	9	
	Macrophage galactose lectin (MGL)	5	includes MGL-Fc *
	LSECtin	10	
	P-Selectin	7	
	Mannose receptor	1	
	Ficolins/Mannose-binding protein	22	check before using *
Galectins	Galectin-1	36	multiple conc. data available
	Galectin-3	25	multiple conc. data available
	Galectin-9	17	multiple conc. data available; includes different species and chimeras *
Siglecs	CD22	1	
	Sialoadhesin	1	
	Siglec-8	4	
	MAG	0	
	Siglec-15	0	
Mammalian trafficking, other	Cation-dependent Mannose-6-phosphate receptor	1	
	Calreticulin	2	2 additional data sets on truncated protein
	Ficolin M (Ficolin 1)	14	
Bacterial adhesions, lectins	PA-IIL	2	
	CBM47	0	
	F17G/GafD	7	
Bacterial toxins	Subtilase cytotoxin (SubAB)	2	
	Botulinum toxin serotype A (BoNT/A)	1	
	C. difficile toxin A (TcdA)	1	
Capsid virus GBPs	Polyomavarus capsid protein (VP1)	0	
	Reovirus hemagglutinin (sigma 1)	0	
	Parvovirus Minute Virus of Mice (MVM)	0	
Enveloped virus GBPs	Influenza hemagglutinin H3	8	check before using *
	Parainfluenza virus type 3 hemagglutinin-neuraminidase	2	
Eukaryotic microbial GBPs	Candida glabrata EPA7	0	
	Cyanovirin-N (CVN)	20	includes 10 homologue *

Appendix 2

Investigator(s) Glycans and Array Type Described in this Workshop

Cummings	glycopeptides, mannose-6-phosphates, glycosphingolipids, modified sialic acids, milk sugars, “shotgun glycomics” arrays from natural sources
Feizi	neoglycolipids, natural and synthetic glycolipids, and “designer arrays” from glycoproteins and polysaccharides
Gildersleeve	neoglycoproteins (glycans displayed on BSA)
Razi, Paulson,	Core H CFG glycan array version 5.0
Boons	heparan sulfate components and motifs
Chen and Paulson	sialoside analogs
Flitsch/ Mrksich	glycans on gold (monitoring of binding and enzymatic modification by MS)
Hirabayashi	glycans on evanescent-field spectrometer surface
Hokke	Schistosome-derived glycans and glycoconjugates
Iyer	comparative arrays: ELISA plate (maleimide + glycan-thiol) *vs.* SPR chip (glycan-biotin + avidin), with variations in spacers and linkers
Joshi	range of N-linked glycans, blood group structures, milk sugars, and glycolipids on polylysine and Nexterion slides Live glycopeptides (focusing on mucins)
Pieters	glycodendrimers on PamGene (porous chip) materials
Reichardt	complex N-glycans (on-chip enzymatic synthesis)
Stevens	sialosides
Wang, D	. nitrocellulose substrate, photogenerated arrays, clustered glycans
Wittmann	glycans with variation in density and multivalency
Wuhrer	tumor-associated glycans, with attention to display orientation