Joint Meeting of the Japanese and American Consortia for Glycomics is Held in Honolulu

An open joint meeting of the Consortium for Functional Glycomics (CFG) and the Japanese Consortium for Glycobiology and Glycotechnology (JCGG) was held on November 21st in Honolulu, Hawaii, after the conclusion of the Joint Meeting of the Society for Glycobiology and the Japanese Society of Carbohydrate Research (November 17-20, 2004). The purpose of the combined Consortia meeting, led by Dr. James Paulson and Dr. Naoyuki Taniguchi, was to give each group a chance to see what the other is doing and to identify synergies and opportunities for cooperative efforts for the future. Approximately 280 scientists were in attendance to hear talks by leading scientists from the US, Europe and Japan.

In the morning sessions the CFG presented a significant update on many aspects of its progress in the last year, including the glycomics initiative, database developments, the glycan arrays and mouse phenotyping. Several Participating Investigators gave presentations of research projects which highlighted data obtained using Consortium resources. In the afternoon sessions, ten leading scientists from the JCGG reported on parallel and unique efforts being undertaken in Japan.

This exciting day was brought to a close with a discussion session led by Drs. Paulson and Taniguchi of areas that seem ready for cooperative efforts. A number of attendees expressed thoughts and suggestions about future directions. It was agreed that the construction of databases is an area of interest to everyone and is ripe for synergistic effort. A distributed database with a single search engine, accessible to everyone, was thought to be a worthy goal. Issues of avoiding duplication of effort, how much overlap in experiments from laboratory to laboratory would be optimal, validation of data before entering it into the database and the
importance of making raw data available to all were discussed. The desirability of all parties meeting again in the future to discuss these issues in more depth was stressed.

Highlights of the CFG presentations follow:

The Glycomics Initiative
An update on the mouse and human glycomics initiative was presented by Dr. Anne Dell, Coordinator of the Analytical Glycotechnology Core (C) at the Imperial College. With the goal of making this initiative a high-throughput effort, the glycan extraction and initial MALDI screening steps are performed at M-SCAN, Inc., with the subsequent spectral interpretation and annotation, and secondary and linkage analyses, being done at the IC.

Dr. Dell pointed out some interesting features of the mouse N- and O-glycan MALDI data that is posted on the Consortium website (http://www.functionalglycomics.org/static/consortium/data/dataCoreC.shtml). A comparison of kidney and liver N-glycans shows that the profiles are very different; kidney tissue has a large number of very complicated tri- and tetra-antennary structures while liver tissue is rich in sialic acid-containing structures. Dr. Dell also showed some preliminary profiles of glycans from human tissues. The first set of human data will be posted on the website soon.

Core C has recently begun profiling populations of cells from the immune system, an effort that will increasingly become the focus of the Core’s activities. Dr. Dell showed profiles of N- and O-glycans from mouse WeHi-3 cells, pointing out that the CT antigen structure is present in both spectra. The sensitivity of the technique allows compounds comprising 0.01% of the total glycan mixture to be detected. The intention is to correlate the emerging glycan structure data for cell populations with microarray data by sending RNA samples to the Gene Microarray Core (E) for analysis on the Glyco-gene chip.

A large number of MALDI spectra are being generated at Core C, and fortunately the interpretation and annotation steps are being greatly facilitated by a program for automated annotation, Cartoonist, which has been developed by Dr. David Goldberg at the Palo Alto Research Center in collaboration with Dr. Dell. This program uses biosynthetic information to assign structures to mass peaks and is seen as being critical to the success of the high-throughput glycan structural analysis effort.
Database Developments

Dr. Rahul Raman, Director of the Bioinformatics Core (B) at the Massachusetts Institute of Technology, talked about the challenges, from a database standpoint, of incorporating all of the emerging Consortium data into a functional platform that integrates the different types of data into a seamless whole.

Dr. Raman gave an on-line demonstration of the power of the object-based relational databases that are being constructed by Core B. For instance, it is envisioned that one might look at the results of a glycan array screening experiment for a particular glycan-binding protein (GBP), and click on a particular high affinity binding glycan to see other GBPs for which it was a high affinity binder or to see in which tissues or cells it is expressed, or what phenotype the knockout mouse has, or access information about the glycosyltransferases responsible for its synthesis. This is fundamentally different from most publicly-available databases, where clicking on an object brings up a flat file. The structure of the relational database allows the user to access all the different types of data regardless of where one enters, and facilitates an integrated approach to functional glycomics. Consortium scientific Core data is being entered into the databases through a data acquisition interface for each Core.

The GBP database (which can be accessed at: http://www.functionalglycomics.org/glycomics/molecule/jsp/gbpMolecule-home.jsp) is currently composed of 146 “molecule pages”, which provide an interface for information from publicly-available databases and data from the Consortium scientific Cores. These pages each have a few cyan-colored fields which are awaiting completion by experts through a web-based system; it is hoped that this task will be completed soon.

The glycosyltransferase (GT) database (a beta version of which can be accessed at: http://www.functionalglycomics.org/static/gt/gtdb.shtml) is a set of glycosylation pathways. Core structures that are unique to each class and extensions and terminal structures are represented in symbol format. Numbered linkages are indicated and link to the CAZY database.

The carbohydrate database is currently under construction and a set of search engines is currently being beta-tested. Its anticipated release date is January 2005. The database will contain approximately 7500 glycan structures from a seed database of glycoprotein and glycolipid glycan structures provided by Glycominds Ltd., non-redundant N- and O-linked glycoprotein glycans from CarbBank, and glycan structures synthesized by the Carbohydrate Synthesis Core (D). This database will continue to be expanded by the incorporation of murine and human N- and O-linked structures identified by the glycomics initiative of the Analytical Technology Core (C).
**The Glycan Arrays**

The **Protein-Carbohydrate Interaction Core (H)** analyzes the carbohydrate-binding specificity of GBPs submitted by investigators; glycan array analysis yields information about the surface-captured oligosaccharide determinants recognized by GBPs and is currently the most popular resource of the Consortium. To date, 54 resource requests for the glycan array screening of over 144 individual samples have been approved by the Steering Committee. **Dr. Richard Cummings**, Coordinator, reported on the progress being made at Core H. The lead platform, which has been used to generate all of the data currently posted on the Consortium website (accessible at: [http://www.functionalglycomics.org/static/consortium/data/dataCoreH.shtml](http://www.functionalglycomics.org/static/consortium/data/dataCoreH.shtml)), uses steptavidin-coated microtiter plates to which biotinylated glycans are attached. Binding of lectins to glycans is detected by ELISA.

Dr. Cummings showed a number of examples of glycan array screening data for a selection of different types of GBPs. The results that have been obtained so far have been consistent with previous findings and extended the knowledge of glycan affinities for some of the known GBPs. In some cases the GBPs are novel, with no previously-available binding information. To date, every GBP that has been analyzed has displayed a unique binding specificity profile.

An alternative covalent glycan array platform has been developed under the direction of **Dr. Ola Blixt** at the **Carbohydrate Synthesis/Protein Expression Core (D)** at the Scripps Research Institute. (For more details about Core D and the development of the covalent array, see the next story in this newsletter.) This new platform has been evaluated with a variety of GBPs and has performed well. While the ELISA and covalent platforms are yielding substantially the same results, there have been some differences in the binding profiles observed. Over the next several months, as Core H transitions from the ELISA to the covalent array, data will be collected from both platforms to gain a better understanding of the differences between them. Both platforms give reproducible data and are reusable. The density of glycans is higher on the covalent array, which uses less of each glycan to construct the arrays and less GBP for the analysis.

The current version of the biotinylated array contains 181 unique glycans comprising a variety of synthetic and natural structurally defined terminal sequences of glycoprotein and glycolipid glycans. Expansion of the structures present on the arrays is considered to be a priority; Cores D and H work together to produce new glycans for the arrays, being guided in part by the information generated by the **Analytical Glycotechnology Core (C)** about the glycan structures present in tissues and cells.

**Dr. Cummings** stressed that Core H has many tools available for use and is anxious to work with individual investigators to address specific research questions. Secondary binding analysis using surface plasmon resonance (using Biocore 3000) is also available by investigator request and Steering Committee approval. **Richard Alvarez**, the Director of Core H, works closely with investigators to ensure that the best possible data are obtained.
Mouse Phenotyping
Dr. Jamey Marth, Coordinator of the Mouse Phenotype Core (G) at the University of California, San Diego, reported that Core G is engaged in measuring more than 100 physiological parameters and responses among genetically altered mice and comparing the findings to those identically obtained from sibling control animals. Data for Galectin-1 and -3, FucT-IV and -VII, ST3Gal-I, ST6 Gal-I and Core 2 GlcNAcT-I knockout strains are available on the Consortium website at: [http://www.functionalglycomics.org/static/consortium/data/coreg1.shtml](http://www.functionalglycomics.org/static/consortium/data/coreg1.shtml).

Dr. Marth highlighted several novel findings that Core G has obtained, including an increase in bleeding time in ST3Gal-I knockout animals which was shown to be correlated with a decrease in the level of Factor V (a protein with many potential glycosylation sites), an increase in oxygen consumption and carbon dioxide production in FucT-IV knockout animals, differences in conditioned fear responses and social dominance behavior in Galectin-3 knockout animals and an increase in the stem cell marker Sca-1 in the bone marrow, blood, lymph node and spleen of Galectin-1 knockout animals.

The phenotyping effort is proceeding in high gear and Core G is increasingly looking for novel strains to phenotype in the interim period before novel knockout mouse strains become available from the Mouse Transgenics Core (F). Dr. Marth encouraged American, European and Japanese investigators with novel strains they would like to see phenotyped to contact him or Dr. Paulson. Suggested strains will be reviewed and prioritized by the Mouse Committee and the Steering Committee.

Investigator Use of Consortium Data
Several talks were presented by investigators which highlighted the use of Consortium data as part of their own research projects.

Dr. Ronald Schnaar presented recently obtained data on behalf of Dr. Bruce Bochner in a study of human Siglec-8 (Glycobiology abstract 303). Cross-linking of Siglec-8, which is expressed on eosinophils, mast cells and basophils, has been shown in Dr. Bochner’s laboratory to induce eosinophil death. A human Siglec-8-IgG1 chimera was submitted to the Protein-Carbohydrate Interaction Core (H) for glycan array analysis, which strikingly revealed high affinity binding to a single glycan structure – 6'-sulfo-sLe\(^\text{X}\). Neither unsulfated sLe\(^\text{X}\), nor an isomer with the sulfate on the 6-position of the GlcNAc residue – 6-sulfo-sLe\(^\text{X}\) – supported detectable
binding. (These data are accessible on the Consortium website at: http://www.functionalglycomics.org/static/consortium/data/dataCoreH.shtml.) Subsequent secondary analysis at Core H using surface plasmon resonance confirmed these results and yielded a $K_D$ value of $2.3 \, \mu M$ for this high specificity interaction.

**Dr. Paul Crocker** shared data from his laboratory concerning expression patterns of mouse CD33-related siglecs on cells of the immune system using antibodies generated in sheep. The generation of monospecific sheep polyclonal antibodies to CD33-related mouse siglecs was performed in Dr. Crocker’s laboratory as a Consortium bridging project. Mouse Siglec-F expression has only been detected on eosinophils, making it a candidate ortholog for human Siglec-8. However, Dr. Crocker showed data indicating that the two species apparently evolved independently. Mouse Siglec-E antibody will become available to investigators through the **Carbohydrate Synthesis/Protein Expression Core (D)** in the near future.

**Dr. James Paulson** presented work from his laboratory on in vitro activation and purification of B cells and T cells from mixed splenocytes. He showed MALDI glycan profiles from these cells done in collaboration with **Dr. Anne Dell’s** laboratory, and some Glyco-gene chip microarray data produced by the **Gene Microarray Core (E)** of the Consortium. In activated CD8$^+$ T cells compared to fresh T cells, sialylated structures are largely gone, replaced by galactose-terminated structures. This correlates with a six to seven-fold decrease in the expression of ST6 Gal1 and a two-fold increase in the expression of $\alpha1-3$ Gal T in these cells. (These data are accessible on the Consortium website at: http://www.functionalglycomics.org/static/consortium/data/dataCoreE.shtml.)
Dr. Yvette van Kooyk presented a talk on dendritic cell and macrophage C-type lectins, incorporating glycan array results obtained from the Protein-Carbohydrate Interaction Core (H) for a human DC-SIGN-Fc chimera and a human macrophage Gal/GalNAc-specific lectin (MGL)-Fc chimera. (These data are accessible on the Consortium website at: http://www.functionalglycomics.org/static/consortium/data/dataCoreH.shtml) Dr. van Kooyk’s research is focused on exploring potential roles for these C-type lectins in the immune system.

**Consortium Core Highlight Story***

**Spotlight on The Carbohydrate Synthesis/Protein Expression Core (D)**

It has been a productive year for Core D at The Scripps Research Institute in La Jolla. Under Ola Blixt’s direction, a very promising alternative carbohydrate microarray platform has been developed, the synthetic compound library has been expanded and the first glycan-binding proteins (GBPs) have been purified for crystallization by the Joint Center for Structural Genomics (JCSG).

**Printed Covalent Glycan Array**

During the Consortium’s first year the ELISA glycan array was developed collaboratively by Core D and the Protein-Carbohydrate Interaction Core (H) (under the direction of Rick Alvarez at the University of Oklahoma). Ola Blixt had previously been involved with Jim Paulson and Chi-Huey Wong in the development of a lipid-based covalent array and had become interested in developing a miniaturized and practical covalent array platform for the Consortium. Discussions with Steve Head, Director of the Consortium’s Gene Microarray Core (E), raised the possibility of using existing printing technology to produce glycan arrays, if a method could be devised to immobilize the glycans. When an amine-reactive N-hydroxy-succinimide- (NHS-) activated glass slide that could potentially be used to couple reactive amino groups using simple and convenient chemistry became commercially available, it seemed that all the necessary pieces were in place to produce a printed covalent array employing Core D’s extensive library of glycans…
During the last year, **Ola Blixt** has actively collaborated with **Steve Head** of **Core E** to generate a prototype covalent glycan array platform. Advantage was taken of the glycan library developed for the ELISA array, comprising over 200 synthetic and natural structurally defined terminal sequences of glycoprotein and glycolipid glycans. Over half of the glycans incorporated into the covalent array were produced in the laboratory of **Nicolai Bovin**, Co-Coordinator for **Core D** at the Shemyakin & Ovchinnikov Institute of Bioorganic Chemistry in Moscow. Other compounds were produced by **Core D**, **Chi-Huey Wong’s laboratory** and **Core H**. Glycans were covalently linked to commercial NHS-activated microglass slides using standard gene microarray printing technology. Another advantage of the reactive amino group coupling strategy is that pronase-digested natural N-glycans can be coupled directly to the slide surface.

The new platform was evaluated with regard to printing optimization and binding interactions using a wide variety of GBP’s. Glycans are printed on the slides at two different concentrations in replicates of six each. The covalent array has performed well with various plant lectins, mammalian lectins, anti-carbohydrate antibodies and viral and bacterial lectins. The results, presented in a *PNAS* paper which has just been published online, have both confirmed binding specificities obtained by other means and yielded novel information about fine binding specificities. Uniformly low backgrounds have been observed, and 100 – 200-fold less protein (0.1-50 micrograms) is required for an optimal signal compared to the ELISA array. The array has also been used to screen the glycan-binding specificities of intact influenza virus particles, as well as to obtain binding profiles for human serum.

Of particular interest so far is the use of the printed array to screen human serum. **Ola Blixt** explained that the binding profiles obtained from 10 healthy donor samples were remarkably consistent, raising the possibility of there being an identifiable “healthy profile” and of the potential use of the array for screening patient serum for the presence of antibodies that could be useful for diagnosis of disease.

While the ELISA and covalent platforms are yielding substantially the same results, there have been some differences in the binding profiles observed. It is not yet clear how to interpret these differences, but geometric and steric factors related to the nature of the multivalent interactions and the density of sugars on the platforms may play a role. **Ola Blixt** believes that the glycan density is probably higher on the printed than on the ELISA array, but points out that differences in spacing and clustering may play a role in the binding of GBP’s to the two platforms. Such factors may be more important in the case of multimeric GBP’s. In general, GBP’s have low intrinsic affinity for their ligands but often engage in multivalent interactions. The **Core D** group has taken the novel approach of enhancing valency where necessary to achieve binding to the array. This has been accomplished through the use of secondary and tertiary antibodies to generate multivalent GBP complexes.

There is a lot of excitement at **Core D** and within the Consortium about the use of the glycan arrays to contribute to a more complete understanding of the specificities of GBP-ligand interactions. **Core D** researcher **Daniela Vasiliu** hopes to see this knowledge lead ultimately to the development of new therapies for a host of diseases. As the Consortium transitions from the
ELISA glycan array to the printed glycan array over the next several months, data will be collected from both platforms to gain a better understanding of the differences between them. Ultimately, the Steering Committee will make a decision about what role the ELISA array will play in the future of the Consortium.

The Carbohydrate Compound Library

The carbohydrate compound library (available at http://www.functionalglycomics.org/static/consortium/resources/resourcecored.shtml) has been increased to 154 structures containing neutral or biotinylated spacers or polyacrylamide polymers (PAA). The library represents terminal structures of glycoprotein and glycolipid glycans, including the following classes of compounds:

- Poly-N-acetyllactosamines
- Lewis series
- Blood group oligosaccharides
- Milk oligosaccharides
- Tumor marker oligosaccharides
- Sialosides
- Ganglioside saccharides
- N-linked glycans
- O-linked glycans
- Sulfated oligosaccharides

**Core D** employs large-scale chemoenzymatic synthesis to efficiently produce these compounds. The complexities of the compounds now being synthesized require multiple enzymatic and purification steps. **Core D’s** capacity to overexpress and purify 28 recombinant glycosyltransferases and accessory enzymes has been invaluable in this effort and has involved generous support from investigators and sponsors in providing recombinant constructs and expression systems. The glycosyltransferases and accessory enzymes are constantly maintained and produced according to synthetic demands. Large-scale production is employed for economy – for example, bacterial cells are cultured in a 100 liter fermentation tank and generate large amounts of active protein.

Sean Paul tends a column used in the purification of oligosaccharides.
Daniela Vasiliu spots fractions from column chromatography of oligosaccharides onto a TLC plate.

The carbohydrate-PAA conjugates are being produced in two different sizes (30 KD and 1 MD) in Nicolai Bovin’s laboratory. These compounds are expected to be valuable tools for investigating the binding specificities of cell surface GBP.s Core D plans to generate PAA conjugates of the entire compound library by sending compounds containing the 2-azido functional group to Nicolai Bovin’s laboratory for further conjugation to PAA. Increasing the number and complexity of N-glycan structures present on the array is a high priority project for Core D in the coming year. Branching natural glycans would be expected to be ligands for many GBP.s, and feedback received from Participating Investigators has indicated a desire to see more of these structures incorporated into the array. One strategy currently under consideration is to cleave N-glycans from glycoproteins in Nicolai Bovin’s laboratory using PNGase F produced by Core D, then send the predominantly biantennary species back to Core D for fractional purification and further enzymatic modification using Core D’s extensive collection of glycosyltransferases and accessory enzymes. Another strategy for obtaining smaller amounts of more complicated structures is to cleave N-glycans from glycoproteins and separate them on a preparative-scale Dionex column. This strategy has been successfully employed in the laboratory of Richard Cummings, Coordinator of Core H. Ola Blixt sees this project as one that will be a real team effort, involving all members of Core D and potentially also Core H.

Production of Glycan-binding Proteins for Crystallization
The protein production efforts at Core D are directed by Nahid Razi. In collaboration with Participating Investigator Margaret Huflejt, full length Galectin-4, as well as its two individual structural domains, have been purified for crystallization by the JCSG. Primary carbohydrate binding studies for all three species were carried out on the printed glycan array, and selected glycans were further evaluated on a Biacore 3000. Based on these studies, it has been possible to make a preliminary assignment of each domain to families of glycans that are distinct from each other. Although both domains can recognize lactose, preferred specificities for each domain were revealed. A number of glycan candidates have been selected for co-crystallization with Galectin-4 and its two individual carbohydrate-binding domains.
The Core D Team

Ola Blixt  
Director

Jim Paulson and  
Chi-Huey Wong  
Co-Coordinators, The Scripps Research Institute, La Jolla

Nicolai Bovin  
Co-Coordinator, Shemyakin & Ovchinnikov Institute of Bioorganic Chemistry, Moscow

Nahid Razi  
Associate Director, Molecular Biology and Protein Expression

Kirk Allin  
Protein expression and purification

Nathan Jacobsen  
Chemical and enzymatic synthesis

Xiaofei Liu  
Vector and cell line construction, protein expression and purification

Daniela Vasiliu  
Chemical and enzymatic synthesis

Yingning Zhang  
Vector and cell line construction, protein expression and purification

Julia Hoffmann  
Research Assistant

Sean Paul  
Research Technician

Matthew Fowler  
Administrative Assistant


*This is the first in an occasional series of articles highlighting Consortium Cores.
Available Resources and Services

The Consortium for Functional Glycomics is producing novel resources and services for Participating Investigators and interested scientists. A link to an advertisement page on the website (http://glycomics.scripps.edu/CFGad.html) resides as a banner on the Consortium home page (http://functionalglycomics.org). Please visit our advertisement page to view available carbohydrate compounds, mouse knockout strains, glycan array screening and glyco-gene microarray analysis. Visitors can also find instructions for completing and submitting resource requests online. Request forms received online are forwarded to the Director and Coordinator of the appropriate Core for evaluation. All requests are given the same consideration regardless of Consortium member status; non-members proposing experiments within the scope of the Consortium agree to submit their data to the Consortium database prior to publication. Most requests, along with the Director's recommendation, are reviewed at the following Steering Committee meeting. The website is updated with new offerings as additional resources become available.

People and News

Glycobiologists rock:
Lucky attendees of the Society of Glycobiology banquet were treated to a surprise appearance of the Blues Brothers (aka Participating Investigators Richard Cummings and Michael Pierce) in a performance that brought the house down and the audience to its feet.

Click here to see the Blues Brothers live in action
### New members:

<table>
<thead>
<tr>
<th>Investigator</th>
<th>Institution</th>
<th>Subgroup</th>
</tr>
</thead>
</table>
| **Gillian Air, PhD**  
Professor | University of Oklahoma | Other |
| **Pedro Bonay, PhD**  
Professor | Universiad Autonoma De Madrid | Galectin |
| **Brian Dean, PhD**  
Head of Laboratory | Mental Health Research Institute | Other |
| **Robert C. Fuhlbrigge, MD, PhD**  
Assistant Professor | Harvard University | C-type lectin |
| **Thomas A. Gerken, PhD**  
Associate Professor | Case Western Reserve | Other |
| **Donald Harm, PhD**  
Professor | Harvard School of Public Health | TCR/CD1/MHC |
| **Shawn Hochman, PhD**  
Assoc. Professor | Emory University School of Medicine | Other |
| **Shie-Liang Hsieh, PhD**  
Professor | National Yang-Ming University | C-type lectin |
| **David Jackson, PhD**  
Professor | Weatherall Institute of Molecular Medicine | Other |
| **David L. Jaye, MD**  
Assistant Professor | Emory University School of Medicine | C-type lectin |
| **Laura Kiessling, PhD**  
Professor | University of Wisconsin | Siglec |
| **Peter Lipke, PhD**  
Professor | Hunter College | Other |
| **Gary Litman, PhD**  
Professor | University of South Florida | Other |
| **Seth Pincus, MD**  
Professor, Director | Louisiana State University | Other |
| **Gabrial Rabinovich, PhD**  
Assistant Professor | University of Buenos Aires | Galectin |
| **Anna Katharina Simon, PhD**  
Investigator | University of Oxford | Other |
| **Willi Vann, PhD**  
Laboratory Chief | Center for Biologics Evaluation and Research, FDA | Other |
| **Herbert W. Virgin IV, MD, PhD**  
Professor | Washington University School of Medicine | Other |
| **Reinhard Vlasak, PhD**  
Associate Professor | University of Salzburg | Other |
| **Peng George Wang, PhD**  
Professor | Ohio State University | Other |
| **Zena Werb, PhD**  
Professor | University of California San Francisco | Galectin |
| **Dapeng Zhou, PhD**  
Assistant Professor | University of Chicago | TCR/CD1/MHC |
Calendar of upcoming events:

- **Combined Participating Investigator and Advisory Committee Meeting**
  NIH campus
  Bethesda, MD
  May 17-18, 2005

- **Gordon Conference on Glycobiology**
  Ventura, CA
  March 6-11, 2005

- **229th American Chemical Society National Meeting**
  Division of Carbohydrate Chemistry
  “Frontiers of Modern Carbohydrate Chemistry”
  March 13-17, 2005
  San Diego, CA
  [http://www.chemistry.org/](http://www.chemistry.org/)

- **6th Carbohydrate Bioengineering Meeting**
  April 3-6, 2005
  Barcelona, Spain

- **Gordon Conference on Carbohydrates**
  June 19-24, 2005
  Tilton, NH

- **Glycoproteomics – Protein Modifications For Versatile Functions**
  June 28-30, 2005
  Dubrovnik, Croatia
  [http://bmb.pharma.hr/glyco2005/](http://bmb.pharma.hr/glyco2005/)

- **13th European Carbohydrate Symposium**
  August 21-26, 2005
  Bratislava, Slovakia

- **XVIII International Symposium on Glycoconjugates**
  August 28 – September 2, 2005
  Florence, Italy
  [http://www.glycoxviii.com](http://www.glycoxviii.com)

- **2nd Human Disease Glycomics/Proteome Initiative Workshop**
  August, 2005
  Munich, Germany