Banbury Center

COLD SPRING HARBOR LABORATORY

2011

BANBURY CENTER

Banbury Center is a 55-acre estate adjoining the waters of Long Island Sound on the north shore of Long Island, barely 40 miles east of downtown Manhattan and some five miles from Cold Spring Harbor Laboratory. The estate was donated to the Laboratory in 1976 by Charles Sammis Robertson, together with funds for necessary architectural conversions and an endowment to cover upkeep of the grounds and the original estate structures. With the Laboratory's international reputation for research and education, the magnificent Banbury grounds and buildings are an ideal site for small conferences in the areas of molecular biology and genetics, especially as they relate to health, social, and policy issues.

What was once the estate's original seven-car garage is now the Conference Room, containing administrative offices, a small library, and—at its center—a room of an ideal shape and size for workshop-style discussion meetings. Complete with extensive, unobtrusive sound and projection facilities as well as wall-to-wall blackboard space, the room can accommodate as many as 40 participants while remaining equally conducive to either formal presentations or informal give-and-take.

The Robertsons' family house, situated on the final promontory before the grounds descend to the shore of Cold Spring Harbor, now serves as the center for participant accommodations and dining, while the extensive grounds, swimming pool, tennis court, and beach present ample recreational resources. On-site accommodations were supplemented by the opening in 1981 of the Sammis Hall guest house—a modern embodiment of the sixteenth century Palladian villas—designed for the Center by the architectural firm of Moore Grover Harper. In 1997, the Meier House, opposite the Conference Center, was added to provide extra housing so that everyone attending a Banbury Center meeting can stay on the estate.

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BANBURY CENTER
EXECUTIVE DIRECTOR'S REPORT

It was another busy year for the Banbury Center. The Center was used for 34 events with a total of 686 participants. There were 24 science-related meetings, together with six lecture courses run by the Meetings and Courses Program and two Watson School *Topics in Biology* courses. Of the 686 participants, 511 were from the United States (from 35 different states) and 96 from Europe (16 different countries). The truly international character of the Center's program is shown by the fact that participants came from a total of 25 countries worldwide.

Banbury Center fosters and promotes research by providing a venue for meetings other than those dealing with scientific topics, for example, by providing training for young scientists and physicians at the beginnings of their careers. The National Institute of Mental Health held its third "Brain Camp" for young physicians, to introduce them to the latest basic research relevant to their work. The Boehringer Ingelheim Fonds returned with their fellows drawn from Europe and North America for a "Communicating Science" workshop. The fellows are subjected to a rigorous training in writing skills, presentation of graphic information, and preparing and delivering a scientific talk, so that they can excel in these skills as well as their research. For the first time, we held a "Leadership in Bioscience" workshop. David Stewart received funding from American Express Foundation under their Leadership Program for a short course where participants were to be instructed in things scientists need to be able to do—in addition to their research—to succeed. The first course was held in 2011, organized by Carl Cohen, coauthor of *Lab Dynamics: Management Skills for Scientists*, published by Cold Spring Harbor Laboratory Press. The course drew participants from institutes throughout the United States.

We also promote research by hosting meetings where a small number of members of groups or associations come together to discuss policy affecting their work. There were four such examples this year. The National Cancer Institute (NCI) established a network of biobanks to act as clearing houses to collect and supply biopsies, DNA, and cell cultures to researchers. In June, representatives of the NCI Biobanks came to Banbury to review the effectiveness and discuss the future of the program. Discussions were guided by Laurence Baker (University of Michigan Cancer Center) and Scott Lowe (CSHL), with input from Harold Varmus, Director of NCI.

We have held several meetings on the chronic fatigue syndrome. and this year, we were delighted to host the Scientific Advisory Board of the Chronic Fatigue and Immune Dysfunction Syndrome (CFIDS) Association. During the past few years, CFS research has received high-profile media attention, for example, over the claim (now discredited) that the XMR virus is a cause of CFS. This has generated both increased interest and unprecedented opportunities for progress. The goals of the meeting were for the Scientific Advisory Board to provide guidance on research strategies as to encourage innovative research focused on early detection, objective diagnosis, and effective treatment.

This group also included a meeting of the editorial board of the Federation of Biochemical Societies (*FEBS*) journal. Banbury Center provided a quiet haven for the board to meet with the journal's staff and discuss the performance and future direction of the journal.

Finally, representatives of the Epigenomics of Plants International Consortium (EPIC), funded by the National Science Foundation (NSF), came to Banbury in November. The Consortium was established to coordinate and promote research on deciphering the plant epigenome. Participants discussed the intellectual questions and transformative methodologies and infrastructure needs required to do this, as well as the means to engage funding agencies and the international research community as a whole.

The broad sweep of scientific topics of Banbury Center meetings changes from year to year. One year, it may be neuroscience and psychiatric disorders, and another year, it may be human genetic disorders. This year, the focus was on cancer, in particular on treatments for cancer. The first meeting, *Curing Melanoma and Other Cancers by Targeted Therapies*, was organized by Joseph Schlessinger (Yale University) and Jim Watson. It could not have been held at a more auspicious moment. In the course of the meeting, Jim Allison (Memorial Sloan-Kettering Cancer Center) learned that the Food and Drug Administration (FDA) had approved a monoclonal antibody therapy for metastatic melanoma that had been developed based on his work.

The second cancer meeting was *Metformin and Neoplasia*. Metformin is an antidiabetic drug used to treat type-2 diabetes. It is the most widely prescribed antidiabetic in the world. Remarkably, epidemiological studies have shown that patients taking metformin have a lower risk of developing cancer. The mechanism(s) underlying this anticancer effect is far from clear and was a focal point of the presentations and discussions at the meeting. Metformin has an added interest in the context of "repurposing" drugs. It is argued that drugs like metformin, which have been given to hundreds of millions of people and whose safety is established, should be fast-tracked for approval for other uses.

As long ago as 1995, Stan Prusiner organized the first Banbury Center meeting on prions. At that time, there were many controversial issues about the nature, replication, and species specificity of these misfolded proteins. Prion-like particles became immensely important to the population of the United Kingdom in 1990 when patients were found suffering from what was called variant Creutzfeldt–Jakob disease. The cause of the disease was demonstrated to be meat contaminated with neural material from cattle suffering with bovine spongiform encephalopathy. As a result a large proportion of the U.K. population had been exposed, leading to almost 200 deaths. Misfolded proteins are found in other disorders, for example, Alzheimer's disease, and there is recent evidence that Alzheimer's disease amyloidosis can be transmitted to primates. That these disorders might be transmissible has important implications for public health, and the time was clearly right for a critical review of the data on transmission of the amyloidoses, the mechanisms involved, and the implications for human health.

Another area in which Banbury Center has long had an interest is the genetics of psychiatric disorders. In the early 1990s, we held several meetings reporting on the progress of finding genes involved in these disorders using the only tools then available, linkage analysis. A later incarnation of this approach, genome-wide association studies, has found many locations associated with psychiatric disorders, but the significance of these remains unknown. Now, new high-through-put DNA sequencing techniques have made, or are about to make, it possible to sequence the whole exomes and genomes of large numbers of individuals. This will provide opportunities to develop new gene-hunting strategies for complex genetic disorders. Our meeting brought together experts to critically assess current strategies and to outline how genome-scale sequencing can be used most effectively and efficiently.

The Cold Spring Harbor Laboratory Corporate Sponsor Program is a mainstay of the Banbury Center program, providing funding each year for a small number of meetings. We are very grateful to members of the Program for their support and happy when they wish to use Banbury Center for a meeting of their own choice. In 2011, both Astellas-OSI Pharmaceuticals and Sanofi-Aventis came to Banbury.

The Banbury Center could not operate at its high level without the hard work of many people. The Center is especially fortunate in having Janice Tozzo and Susanne Igneri ensuring that the meetings run smoothly, and Basia Polakowski making sure that participants are welcome in Robertson House. Sonny Leute, Fredy Vasquez, and Joseph McCoy look after the grounds, dealing with vast amounts of leaves in the fall and, this year, vast amounts of snow in the winter. Jon Parsons is indefatigable in handling audio-visual requirements, and Connie Brukin enlivens this report with her photographs. Culinary Services feeds our participants and Housekeeping copes admirably with the rapid turnover of guests.

Garage

Renovations, 1976

It is now 35 years since the garage of the Robertsons' estate was converted into the Conference Room, and for the first time in that period, the room is undergoing a complete renovation. It is long overdue. In particular, the original wiring was not designed to take the load imposed by all the computers that participants bring or the demands of modern projectors and copying machines. We will also upgrade all the ethernet cabling and generally bring the facility into the 21st century. The building has been emptied and turned over to the electricians, carpenters, and painters—and we look forward to hosting meetings for the next 35 years!

Jan Witkowski
Executive Director

BANBURY CENTER MEETINGS

Leadership in Bioscience Workshop

February 18–21

FUNDED BY **The American Express Foundation**

ARRANGED BY **C. Cohen,** Science Management Associates, Newton, Massachusetts
D. Kennedy, WorkLab, LLC, New York

A scientist running a laboratory is essentially running a business, small to begin with but likely to get larger with time. And so scientists need to develop skills akin to those needed to run a business: identifying and resolving conflicts, dealing with difficult people, leading effective and productive meetings, and communicating effectively within the laboratory and with the outside world. These skills, if acquired at all, are usually learned haphazardly, after the fact. How much better to learn them systematically and in advance of needing them! So, David Stewart, Executive Director of the Meetings and Courses Program, applied to the American Express Foundation for funding from the Foundation's Leadership Program. He was successful and the "Leadership in Bioscience Workshop" was the result.

SESSION 1: Who We Are

Participants read 50–100 word "Who I am and what I hope to get from this workshop" aloud to entire group. They revealed to the group what they would be if they were not scientists.

SESSION 2: Introduction: What Is Leadership and What Makes a Great Scientist/Leader?

Part 1 Small groups proposed attributes of leadership especially in a scientific context, and they discussed examples of effective and ineffective leadership based on their own experience and observations.

Part 2 Small groups reported to the entire group. The goal was to develop attributes of excellent leaders that will serve as a reference point for the rest of the conference.

SESSION 3: Difficult Conversations and Interactions

The types of situations that scientists find difficult as they transition into leadership positions and provided a practical toolkit to use in those situations.

- Learning to listen and to seek out underlying interests
- Fundamental tools for negotiating difficult conversations
- Dealing with difficult people

SESSION 4: Keynote Speaker: Zia Khan, Vice President, Strategy and Evaluation, Rockefeller Foundation, New York

SESSION 5: Case Studies

Attendees were instructed to bring with them a one-page case study describing a difficult management situation or leadership challenge they faced or are facing.

Part 1 In small groups, each attendee read their case aloud. A structured discussion guide was provided to elicit comments, discussion, and suggestions from the group in the context of the work already done in the workshop. Each small group selected one case that best illustrated a key leadership challenge for presentation in summary to the entire group.

Part 2 Each small group made a 1-minute summary of its selected case to the large group, which then chose just one or more cases to discuss in the large group. Large groups' ideas/suggestions/approaches were compared with those of the small group. A discussion of leadership characteristics was tied in from Session 1.

SESSION 6: Group Dynamics and Meetings

- How to run/lead meetings.
- How to structure and encourage open discussion, ensuring participation.
- How to deal with silence and non-participants.
- How to recognize and manage impediments to effective group problem solving.

SESSION 7: Projecting Leadership

Volunteer(s) were selected to deliver a "pitch" about their institution, department, or group. The large group provided feedback in the context of what was learned so far in the workshop.

SESSION 8: Science in the Public Eye

Facilitator: K.R. Miller, Brown University, Providence, Rhode Island

SESSION 9: Concluding Group Discussion

What did we learn? What did we not learn that we would have liked to learn?

SCOR Retreat

March 15–17

FUNDED BY **The Leukemia & Lymphoma Society**

ARRANGED BY **S. Lowe,** Cold Spring Harbor Laboratory, New York

SCOR (Specialized Center of Research) is a program of the Leukemia & Lymphoma Society. The cornerstone of the SCOR program is its collaborative structure: Every recipient works with a cross-disciplinary team of leading researchers from their own and other universities and medical institutions. In this case, researchers from Cold Spring Harbor Laboratory collaborate with researchers at the Universities of Minnesota, California, San Francisco, and Chicago. This meeting provided an opportunity for those involved to present their data and to interact with each other in person.

OPENING SESSION

J. Zuber, Cold Spring Harbor Laboratory: Leukemia maintenance genes.

SESSION 1: Genetics and Biology of 5q/7q Deletions

M. Le Beau, University of Chicago, Illinois: Commonly deleted intervals in human leukemias with del 5q/7q.

R. Bergerson, University of Chicago, Illinois: Characterization of candidate haploinsufficient genes on chromosome 5.

A. Stoddart, University of Chicago, Illinois: Characterization of the genetic pathways leading to t-MN with a del 5q.

J. Wong, University of California, San Francisco: Modeling 7q deletions in the mouse.

S. Lowe, Cold Spring Harbor Laboratory: Is MLL3 a 7q tumor suppressor?

SESSION 2: Signaling in AML

H. Liu, University of Chicago Hospital, Illinois: Targeting PI3K/mTOR and MEK pathways in AML.

E. Diaz-Flores, University of California, San Francisco: Biochemical profiling of primary leukemias using phosphoflow cytometry.

Z. Zhao, Cold Spring Harbor Laboratory: Ras feedback signaling in leukemogenesis and therapy response.

SESSION 3: Therapy in AML

S. Rathe, University of Minnesota, Minneapolis: This, that, and the other thing.

E. Dolan, University of Chicago, Illinois: Pharmacogenetics of Ara-C.

SESSION 4: Lymphoid Malignancies

M. Dail, University of California, San Francisco: Response and resistance to PI3K inhibition in T-lineage leukemia.

C. Scuoppo, Cold Spring Harbor Laboratory: New tumor suppressor networks in lymphoma.

C. Miething, Cold Spring Harbor Laboratory: Biology of PTEN in lymphoma.

The Third NIMH-Sponsored Brain Camp

March 18–21

FUNDED BY **National Institute of Mental Health**

ARRANGED BY **M. Akil,** National Institute of Mental Health, Bethesda, Maryland
T. Insel, National Institute of Mental Health, Bethesda, Maryland

M. Akil

For the third year, the Banbury Center was very pleased to host the NIMH-sponsored "Brain Camp." The goal of the Brain Camp is to identify areas of neuroscience that are of interest and relevance to psychiatrists and to communicate these to a small group of outstanding psychiatry residents and research fellows. Some of the most distinguished and thoughtful neuroscientists in the country took part in the meeting. The outcome of the meeting will be the start of a neuroscience curriculum that can eventually be shared with psychiatry training programs around the country.

Introduction and Charge: **T. Insel,** National Institute of Mental Health, Bethesda, Maryland

Special Lecture: **E. Kandel,** Columbia University, New York: Mice, Men, and Mental Illness: Animal Models of Mental Disorders.

SESSION 1: Genetics and Genomics

P. Sklar, Mount Sinai School of Medicine, New York: Toward understanding schizophrenia and bipolar disorder genetics.

J. Gordon, Columbia University, New York: So you've cloned the gene... Now what?

SESSION 2: Developmental Neurobiology

P. Shaw, National Institute of Mental Health, Bethesda, Maryland: In for the long haul: Using longitudinal neuroimaging to understand attention-deficit/hyperactivity disorder.
J. Huang, Cold Spring Harbor Laboratory: Toward a genetic dissection of GABAergic circuits in cerebral cortex: Chandeliers light up the path from genes to cognition.
T. Bale, University of Pennsylvania, Philadelphia: Epigenetics in neurodevelopment: Gene × environment × development × sex.

SESSION 3: Cognitive Neuroscience

C. Carter, University of California, Davis, Sacramento, and A. MacDonald, III, University of Minnesota, Minneapolis: Circuits and symptoms: The cognitive neuroscience of executive control in health and disease.

SESSION 4: Social Neuroscience

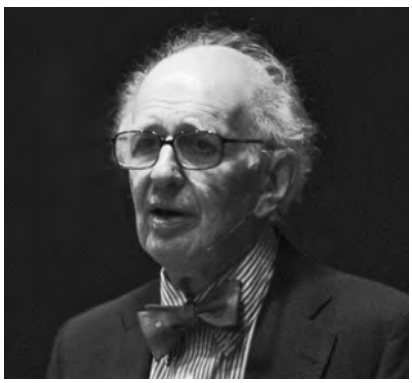
K. Pelphrey, Yale University, New Haven, Connecticut: Neural signatures of autism.
T. Insel, National Institute of Mental Health, Bethesda, Maryland: Social neuroscience: A new basic science for psychiatry.

Round Table Discussion with All Speakers: Future Directions in Neuroscience and Psychiatry

SESSION 5: Circuits and Microcircuits

B. Rosen, Massachusetts General Hospital, Charlestown: Multimodal functional neuroimaging.
K. Hong Wang, National Institute of Mental Health, Bethesda, Maryland: Illuminating the functional organization and plasticity of cortical microcircuits.

K. Pelphrey, L. Sjulson



E. Kandel

Curing Melanoma and Other Cancers by Targeted Therapies

March 22–25

FUNDED BY **Hazen Polsky Foundation and the Melanoma Research Alliance**

ARRANGED BY **J. Schlessinger,** Yale University School of Medicine, New Haven, Connecticut
J.D. Watson, Cold Spring Harbor Laboratory, New York

A wealth of genetic and biochemical analyses combined with novel approaches for drug discovery is offering, for the first time, hope for effective new therapies for untreatable cancers such as melanoma. The goal of the meeting was to present new data about targeted therapies that have been recently developed for the treatment of melanoma and other cancers. Genetic and biochemical studies describing novel targets and new approaches for targeted therapies were also described. Finally, molecular mechanisms underlying drug resistance that take place in patients treated with targeted therapies and new approaches for overcoming this problem were reviewed.

S. Topalian, J. Watson

Welcoming Remarks: **J.A. Witkowski,** Banbury Center, Cold Spring Harbor Laboratory, New York
Introductory Remarks: **J.D. Watson,** Cold Spring Harbor Laboratory, New York

SESSION 1: Genetic and Molecular Basis for Melanoma
Chairperson: M. Herlyn, The Wistar Institute, Philadelphia, Pennsylvania

M. Herlyn, The Wistar Institute, Philadelphia, Pennsylvania: Tumor heterogeneity and the consequences of therapy.

D.E. Fisher, Massachusetts General Hospital, Boston: BRAF-MAPK targets the melanocytic master transcriptional regulator MITF: Targeted therapy and lineage differentiation.

R. Halaban, Yale University School of Medicine, New Haven, Connecticut: Insights from sequencing the melanoma transcriptome and exome.

T. Wiesner, Memorial Sloan-Kettering Cancer Center, New York: Germline mutations in BAP1 predispose to melanocytic tumors.

SESSION 2: Signaling Pathways and Targeted Therapies in Melanoma
Chairperson: J. Schlessinger, Yale University School of Medicine, New Haven, Connecticut

G. Bollag, Plexxikon, Berkeley, California: Discovery of kinase inhibitors for melanoma.
M.J. Weber, University of Virginia, Charlottesville: Compensatory signaling: A mechanism of resistance and a guide to combination therapy.
N. Rosen, Memorial Sloan-Kettering Cancer Center, New York: Resistance to ERK inhibition: Pharmacologic and biologic issues.
R. Marais, Institute of Cancer Research, London, England: Targeting BRAF in melanoma: Synthetic lethality as an approach to treating cells expressing BRAF and other oncogenes.

SESSION 3: Resistance Mechanisms in Melanoma and Other Cancers
Chairperson: B. Stillman, Cold Spring Harbor Laboratory

D.A. Tuveson, CRUK Cambridge Research Institute, Cambridge, United Kingdom: Stromal barriers in pancreatic cancer medicine.
R. Lo, University of California, Los Angeles: Overcoming acquired resistance to BRAF inhibitors.
L.A. Garraway, Dana-Farber Cancer Institute, Boston, Massachusetts: Systematic characterization of resistance to RAF inhibition in melanoma.
P.D. Nisen, GlaxoSmithKline, Collegeville, Pennsylvania: A multifaceted approach to melanoma therapy: BRAF, MEK, MAGE3, and PD-1.

SESSION 4: Epigenetic Pathways in Melanoma and Other Cancers
Chairperson: C.J. Sherr, St. Jude Children's Research Hospital, Memphis, Tennessee

E. Bernstein, Mount Sinai School of Medicine, New York: Unraveling the melanoma epigenome.
J.E. Bradner, Dana-Farber Cancer Institute, Boston, Massachusetts: Direct inhibition of epigenetic reader proteins in cancer therapy.
C. Vakoc, Cold Spring Harbor Laboratory: RNAi Screening to identify epigenetic vulnerabilities in acute myeloid leukemia.

SESSION 5: Immunotherapies for Melanoma Treatments
Chairperson: J.P. Allison, Memorial-Sloan Kettering Cancer Center, New York

J.P. Allison, Memorial-Sloan Kettering Cancer Center, New York: Immune checkpoint blockade in melanoma therapy.
S. Topalian, Johns Hopkins University School of Medicine, Baltimore, Maryland: Targeting immunological pathways: B7-H1/PD-1 blockade in cancer.
T.F. Gajewski, University of Chicago, Illinois: Regulation of antitumor immunity at the tumor microenvironment.

SESSION 6: Differentiation, Stem Cells, and EMT
Chairperson: H. Varmus, National Cancer Institute, Bethesda, Maryland

K. Struhl, Harvard Medical School, Boston, Massachusetts: Metformin-based combinatorial therapy: New xenograft data on melanoma cell lines.
R. Nusse, Stanford University Medical Center, California: WNT signaling and stem cell control.
R. Kalluri, Beth Israel Deaconess Medical Center, Boston, Massachusetts: Hypoxia-induced epithelial to mesenchymal transition and metastasis.

SESSION 7: Perspectives on Melanoma, Biomarkers, and Targeted Therapies
Chairperson: D.M. Epstein, Astellas–OSI Oncology, Inc., Farmingdale, New York

I. Mellman, Genentech, S. San Francisco, California: The practical empiricist's guide to developing targeted cancer therapies.
D.M. Epstein, Astellas–OSI Oncology, Inc., Farmingdale, New York: Dual IGF-1R blockage in cancer therapy.
J.E. Darnell, The Rockefeller University, New York: STAT 3, why we must learn to inhibit it and new ideas that might work.

SESSION 8: Animal Models and Melanoma: What Can We Learn?
Chairperson: D.A. Tuveson, CRUK Cambridge Research Institute, Cambridge, United Kingdom

M. McMahon, University of California, San Francisco: Modeling the effects of pathway-targeted therapeutics in genetically engineered mouse models of cancer.
M. Bosenberg, Yale University School of Medicine, New Haven, Connecticut: Optimizing mouse models of melanoma for reclinical testing.
L. Dow, Cold Spring Harbor Laboratory: Using inducible RNAi in vivo to investigate the role of Wnt signaling in melanoma progression.

SESSION 9: Fighting Mesenchymal Cancers
Chairperson: J. Schlessinger, Yale University School of Medicine, New Haven, Connecticut

G.F. Vande Woude, Van Andel Institute, Grand Rapids, Michigan: Targeting c-MET in cancer.
G. Demetri, Dana-Farber Cancer Institute, Boston, Massachusetts: Parsing pathogenetic pathways to accelerate drug development: Universal lessons from GIST and other sarcomas.
R. Sordella, Cold Spring Harbor Laboratory: Intrinsic and extrinsic regulation of metastatic spread of NSCLC.

Closing Remarks and Discussion: J. Schlessinger, Yale University School of Medicine, New Haven, Connecticut

L. Garraway, R. Nusse, H. Varmus

J. Schlessinger

Neuronal Response Variability and Cortical Computation

April 3–6

FUNDED BY **The Swartz Foundation** and **The Gatsby Charitable Foundation**

ARRANGED BY **L. Abbott,** Columbia University, New York
J. Reynolds, Salk Institute for Biological Studies, La Jolla, California

It is becoming increasingly clear that neuronal response variability, in particular low-frequency response correlations, have a profound impact on how populations of neurons encode information and provide an important window into neural circuit function. The goal of the meeting was to bring together experimentalists and theorists seeking to understand neuronal response variability and its implications for cortical computation and to provide a more unified way to think about variability and correlations. Participants examined such questions as: Is variability "noise" or is it a signature of important computations that we have yet to understand? How do neural circuits distinguish intrinsic variability in the neural signal from the stimulus-induced variability? How can we best exploit our ability to measure variability and correlations to maximize what we learn about neural circuits?

Welcoming Remarks: **J.A. Witkowski,** Banbury Center, Cold Spring Harbor Laboratory, New York
Introductory Remarks: **Why Are We Here? L. Abbott,** Columbia University, New York

SESSION 1: Correlations in Data and Models
Chairperson: L. Abbott, Columbia University, New York

A. Kohn, Albert Einstein College of Medicine, Bronx: Signal propagation between V1 and V2.
M. Smith, University of Pittsburgh, Pennsylvania: Structure of neuronal correlation: Depth, distance, and dynamics.
A. Tolias, Baylor College of Medicine, Houston, Texas: Structure of network activity in the neocortex.
A. Renart, Champalimaud Centre for the Unknown, Lisbon, Portugal: Temporal correlations in recurrent neural networks with balanced excitation and inhibition.
J. Curtis, Salk Institute for Biological Studies, La Jolla, California: Changes in neuronal gain modulate neuronal synchronization and correlation.
M. Cohen, Harvard Medical School, Boston, Massachusetts: Using the variability of neuronal populations to compare spatial and feature attention.

SESSION 2: Effects of Stimuli and Attention on Variability and Correlations
Chairperson: H. Sompolinsky, The Hebrew University, Jerusalem, Israel

M. Churchland, Stanford University, California: Stimulus onset quenches neural variability: A widespread cortical phenomenon.
K. Rajan, Princeton University, New Jersey: Stimulus-dependent suppression of chaos in recurrent neural networks.
E. Anderson, Salk Institute for Biological Studies, La Jolla, California: Burstiness and attentional modulation in V4.
T. Pasternak, University of Rochester, New York: Trial–trial variability of cortical neurons reveals the nature of their engagement in a visual discrimination task.
K. Shenoy, Stanford University, California: Toward a single-trial understanding of motor preparation and variability.

SESSION 3: Decisions and Choice Probability
Chairperson: T. Pasternak, University of Rochester, New York

J. de la Rocha, IDIBAPS, Barcelona, Spain: A model for choice probability: Disambiguating whether response variability biases the decision or vice versa.
A. Fontanini, SUNY Stony Brook, New York: Effects of anticipatory cues on gustatory processing in actively sensing rats.
X.-J Wang, Yale University School of Medicine, New Haven, Connecticut: A reservoir of time constants for memory traces in cortical neurons.
M. Shadlen, University of Washington, Howard Hughes Medical Institute, Seattle, Washington: Variance as a signature of neural computations during decision-making.
D. Ringach, University of California, Los Angeles: Coding by population variance.

SESSION 4: Variability and Correlations in Coding and Circuits
Chairperson: X.-J. Wang, Yale University School of Medicine, New Haven, Connecticut

B. Averbeck, National Institutes of Health, Bethesda, Maryland: Noise correlations and information encoding and decoding.
K. Padmanabhan, Carnegie Mellon University, Pittsburgh, Pennsylvania: Intrinsic biophysical diversity neuronal firing while increasing information content.
M. Corbetta, Washington University School of Medicine, St. Louis, Missouri: Bold signal noise and behavior.
N. Brunel, Université Paris Descartes, Paris, France: Response of networks of excitatory and inhibitory neurons to time-dependent inputs.
H. Sompolinsky, The Hebrew University, Jerusalem, Israel: Sensory processing in random cortical networks.

SESSION 5: Variability and Correlation in Visual Processing
Chairperson: J. Reynolds, Salk Institute for Biological Studies, La Jolla, California

Y. Fregnac, CNRS UNIC, Gif sur Yvette, France: Contextual dependency of signal reliability and noise in V1 during sensory processing/adaption of the simple or complex nature of V1 receptive fields to visual statistics.
L. Osborne, University of Chicago, Illinois: Variability in smooth pursuit eye movements and its origin in the brain: Information coding of visual motion in cortical area MT in single units and populations.
V. Dragoi, University of Texas, Houston Medical Center,: Correlated variability in laminar cortical circuits.
W. Geisler, University of Texas, Austin: Optimal receptive fields for natural tasks: Efficiency, redundancy, and neural noise.

Closing Remarks and Discussion: J. Reynolds, Salk Institute for Biological Studies, La Jolla, California

V. Dragoi

Lyme Disease in the Proteomics–Genomics Era

April 10–13

FUNDED BY **Time for Lyme, Inc.**

ARRANGED BY **B. Budowle,** University of North Texas Health Science, Fort Worth
S. Schutzer, UMDNJ–New Jersey Medical School, Newark

We are now in the proteogenomic era, characterized by a revolution in high throughput technologies, most notably in DNA sequencing and protein identification. These new technologies not only do more faster, they enable us to think about doing things differently, to exploit their power to devise new strategies. The goals of this meeting were to explore how new technologies might be used in conjunction with existing techniques, to develop new diagnostic strategies, to forecast promising future tests, and to identify the problems that need to be overcome including supporting biorepositories. Participants included not only those with experience in Lyme disease but also a number of individuals whose expertise in proteomics, genomics, and other areas can help move the field forward.

S. Schutzer, A. Hassett

Welcoming Remarks: **J.A. Witkowski,** Banbury Center, Cold Spring Harbor Laboratory, New York

What Do We Hope to Accomplish Here?: **S. Schutzer,** UMDNJ–New Jersey Medical School, Newark

SESSION 1: Overview Talks
Chairperson: S. Schutzer, UMDNJ–New Jersey Medical School, Newark

A.C. Steere, Massachusetts General Hospital, Boston: Evolution of lyme disease in the United States covering the clinical spectrum of lyme.

M.E. Schriefer, Centers for Disease Control and Prevention, Ft. Collins, Colorado: Current state of lyme disease laboratory tests and immediate future hopes.

B. Budowle, University of North Texas Health Science, Fort Worth: Things to keep in mind throughout the conference: What if we did have a promising technique, can it be made into a good test and what would be the elements of a good and bad test?

SESSION 2: Animal Models
Chairperson: S. Schutzer, UMDNJ–New Jersey Medical School, Newark

S.W. Barthold, University of California, Davis: Role of animal models in the future.

SESSION 3: Genomic Strategies for Detection and Diagnosis of the Microbe
Chairperson: B. Budowle, University of North Texas Health Science, Fort Worth

D. Ecker, Ibis Biosciences, Inc., Carlsbad, California: Rapid detection of the microbe when culturing is challenging.
P. Chain, Los Alamos National Laboratory, New Mexico: What can we deliver on a large scale?
S. Casjens, University of Utah School of Medicine, Salt Lake City: What has it delivered for Lyme disease, Is it a game changer?
M. Eshoo, Ibis Biosciences, Inc., Carlsbad, California: Technological methods: Whole-genome amplification in host and vector background. Microbes are unknown.

SESSION 4: Genomics and Proteomics
Chairperson: A.C. Steere, Massachusetts General Hospital, Boston

R.W. McCombie, Cold Spring Harbor Laboratory: What are genomics and sequencing able to deliver in general?
S. Salzberg, University of Maryland, College Park: Bioinformatics of complex genetic data.
T.E. Angel, Pacific Northwest National Laboratory, Richland, Washington: What are integrated strategies to be incorporated into mass spectrometry and protein fractionation? How to maximize the strengths and overcome the challenges.
General Discussion: S. Schutzer, UMDNJ–New Jersey Medical School, Newark, and
T.E. Angel, Pacific Northwest National Laboratory, Richland, Washington
B. Luft, SUNY Stony Brook, New York: Protein arrays I.
P. Felgner, University of California, Irvine: Protein arrays II.
M. Eshoo, Ibis Biosciences, Inc., Carlsbad, California: Can we identify multiple species and genotypes in the ticks and humans?

SESSION 5: Issues for Assay Use and Interpretation on Broad Scale
Chairperson: B. Budowle, University of North Texas Health Science, Fort Worth

M. Lewinski, University of California, Los Angeles: Use in a large clinical laboratory, gold standards, technological and regulatory hurdles.
J. Aucott, Johns Hopkins at Greenspring Station, Lutherville, Maryland: Role of the immune system as a barometer.

SESSION 6: Strategies for Analysis of Genetic Data and Specimen Banks
Chairperson: S. Schutzer, UMDNJ–New Jersey Medical School, Newark

S. Schutzer, UMDNJ–New Jersey Medical School, Newark: Can compartmental genomics and proteomics be used to diagnose a disease and distinguish it from others?
R. Chakraborty, University of North Texas Health Science, Fort Worth: Real-life examples: Getting the right specimens for repository and errors if you fail to do so.
J. S. Fowler, Brookhaven National Laboratory, Upton, New York: PT scan and other methodologies to detect neurological disease.

SESSION 7: Tracking Infection in Animals and Man
Chairperson: S. Schutzer, UMDNJ–New Jersey Medical School, Newark

M. Rusckowski, University of Massachusetts Medical School, Worcester: Can we track the infection as it moves throughout the body?
P. Fox, Animal Medical Center, New York: The dog as a sentinel.
S. Hojvat, Center for Devices and Radiological Health, Rockville, Maryland: Path to FDA clearance.

SESSION 8: Biorepositories and How to Maintain Them and Ensure Their Integrity
Chairperson: A. Hassett, University of Michigan Health System, Ann Arbor

S. Miller, National Museum of Natural History, Washington, DC: Past repositories at Smithsonian and future ones for biodefense. Distinctions and defining the purpose.
B. Budowle, University of North Texas Health Science, Fort Worth: Experience with human genetic and microbial repositories.
Closing Remarks and Discussion: S. Schutzer, UMDNJ–New Jersey Medical School, Newark, and B. Budowle, University of North Texas Health Science, Fort Worth

Communicating Science

April 29–May 5

FUNDED BY **Boehringer Ingelheim Fonds Foundation for Basic Research in Medicine**

ARRANGED BY **A. Hoffmann,** Boehringer Ingelheim Fonds, Heidesheim, Germany
C. Walther, Boehringer Ingelheim Fonds, Heidesheim, Germany

The Boehringer Ingelheim Fonds has an international program of support for Ph.D. fellowships. It first brought its fellows to the Banbury Center for their annual North American retreat in 2005. It has been a great pleasure to have them return and their 2011 stay at Banbury was the fourth occasion they have been here. At Banbury, they receive intensive instruction in matters such as giving presentations and writing papers, topics usually learned by default (and often poorly) during graduate research.

Opening Remarks: **C. Walther,** Boehringer Ingelheim Fonds, Heidesheim, Germany

SPEAKERS
Chairperson: R. Berwick, Massachusetts Institute of Technology, Cambridge

W. Wells, Global Alliance for TB Drug Development, New York: Writing techniques and how to structure papers. First writing assignment.
B. Tansey, Vanderbilt University Medical Center, Nashville, Tennessee: Presentation of graphic information and how to prepare and deliver a scientific talk.
J. Hudspeth, Rockefeller University, New York: What makes success in science?

SPECIAL LECTURES

M. Huse, Memorial Sloan-Kettering Cancer Research Institute, New York: Using photoactivation to study cytoskeletal dynamics in lymphocyte activation and inhibition.
S. Webb, National Association of Science Writers, New York: Science in the media.
K. Ris-Vicari, Katie Ris-Vicari Graphic Design, New York, and M. Hansen, Nature Publishing Group, New York: How to design figures.
C. Walther, Boehringer Ingelheim Fonds, Heidesheim, Germany: All about BIF.

Antibiotic Resistance: Past, Present, Future

May 15–18

FUNDED BY **Oliver Grace Fund**

ARRANGED BY **J. Davies,** University of British Columbia, Vancouver, Canada
S. Levy, Tufts University School of Medicine, Boston, Massachusetts
J.H. Miller, University of California, Los Angeles
J.D. Watson, Cold Spring Harbor Laboratory, New York

S. Levy, J. Miller, J. Davis

Antibiotics (together with vaccines) are biomedical research's greatest contribution to human health. But the introduction of antibiotics in the early 1940s was accompanied by the development of antibiotic resistance. Initially, resistance occurred by mutation (usually during the course of therapy), but in the 1950s, transmissible resistance was identified. In more recent times, this threat has been magnified because of the emergence of multidrug-resistant clinical strains coupled with the paucity of efforts to find and develop new antibiotics. There is even talk of a return to the pre-antibiotic era. The pharmaceutical industry has tried to keep up with bacterial evolution, but in vain. The need for novel antibiotics and methods of suppressing resistance has never been greater, and the Banbury conference addressed these needs. Participants examined the history of the emergence of antibiotic resistance and of the strategies that have been pursued to combat it. This historical background provided a context for discussion of current practical approaches to restoring effective antimicrobial therapy and what paths may prove promising in the future.

Welcoming Remarks: **J.A. Witkowski,** Banbury Center, Cold Spring Harbor Laboratory, New York
Introductory Remarks: **J.H. Miller,** University of California, Los Angeles

SESSION 1: Defining the Parameters
Chairperson: J. Davies, University of British Columbia, Vancouver, Canada

J. Davies, University of British Columbia, Vancouver, Canada: A brief history of coevolution of antibiotics and their resistance.
J.H. Miller, University of California, Los Angeles: Antibiotic sensitivities as codrug targets; some consequences of low amounts of antibiotics.
B. Kreiswirth, UMDNJ, Newark, New Jersey: The challenges of XDR-TB.
W. Witte, Robert Koch Institute, Wernigerode, Germany: Spread of livestock-associated MRSA and the risk posed to humans.
G.A. Jacoby, Lahey Clinic, Burlington, Massachusetts: Plasmid-mediated quinolone resistance.

SESSION 2: Ecological Considerations
Chairperson: G. Wright, McMaster University, Hamilton, Canada

G. Wright, McMaster University, Hamilton, Canada: Origins and ecology of resistance: Inhibition of resistance mechanisms.
G. Dantas, Washington University in St. Louis School of Medicine, St. Louis, Missouri: Antibiotic resistome of the commensal microbiota.
R. Kishony, Harvard Medical School, Boston, Massachusetts: The ecology of antibiotic resistance.
A. Tomasz, The Rockefeller University, New York: From resistance gene to the resistant phenotype.
P. Courvalin, Institut Pasteur, Paris, France: Successful resistance determinants are selectively neutral.
C. Thomas, University of Birmingham, United Kingdom: Role of the second eukaryotic-like, isoleucyl tRNA synthetases in a variety of bacteria as a source of resistance to mupirocin and related antibiotics.

SESSION 3: Decline and Fall of β-Lactams
Chairperson: K. Bush, Indiana University, Bloomington

K. Bush, Indiana University, Bloomington, Indiana: β-Lactamase evolution: Current issues of carbapenemases.
S. Mobashery, University of Notre Dame, Notre Dame, Indiana: Molecular mechanism of resistance to β-lactam antibiotics in methicillin-resistance in *Staphylococcus aureus*.
P. Tulkens, Université Catholique De Louvain, Bruxelles, Belgium: Efflux transporters: Impact of patient treatment and role in decreased susceptibility of sparely used or non-used antibiotics.
O. Lomovskaya, Mpex Pharmaceuticals, San Diego, California: Use of efflux inhibitors as a strategy to overcome and reduce resistance.
H. Zgurskaya, University of Oklahoma, Norman: The assembly and mechanism of multidrug efflux pumps in Gram-negative bacteria.

SESSION 4: Biology and Discovery
Chairperson: K. Lewis, Northeastern University, Boston, Massachusetts

K. Lewis, Northeastern University, Boston, Massachusetts: Tolerance, resistance, and opportunities for antibiotic discovery.
B. Eisenstein, Cubist Pharmaceuticals, Lexington, Massachusetts: The antibiotic pipeline: Where it is, what needs fixing.
L. Piddock, University of Birmingham, United Kingdom: Barriers to overcome to get from drug discovery to new antibiotics in patients.
T.R. Walsh, Cardiff University, Cardiff, United Kingdom: The similarities between global antibiotic resistance and global warming: When two worlds collide.
M. Mulvey, National Microbiology Laboratory, Manitoba, Canada: Antimicrobial resistance in Canada.
S. Projan, Medimmune, Gaithersburg, Maryland: Immunoprophylaxis for the prevention of bacterial infections, better than a cure.

SESSION 5: What Is Next?
Chairperson: S. Levy, Tufts University, Boston, Massachusetts

P. Huovinen, University of Turku, Finland: Targeted use of antibiotics: Rapid diagnostics and human microbiota.
S. Levy, Tufts University, Boston, Massachusetts: Circumventing antibiotic resistance: Prevention, not treatment.
E. Kutter, Evergreen State College, Olympia, Washington: Bacteriophages as natural, self-replicating and self-limiting antimicrobials.
S. Lerner, Wayne State University, Detroit, Michigan: Educating the community about the problem of antibiotic resistance.

NSF Workshop: The Future of Plant Genome Sequencing and Analysis

May 18–20

FUNDED BY **National Science Foundation**

ARRANGED BY **W.R. McCombie,** Cold Spring Harbor Laboratory, New York
M.C. Schatz, Cold Spring Harbor Laboratory, New York
J.A. Witkowski, Banbury Center, Cold Spring Harbor Laboratory, New York

In just the past few years, sequencing instrument capabilities have increased more than 1000-fold and are likely to continue to increase about fivefold each year for the next several years. However, analysis methods have not improved nearly as much during the same time period and a variety of technical limitations of these new instruments make it even more difficult to carry out whole-genome sequencing of novel genomes (de novo sequencing). The goals of this meeting were to assess the current state of de novo sequencing, predict what can be expected to develop in the near future, and determine how these exciting technologies could be used to carry out de novo sequencing of entire complex plant genomes.

W.R. McCombie

Welcoming Remarks: **J.A. Witkowski,** Banbury Center, Cold Spring Harbor Laboratory, New York

Challenges and Opportunities in Plant Genomics: Goals of the Meeting: W.R. McCombie, Cold Spring Harbor Laboratory, New York

SESSION 1: Defining the Challenges
Chairperson: W.R. McCombie, Cold Spring Harbor Laboratory

K. Devos, University of Georgia, Athens: The challenges of complex genomes.
D. Neale, University of California, Davis: The nature of the size and complexity of the conifer genome.
R. Ming, University of Illinois, Urbana: Assembly of papaya sex chromosomes.
J. Mudge, National Center for Genome Resources, Santa Fe, New Mexico: Integration of alternative data types.
D. Main, Washington State University, Pullman: Plant community databases: The stewards of knowledge.
J. Romero-Severson, University of Notre Dame, Indiana: Nonmodel, highly heterozygous, outcrossing disomic polyploids with large genomes.

General Discussion and Listing of Key Points

SESSION 2: Technologies
Chairperson: T. Michael, Monsanto Company, Chesterfield, Missouri

D. Schwartz, University of Wisconsin, Madison: Optical mapping and nanocoding systems for genome assembly and analysis.
H. Cao, BioNanomatrix, Inc., Philadelphia, Pennsylvania: High-throughput single-molecule-level imaging of the linear genome for assembly with nanochannel rays.
S. Turner, Pacific Biosciences, Inc., Menlo Park, California: Application of SMRT sequencing to assembly problems.

Discussion and Listing of Key Points

SESSION 3: Assembly
Chairperson: M.C. Schatz, Cold Spring Harbor Laboratory

T. Michael, Monsanto Company, Chesterfield, Missouri: Building tools, pipelines, and processes to utilize long, single-molecule PacBio reads to assemble plant genomes.
A. Zimin, University of Maryland, College Park, Maryland: Efficient assembly of large genomes from short reads.
M. Schatz, Cold Spring Harbor Laboratory: Computational challenges of plant genome assembly.
I. Birol, British Columbia Cancer Research Centre, Vancouver, Canada: Haploid assembly of diploid genomes.
M. Caccamo, Genome Analysis Centre, Norwich, United Kingdom: Assembly of large genomes with cortex.
S. DesChamps, Dupont Experimental Station, Wilmington, Delaware: Local and global de novo assemblies in complex crop genomes.
S. Gnerre, Broad Institute, Cambridge, Massachusetts: Assembling large and small genomes with ALLPATHS-LG.
P. Kersey, European Bioinformatics Institute, Cambridge, United Kingdom: Squeezing through the bottlenecks: Strategies for assembling large genomes.
K. Mockaitis, Indiana University, Bloomington: Using transcriptome data to facilitate genome assembly.
T. Tatusova, National Center for Biotechnology, Bethesda, Maryland: NCBI efforts to support assembly submissions.

General Discussion and Listing of Key Points

Summary Discussion and Future Developments

K. Mockaitis

D. Schwartz

Future of Biomarker Discovery and Biobanks in Cancer Diagnosis, Prognosis, and Therapy

June 23–24

FUNDED BY **SWOG**

ARRANGED BY **L. Baker,** University of Michigan, Ann Arbor
S. Lowe, Cold Spring Harbor Laboratory, New York

The availability of suitable biomarkers to identify appropriate patient populations and tissue-specific drug activation indices is crucial for maximizing the efficacy of many existing and developing therapies and for trial design for drug development. In turn, the successful identification and validation of new biomarkers requires the availability of biospecimens for clinical research. Patient specimens obtained from clinical trials sponsored by NCI-designated cooperative groups such as SWOG provide an incredibly rich source of tissue for the advancement of cancer research, biomarker discovery, and patient care. This meeting examined the optimization of biospecimen repositories as well as the cutting-edge approaches and technologies that may be brought to bear on biomarker discovery.

R. Sordella, S. Powers, S. Lowe

Welcoming Remarks: **J.A. Witkowski,** Banbury Center, Cold Spring Harbor Laboratory, New York

Meeting Expectations and Goals: S. Lowe, Cold Spring Harbor Laboratory, New York
Cooperative Overview and Challenges: L. Baker, University of Michigan, Ann Arbor

SESSION 1: Improving Therapy through Analysis of Clinical Specimens
Chairpersons: H. Varmus, National Cancer Institute, Bethesda, Maryland, and **R. Fisher**, University of Rochester, New York

A. Types of Scientific Questions That Can Be Addressed with Biobank Tissues

T. Tlsty, University of California, San Francisco: Stratifying DCIS biopsies for risk of future tumor formation.
R. Levine, Memorial Sloan-Kettering Cancer Center, New York: Use of clinical trial leukemia samples to gain novel insights into AML pathogenesis.
P. Kantoff, Dana Farber Cancer Institute, Boston, Massachusetts: Genetic variants in antioxidant pathways and risk of prostate cancer.
R. Sordella, Cold Spring Harbor Laboratory: Intrinsic and extrinsic mechanisms of erlotinib resistance.

B. On the Horizon: New Technologies and Approaches

J. Hicks, Cold Spring Harbor Laboratory: Biomarkers from sequencing, copy number, and single cells.
S. Powers, Cold Spring Harbor Laboratory: Using genomics to develop biomarkers for hepatocellular carcinoma.
A. Van Oudenaarden, Massachusetts Institute of Technology, Cambridge: Single-cell transcript counting in tissue.
L. Wickerham, NSABP Foundation, Pittsburgh, Pennsylvania: Case study.

SESSION 2: How Are We Doing?
Chairperson: T. Tlsty, University of California, San Francisco

A. Lessons from the Cooperatives and Overview of Repositories

S. Hamilton, University of Texas MD Anderson Cancer Center, Houston, Texas: The ECOG experience and next-gen clinical trials.
P. Febbo, University of California, San Francisco: Lessons from the cooperative groups and overview of repositories: Cancer and leukemia group B.
W. Franklin, University of Colorado School of Medicine, Aurora: Best practices in cooperative group biobanks: What we have and what we need.

B. Overview of Committees and Selection Process: Who Gets Tissues and How

C. Hoban, SWOG, Ann Arbor, Michigan: Life cycle of biospecimen use in SWOG: Promoting access and overview of distribution process.

C. Ways Cooperative Groups and BioBank Tissue Inform Scientific and Medical Advance

R. Comis, Eastern Cooperative Oncology Group, Philadelphia, Pennsylvania: Role of the cooperative groups in the translational cancer research continuum.
R. Fisher, University of Rochester, New York: LLMPP: A consortium designed to develop a new molecular understanding of lymphoma resulting in targeted therapeutic initiatives.

SESSION 3: Biomarker Discovery Beyond the Cooperative Groups: What Can We Learn?
Chairpersons: P. Febbo, University of California, San Francisco, and **S. Hamilton,** University of Texas MD Anderson Cancer Center, Houston

N. Rosen, Memorial Sloan-Kettering Cancer Center, New York: Dynamic markers of tumor adaptation to therapy.
J. Derry, Sage Bionetworks, Seattle, Washington: The need for sharing data and models.

SESSION 4: Banking Strategies That Facilitate Biomarker Discovery
Chairpersons: N. Rosen, Memorial Sloan-Kettering Cancer Center, New York, and **P. Kantoff,** Dana Farber Cancer Institute, Boston, Massachusetts

K. Shaw, National Cancer Institute, Bethesda, Maryland: Banking.
W. McCaskill-Stevens, National Cancer Institute, Bethesda, Maryland: Banking of biospecimens from clinical trials: Lessons, challenges, and future opportunities.
N. Ramirez, Nationwide Children's Hospital, Columbus, Ohio: COG and GOG biospecimen resources: More than "tissue bank."
J.-G. Foster, Nationwide Children's Hospital, Columbus, Ohio: Hand in hand: Centralized reference laboratory testing and optimization of cooperative group banking.
S. Paik, NSABP Foundation, Pittsburgh, Pennsylvania: Why great science often fails to become good clinical tests: Development of predictive test for adjuvant Trastuzumab using archived tumor blocks from NSABP trial B-31.

General Discussion: Banking Strategies That Facilitate Biomarker Discovery
Moderator: L. Baker, University of Michigan, Ann Arbor

SESSION 5: Meeting Wrapup: Framing the Future
Chairperson: Scott Lowe, Cold Spring Harbor Laboratory

Discussion

Translation of Cellular and Molecular Mechanisms of Aging to Geriatric Disorders

September 11–13

FUNDED BY **The Therapeutic Strategic Unit of Aging–Sanofi US**

ARRANGED BY **B. Baron,** Sanofi-Aventis, Bridgewater, New Jersey
C. Marta, Sanofi-Aventis, Bridgewater, New Jersey
E. Tamer, Sanofi-Aventis, Bridgewater, New Jersey

The Center and the Laboratory are indebted to members of the CSHL Corporate Sponsor Program, and we are pleased when members of the Program make use of the benefits of the Program. One of these is to hold meetings at Banbury on a topic of their own choosing, and we were happy to welcome members of the Sanofi Therapeutic Strategic Unit of Aging. The meeting brought together key experts with Sanofi scientists to critically evaluate two areas with major implications for aging: (1) the contribution of mitochondrial dysfunction and oxidative stress to aging and its associated disorders and (2) the impact of aging on the immune system and immunosenescence. The focus was on connecting clinical observations to underlying mechanisms and using this knowledge to compare the relevance of potential interventions and to predict the most appropriate patient populations and outcome parameters.

Welcoming Remarks: **J.A. Witkowski,** Banbury Center, Cold Spring Harbor Laboratory, New York
Keynote Address: **Translating Novel Scientific Findings in Aging into Therapies for Geriatric Practice**
R. Hodes, National Institute on Aging, Bethesda, Maryland

OPENING SESSION: From biology of aging to treatment of aging disorders
Chairperson: R. Belder, Sanofi-Aventis, Bridgewater, New Jersey

Introduction of TSU-Aging Strategy and Therapeutic Goals

Opening Remarks: R. Belder, Sanofi-Aventis, Bridgewater, New Jersey

SESSION 1: Mitochondrial Dysfunction, Oxidative Stress, and Translational Interventions
Chairperson: S. Kahn, Gencia Biotechnology, Charlottesville, Virginia

G. Gibson, Weill Medical College, White Plains, New York: The brain's use of glucose and calcium is abnormal in Alzheimer's disease. Why? Does it matter? Can we do anything about it?
R. De Cabo, Biomedical Research Center, NIH, Baltimore, Maryland: Dietary manipulations for healthy aging.
V. Bohr, National Institutes of Health, Baltimore, Maryland: Nuclear and mitochondrial DNA repair defects in aging.
S. Melov, Buck Institute for Research on Aging, Novato, California: A murine mitochondrial model for age-related cardiovascular disease.

Special Lecture
P. Shiels, University of Glasgow, Glasgow, United Kingdom: Cellular and molecular basis of the diseases of aging.

SESSION 1 (*continued*): Mitochondrial Dysfunction, Oxidative Stress, and Translational Interventions
Chairperson: M. Flint Beal, Cornell University, New York

J.M. Cook-Mills, Northwestern University, Chicago, Illinois: Vitamin E isoforms differentially regulate inflammation.
G.S. Shadel, Yale University School of Medicine, New Haven, Connecticut: Regulation of life span by adaptive mitochondrial ROS signaling.
D. Wallace, University of Pennsylvania, Philadelphia: The mitochondrial bioenergetic origin of complex diseases.

SESSION 2: Immunosenescence: Alterations in the Functional and Regenerative Capacity of the Immune System during Immunosenescence. Lessons Learned from Translational Studies
Chairperson: D. Unutmaz, New York University School of Medicine

G. Pawelec, University of Tübingen Clinical School, Germany: Models and mechanisms of human immunosenescence.
B. Grubeck-Loebenstein, Austrian Academy of Sciences, Innsbruck, Austria: Age-related changes in the CD8 T-cell pool and their consequences.

SESSION 2 (*continued*): Immunosenescence: Alterations in the Functional and Regenerative Capacity of the Immune System during Immunosenescence. Lessons Learned from Translational Studies
Chairperson: G. Pawelec, University of Tübingen Clinical School, Germany

D. Unutmaz, New York University: Does chronic inflammation accelerate immunosenescence?
L. Haynes, Trudeau Institute, Saranac Lake, New York: How aging impacts CD4 T cells.
J. Goronzy, Stanford University School of Medicine, California: Receptor threshold calibration in T cells: Implications for T-cell homeostasis and responses with age.
H. Geiger, Cincinnati Children's Hospital Medical Center, Ohio: DC42 activity regulates hematopoietic stem-cell aging and rejuvenation.


D. Wallace


M. Beal

Scientific and Technological Barriers to Global Real-Time Risk Assessment of Vector-Borne Infections

September 18–21

FUNDED BY **Defense Threat Reduction Agency, Department of Defense**

ARRANGED BY **D. Barnard,** Agricultural Research Service, USDA, Gainesville, Florida
R. Breeze, Global Security Directorate, Lawrence Livermore National Laboratory, Livermore, California
D. Fish, Yale University, New Haven, Connecticut
A. Rudolph, Chemical and Biological Defense Directorate, Defense Threat Reduction Agency, Fort Belvoir, Virginia

In 1991, the Banbury Center held its first meeting on Lyme disease, then a newly emerging disease. From that first meeting has developed a series of meetings on newly emerging diseases and the threat that they pose to world health. New pathogens emerge regularly in many regions of the world, and they are often zoonotic, making the jump from a wild or domestic animal reservoir or an arthropod vector to humans. This meeting supported by the U.S. Department of Defense—which has long focused on protecting the health of its forces deployed overseas from numerous infectious diseases not indigenous to the United States—examined what is being done and what could be done to detect such diseases. Questions discussed included What data are available from existing and evolving vector-borne disease surveillance and risk assessment activities and how might these data be enhanced? How might data be generated in low-resource countries, mega cities, and remote regions without long-term and costly investments in human and physical capital? What do we need to know about the ecology of the microbes, vectors, and hosts, including microbial variants that provide early indications of disease activity?

J. Richardson, W. Lipkin, D. Fish

Welcoming Remarks: **J.A. Witkowski,** Banbury Center, Cold Spring Harbor Laboratory, New York
Introductory Remarks: **A. Rudolph,** Chemical and Biological Defense Directorate, Fort Belvoir, Virginia

SESSION 1: A World of Vector-Borne Threats
Chairperson: R. Breeze, Global Security Directorate, Lawrence Livermore National Laboratory, California

C. Phillips, Texas Tech University, Lubbock: Global disease surveillance, emergent disease preparedness and national security.
W. Reisen, University of California, Davis: Arbovirus surveillance in California.
D. Fish, Yale University, New Haven, Connecticut: Disease emergence: Lessons from ticks.
G. Glass, Johns Hopkins University, Baltimore, Maryland: Observations on some challenges of finding what you are looking for.
P. Daszak and W. Karesh, EcoHealth Alliance, New York: Predicting the origins and spread of vector-borne diseases.
M. Kilpatrick, University of California, Santa Cruz: A mathematical framework and research plan for predicting which vector-borne pathogens could cause epidemics in North America.
D. Impoinvil, University of Liverpool, United Kingdom: QWeCI and LUCINDA.
D. Knowles, USDA Agricultural Research Service, Pullman, Washington: Determinants contributing to the reemergence of a foreign animal tick-borne infection in the U.S.
T. Myers, Armed Forces Health Sciences Center, Silver Spring, Maryland: The Global Emerging Infections Surveillance and Response System (GEISS).
R. Jarman, Walter Reed Army Institute of Research, Silver Springs, Maryland: Pathogen and disease surveillance: Lessons from dengue cohort studies in Northern Thailand.
K. Gage, Centers for Disease Control and Prevention, Fort Collins, Colorado: Selection of sites to evaluate newly developed techniques for assessing global risks of vector-borne infections.

Somalia Scenario and Conference Discussion (Part 1)

SESSION 2: Technologies and Technology Gaps
Chairperson: E. Van Gieson, Chemical and Biological Defense Directorate, Fort Belvoir, Virginia

D. Barnard, USDA Agricultural Research Service, Gainesville, Florida: Detection systems for dipteran vectors.

Discussion led by **W. Reisen,** University of California, Davis
R. Baker, Texas Tech University, Lubbock: The significance of knowing mammalian reservoir species.
T. Briese, Columbia University, New York: Strategies for comprehensive pathogen surveillance and discovery.
I. Lipkin, Columbia University, New York: Microbe hunting.
P. Naraghi-Arani, Lawrence Livermore National Laboratory, California: Novel detection technologies applicable to vector-borne disease surveillance.
M. Eshoo, IBIS Biosciences, Carlsbad, California: The use of PCR/ESI-MS to detect known and novel vector-borne pathogens.

SESSION 3: The Virtual World
Chairperson: B. Knols, Soper Strategies, Amsterdam, The Netherlands

J. Brownstein, Harvard University, Cambridge, Massachusetts: HealthMap: Harvesting informal sources for public health surveillance.
L. Eisen, Colorado State University, Fort Collins: Data management system/decision support system for surveillance and control of vectors and vector-borne diseases.
J. Richardson, Walter Reed Army Institute of Research, Silver Spring, Maryland: Vector map.
B. Knols, Soper Strategies, Amsterdam, The Netherlands: Malariaworld.

Somalia Scenario and Conference Discussion (Part 2)

SESSION 4: Dynamic Spatial Risk Maps
Chairperson: D. Fish, Yale University, New Haven, Connecticut

A. Tatem, University of Florida, Gainesville: Mapping and modeling population and vector-borne infection movements in resource-poor settings.
C. Lord, University of Florida, Gainesville: Scale in models of vector-borne diseases.
B. Blumenthal, Columbia University, New York: Real-time provision of climate analysis for vectoral environment evaluation.
M. Thomson, Columbia University, New York: Climate information for the prediction and prevention of vector-borne diseases.
N. Nurthen, Chemical and Biological Defense Directorate, Fort Belvoir, Virginia: Data sharing/access issues for global real-time risk assessment of vector-borne infections.

Somalia Scenario and Conference Discussion (part 3)

Strategic Research Initiative for CFS

September 25–27

FUNDED BY **CFIDS Association of America**

ARRANGED BY **K.K. McCleary,** CFIDS Association of America, Charlotte, North Carolina
S. Vernon, CFIDS Association of America, Charlotte, North Carolina

S. Vernon

Banbury Center has held several meetings on chronic fatigue syndrome and related disorders and the Center was pleased to be the site for the inaugural meeting of the Scientific Advisory Board of the CFIDS Association of America. During the past few years, CFS research has received high-profile media attention, generating both increased interest and unprecedented opportunities for progress. The Association was looking to its new SAB for guidance on research strategy, so as to encourage innovative research focused on early detection, objective diagnosis, and effective treatment. Banbury takes great pride in the role the Center has had in helping foster research on CFS.

Welcoming Remarks: **J.A. Witkowski,** Banbury Center, Cold Spring Harbor Laboratory, New York
Introductory Remarks: **S. Vernon,** CFIDS Association of America, Charlotte, North Carolina
K.K. McCleary, CFIDS Association of America, Charlotte, North Carolina: 25 Years of Service: Where the CFIDS Association Stands Today

L. Bateman

SESSION 1: Background on the Association and CFS
Chairpersons: R. Silverman, Learner Research Institute, Cleveland, Ohio, and **R. Dodd,** American Red Cross, Holland Laboratory, Rockville, Maryland

A. Lesser, CFIDS Association of America, San Francisco, California: From advocacy to research.
A. Divine, Boulder, Colorado, J. Spotila, King of Prussia, Pennsylvania, and P. Venetucci, Park Ridge, Illinois: Illness narratives.

S. Vernon, CFIDS Association of America, Charlotte, North Carolina: What's in a name?
L. Bateman, The Fatigue Consultation Clinic, Salt Lake City, Utah: A clinical perspective of CFS.
N. Klimas, University of Miami School of Medicine, Florida: Plausible causes/triggers of CFS (as we know it today).
G. Broderick, University of Alberta, Edmonton, Canada: A system biology perspective of CFS.
V. Racaniello, Columbia University Medical Center, New York: Lessons learned from XMRV.

SESSION 2: Transforming CFS Research
Chairpersons: K. Moran, Integrated Strategy, LLC, Greenwood Village, Colorado, and **P. DeStefano,** McDermott Will & Emery, Menlo Park, California

S. Vernon, CFIDS Association of America, Charlotte, North Carolina, and K.K. McCleary, CFIDS Association of America, Charlotte, North Carolina: Strategic and promising areas of research.
E. Aslakson, Centers for Disease Control and Prevention, Atlanta, Georgia: Biomarker hit lists and hypothesis generation.
I. Biaggioni, Vanderbilt University School of Medicine, Nashville, Tennessee: Common platforms for progress.
D. Papanicolaou, Merck Research Laboratories, Kenilworth, New Jersey: Piquing the interest of the pharmaceutical industry.
R. Bromley, Redwood City, California: Not-for-profit research organization successes and failures.
B. Raidt, River Forest, Illinois, and P. Venetucci, CFIDS Association of America, Park Ridge, Illinois: Weaving CFS into the social and medical fabric.

SESSION 3: Transforming Research with the Help of the SAB
Chairperson: K. Frick, CFIDS Association of America, San Francisco, California

R. Bromley, Redwood City, California: Strategic issues: What is next? Strategic governance for research support organizations.

B. Allshouse, L. Bateman

K. Moran

FEBS Journal Editorial Board Meeting

September 30–October 2

FUNDED BY ***FEBS Journal*, John Wiley & Sons, Ltd., New York**

ARRANGED BY **N. Tonks,** Cold Spring Harbor Laboratory, New York
V. Wilkinson, *FEBS Journal*, Cambridge, United Kingdom

The Banbury Center takes a broad perspective on its mission to promote biomedical research. We have, for example, held meetings to discuss scientific fraud, funding for research, and open access journals. This meeting provided an opportunity for the editorial board of the *FEBS Journal* to meet with the journal's staff and discuss the performance and future direction of the journal.

Editorial Office Statistics and update

V. Johnson and D. Nicholson, Wiley-Blackwell, Oxford, United Kingdom: Wiley-Blackwell presentation and structured brainstorming session

Editorial Board meeting

R. Apweiler, European Bioinformatics Institute, Cambridge, United Kingdom
M. Hall, University of Basel, Switzerland
J. Hardy, University College, London, United Kingdom
D. Michele, University of Michigan, Ann Arbor
P. Munoz-Canoves, University Pompeu Fabra, Barcelona, Spain
R. Perham, University of Cambridge, United Kingdom
N. Scrutton, The University of Manchester, United Kingdom
N. Tonks, Cold Spring Harbor Laboratory, New York
A. Wlodawer, National Cancer Institute, Bethesda, Maryland

Dosage, Epigenetics, and the Biology of Hybridization and Hybrids

October 10–13

FUNDED BY **Cold Spring Harbor/Pioneer DuPont Joint Collaborative Project**

ARRANGED BY **Z. Lippman,** Cold Spring Harbor Laboratory, New York
R. Martienssen, Cold Spring Harbor Laboratory, New York
R. Williams, DuPont Experimental Station, Wilmington, Delaware

Each year, members of the Cold Spring Harbor–Pioneer DuPont Joint Collaborative group meet to review the progress of the collaboration. In addition, a small number of researchers not part of the collaboration come to the meeting for discussion of an important topic related to the work of the collaboration. This year, the topic dealt with the molecular biology of hybridization, exploring the roles of gene expression in phenotypic variation, with a particular emphasis on changes not easily explained by simple nucleotide changes, for example, chromosome structure, genome organization, epigenetics, and regulatory RNA. These mechanisms are likely to have effects on plant development, response to stress, heterosis, and evolution.

Welcoming Remarks: **J.A. Witkowski,** Banbury Center, Cold Spring Harbor Laboratory, New York
Introductory Remarks: **Z. Lippman,** Cold Spring Harbor Laboratory, New York

SESSION 1: Genomics and Epigenomics
Chairperson: A. Rafalski, DuPont Experimental Station, Wilmington, Delaware

J.-M. Chia, Cold Spring Harbor Laboratory: HapMap II.
J. Lu and M. Regulski, Cold Spring Harbor Laboratory: Progress on epigenetic variation profiling.
V. Llaca, DuPont Experimental Station, Wilmington, Delaware: The maize methylome pipeline.
M. Dotto, Cold Spring Harbor Laboratory: Small RNAs in lbl1 mutants: Genome-wide search for ta-siRNA loci in maize.
F. Van Ex, Cold Spring Harbor Laboratory: Alternate regulation of RNAi components as an epigenetic basis for apomixis.
A. Eveland, Cold Spring Harbor Laboratory: Systems approaches in maize inflorescence architecture.

SESSION 2: Mechanisms of Reproductive Development
Chairperson: D. Jackson, Cold Spring Harbor Laboratory

C. MacAlister, Cold Spring Harbor Laboratory: Control of meristem formation and homeostasis at the transition to flowering in tomato: Role of terminating flower and fasciated flower.

J. Habben, Pioneer Hi-Bred International, Inc., Johnston, Iowa: Testing of maize transgenics for drought tolerance.

B. Il Je, Cold Spring Harbor Laboratory: New players in maize fasciated pathways and seed row number.

D. Jackson, Cold Spring Harbor Laboratory: A new pathway for meristem maintenance in maize: Uniting fasciated and abphyl phenotypes.

B. Li, DuPont Experimental Station, Wilmington, Delaware: Cloning of maize mutant genes involved in reproductive development.

S. Lawit, Pioneer Hi-Bred International, Johnston, Iowa: Paths toward self-reproducing hybrids.

SESSION 3: Dosage, Development and Hybridization
Chairperson: Z. Lippman, Cold Spring Harbor Laboratory

Z. Lippman, Cold Spring Harbor Laboratory: Dynamics of meristem maturation and the evolution of inflorescence architecture.

O. Danilevskaya, Pioneer Hi-Bred International, Johnston, Iowa: Functional analysis of the PEBP gene family from maize.

O. Loudet, INRA, Versailles, France: Natural variation for growth and allelic incompatibilities in *Arabidopsis thaliana*.

M. Tanurdzic, Cold Spring Harbor Laboratory: RNAi and inheritance of epigenetic states in plant interspecific hybrids.

L. Comai, University of California, Davis: Dosage-dependent interspecific incompatibility in *Arabidopsis*.

M. Freeling, University of California, Berkeley: Ancient epigenetic origins of genome dominance following paleopolyploidies, and gene regulatory consequences.

SESSION 4: Epigenetics
Chairperson: R. Martienssen, Cold Spring Harbor Laboratory

R. Mosher, University of Arizona, Tucson: Pol IV-dependent siRNAs in *Arabidopis* seeds.

J. Reinders, DuPont Experimental Station, Wilmington, Delaware: Dynamic retroelement transmission rates during sexual reproduction of *Arabidopsis*.

M. Hudson, University of Illinois, Urbana: The genetics and effects of small RNA expression in *Arabidopsis* and maize hybrids.

R. Martienssen, Cold Spring Harbor Laboratory: Heterochromatin, small RNA, and the epigenetic control of gametogenesis.

M. Timmermans, Cold Spring Harbor Laboratory: Generation of robust development patterns by opposing gradients of mobile small RNAs.

J. Birchler, University of Missouri, Columbia: Studies at the intersection of ploidy and heterosis.

SESSION 5: Tackling Genomics and Phenomics
Chairperson: R. Williams, DuPont Experimental Station, Wilmington, Delaware

M. Schatz, Cold Spring Harbor Laboratory: Challenges and solutions for plant genome assembly.

K. Creasey, Cold Spring Harbor Laboratory: Epigenetically activated small RNA mediates transgenerational phenotypes in *Arabidopsis*.

M. Frank, Pioneer Hi-Bred International, Johnston, Iowa: NUE screens: A chimeric approach.

C. Lu, DuPont Experimental Station, Wilmington, Delaware: Forward genetic screens in drought discovery.

S. Pasternak, Josh Stein, Andrew Olson, Cold Spring Harbor Laboratory: What up with wheat? Progress on wheat genome sequencing.

D. Ware

M. Freeling

T. Michael

Genotype to Phenotype: Deriving Biological Knowledge from Large Genomic Data Sets

October 16–19

FUNDED BY **The Cold Spring Harbor Laboratory Corporate Sponsor Program**

ARRANGED BY **T. Michael,** Monsanto Company, Chesterfield, Missouri
P. Schnable, Iowa State University, Ames

In the past few years, sequencing instrument capabilities have increased more than 1000-fold and are likely to continue to increase about fivefold each year for the next several years. However, analysis methods have not improved nearly as much during the same time period, and a variety of technical limitations of these new instruments make it even more difficult to carry out whole-genome sequencing of novel genomes (de novo sequencing). The goals of this meeting were to assess the current state of de novo sequencing, predict what can be expected to develop in the near future, and determine how these exciting technologies could be used to carry out de novo sequencing of entire complex plant genomes.

Welcoming Remarks: **J.A. Witkowski,** Banbury Center, Cold Spring Harbor Laboratory, New York
Goals and Structure of Meeting: **T. Michael,** Monsanto Company, Chesterfield, Missouri, and **P. Schnable,** Iowa State University, Ames

SESSION 1

R. Reiter, Monsanto Company, St. Louis, Missouri: Large breeding data sets.
E. Spalding, University of Wisconsin, Madison: Phenotyping in the laboratory.
T. Harkins, Life Technologies, Carlsbad, California: Future of next-gen sequencing technologies.
L. Comai, University of California, Davis: Sexual incompatability in a genomic context.
R. Flavell, Ceres, Inc., Thousand Oaks, California: Bold ideas for energy crops.
D. Fischoff, Monsanto Company, St. Louis, Missouri: Future opportunities in Biotech-breeding.

General Discussion and Focus Challenge

SESSION 2

M. Schatz, Cold Spring Harbor Laboratory: Novel genome assembly strategies.
T. Michael, Monsanto Company, Chesterfield, Missouri: Novel genomes.
A. Paterson, University of Georgia, Athens: Comparative genomics.
S. Jackson, University of Georgia, Athens: Economically important crop genomes.
W.R. McCombie, Cold Spring Harbor Laboratory: Strategies for next-gen sequencing.
T. Mockler, Oregon State University, Corvallis: Genome features.

SESSION 3

Moderators: T. Michael, Monsanto Company, Chesterfield, Missouri, and **P. Schnable,** Iowa State University, Ames

General Discussion and Focus Challenge

SESSION 4

Introduction and Day-1 Summary: T. Michael, Monsanto Company, Chesterfield, Missouri

R. Last, Michigan State University, Lansing: Metabolomics.
P. Benfey, Duke Institute for Genome Sciences and Policy, Durham, North Carolina: Transcriptomics.
R. Martienssen, Cold Spring Harbor Laboratory: Epigenomics.
S. Briggs, University of California, San Diego: Proteomics.
I. Baxter, U.S. Department of Agriculture, St. Louis, Missouri: Ionomics.
T. Altmann, Leibniz Institute of Plant Genetics and Crop Plant Research, Gatersleben, Germany: Phenomics.

General Discussion and Focus Challenge

SESSION 5

E. Buckler, Cornell University, Ithaca, New York: Genotype to phenotype in cross-pollinated crops.
N. Springer, University of Minnesota, St. Paul: Methylation variation.
P. Schnable, Iowa State University, Ames: Structural variation.
N. Stein, Leibniz Institute of Plant Genetics and Crop Plant, Gaterlseben, Germany: Genotype to phenotype in self-pollinated crops.
O. Loudet, INRA Versailles, France: Natural variation.
D. Kliebersteín, University of California, Davis: Statistical quantitative genetics.

SESSION 6

Moderators: T. Michael, Monsanto Company, Chesterfield, Missouri, and **P. Schnable,** Iowa State University, Ames

General Discussion and Focus Challenge

SESSION 7

Introduction and Day 2 Summary: P. Schnable, Iowa State University, Ames

V. Walbot, Stanford University, California: Studying development in a genomic context.
S. Goff, University of Arizona, Tucson: Model-based approaches to molecular breeding.
J. Bennetzen, University of Georgia, Athens: Interactions between plant genotypes and soil microflora.
M. Timmermans, Cold Spring Harbor Laboratory: Small RNAs regulating shoot meristem function.

SESSION 8

Moderators: T. Michael, Monsanto Company, Chesterfield, Missouri, and **P. Schnable**, Iowa State University, Ames

General Discussion and Focus Challenge

Metformin and Neoplasia

October 30–November 2

FUNDED BY **Oliver Grace Cancer Fund**

ARRANGED BY **M. Pollak,** McGill University, Montreal, Canada
C. Thompson, Memorial Sloan-Kettering Cancer Center, New York

Metformin is widely prescribed for type II diabetes, and it is known to be a safe and effective agent for this condition. Recent retrospective epidemiologic data suggest that use of metformin or related biguanides is associated with substantially reduced cancer incidence and/or improved cancer outcomes. Furthermore, these compounds have been shown to reduce tumor growth in several in vivo models and to reduce tumor formation in carcinogenesis assays. Participants at this meeting reviewed and critically assessed the most recent results in the field and discussed the many proposed mechanisms of action. The question of potential clinical applications for treatment or prevention was also considered, and gaps in knowledge such as how to optimize pharmacokinetics, identification of predictive biomarkers to select patients who may benefit, and the definition of rational combinations were considered.

Welcoming Remarks: **J.A. Witkowski,** Banbury Center, Cold Spring Harbor Laboratory, New York
Introductory Remarks: **M. Pollak,** McGill University, Montreal, Canada, and
C. Thompson, Memorial Sloan-Kettering Cancer Center, New York

SESSION 1

History

C. Bailey, Aston University, Birmingham, United Kingdom: History of biguanides and development of metformin as an antidiabetic.

Pharmaco-Epidemiology

J. Johnson, University of Alberta, Edmonton, Canada: Epidemiologic evidence for an influence of metformin on neoplasia.

Cancer Models

P. Dennis, National Cancer Institute, Bethesda, Maryland: Metformin as a chemopreventive agent in mouse models of cancer.

M. Martin, Institute of Cancer Research, London, United Kingdom: Investigating the potential for metformin as an antimelanoma agent.

B. Zheng, Columbia University, New York: Cross-talk between LKB1-AMPK and BRAF signaling pathways and its implication for melanoma therapy.

D. Sabatini, Whitehead Institute for Biomedical Research, Cambridge, Massachusetts: Nutrient sensing by the mTOR pathway.

SESSION 2: Cancer Models

K. Struhl, Harvard Medical School, Boston, Massachusetts: Metformin selectively kills cancer stem cells and acts together with chemotherapy to prolong remission.
F. Bost, INSERM U895, University of Nice Sophia-Antipolis, France: The multiple biological actions of metformin on cancer cells.
M. Schwab, Dr Margarete Fischer-Bosch Institute of Clinical Pharmacology, Stuttgart, and University Tübingen, Germany: Pharmacokinetics and pharmacogenomics of metformin.

Mechanistic Aspects I: Mitochondria
B. Guigas, Leiden University Medical Center, The Netherlands: Role of mitochondria in the mechanism of action of metformin.
M. Vander Heiden, Dana-Farber Cancer Institute, Boston, Massachusetts: Metabolic pathway regulation in cancer.

SESSION 3: Mechanistic Aspects II: Cellular Physiology

M. Haigis, Harvard Medical School, Boston, Massachusetts: Role of sirtuins in metabolism.
D. Shackelford, University of California, Los Angeles: Phenformin as a cancer therapeutic.
G. Hardie, University of Dundee, United Kingdom: AMPK:A target for metformin that is down-regulated in cancer cells and during viral infection.
G. Rocha, Universidade Estadula de Campinas, Sao Paulo, Brazil: Metformin and chemotherapy.
A. Selvaraj, University of Cincinnati, Ohio: Metformin and TOR pathway.
N. Sonenberg, McGill University, Montreal, Canada: Metformin alters the translatome.
I. Topisirovic, McGill University, Montreal, Canada: Effects of biguanides and mTOR inhibitors on protein synthesis and energy metabolism.

SESSION 4: Mechanistic Aspects II: Cellular Physiology (*continued*)

C.L. Walker, MD Anderson Cancer Center, Smithville, Texas and J. Pouyssegur, University of Nice, France: Targeting lactic acid export of glycolytic tumors. Best anticancer benefit: Metformin or AMPK block?
F. Wondisford, Johns Hopkins University, Baltimore, Maryland: Molecular mechanism of metformin action.
B. Viollet, Institut Cochin Université Paris Descartes, France: Metformin actions in the liver to inhibit gluconeogenesis: Insights to possible mechanisms relevant to oncology.
M. Driscoll, Rutgers University, Piscataway, New Jersey: Metformin engages pathways that promote healthy aging in *C. elegans*.
M. Pollak, McGill University, Montreal, Canada: Metformin can influence tumor growth as an indirect consequence of actions on the liver.
G. Hardie, University of Dundee, United Kingdom: Relationship between ATM and metformin action.

Early Clues from the Clinic
G. Hardie, University of Dundee, United Kingdom: Results of biomarker trial in breast cancer.

SESSION 5: Early Clues from the Clinic

S. Jiralerspong, Baylor College of Medicine, Houston, Texas: Clinical evidence regarding metformin antineoplastic activity.

Novel Aspects
G. Ferbeyre, University of Montreal, Canada: Metformin reduces DNA damage and mutations due to endogenous reactive oxygen species.
R. Jones, McGill University, Montreal, Canada: Metformin effects on immunity of possible relevance to oncology.

Repurposing Drugs
A. So, Duke University, Durham, North Carolina: Repurposing drugs: Policy challenges and economic prospects.

Concluding Remarks and General Discussion: M. Pollak, McGill University, Canada, and **C. Thompson,** Memorial Sloan-Kettering Cancer Center, New York

Workshop: The Future of the Epigenomics of Plants International Consortium

November 2–4

FUNDED BY **Epigenomics of Plants International Consortium**

ARRANGED BY **R. Martienssen,** Cold Spring Harbor Laboratory, New York
C. Pikaard, Indiana University, Bloomington
D. Wagner, University of Pennsylvania, Philadelphia

Plant research is leading the way in many areas of epigenomics and the Epigenomics of Plants International Consortium (EPIC) is a National Science Foundation (NSF)-funded research coordination initiative to form an International Consortium to decipher the plant epigenome. It has been clear for many years that epigenetic interactions with the environment shape the plant body plan during development and control growth and survival responses of these sessile organisms. As a result, plants have a sophisticated epigenomic "toolkit" that modulates genome accessibility. Deciphering the plant epigenome is a large task and will be most effectively achieved via an internationally coordinated effort. This conference discussed the intellectual questions, transformative methodologies, and infrastructure needs required to achieve this goal, as well as the means to engage funding agencies and the international research community as a whole.

Welcoming Remarks: **J.A. Witkowski,** Banbury Center, Cold Spring Harbor Laboratory, New York
Overview of EPIC: **D. Wagner,** University of Pennsylvania, Philadelphia: Our mandate, relevance to recent U.S. Plant Science Summit and 10-year goals, EPIC's accomplishments to date, challenges ahead.

SESSION 1: Defining the Mission
Concurrent meeting of breakout groups led by C. Pikaard (Group A) and D. Wagner (Group B).

Group A: Potential grand challenges, gaps in our understanding or capabilities, long- and short-term goals.
Group B: Epigenetic modifications to be examined, what "reference epigenomes" are needed, model systems vs. crops, conditions, (e.g., developmental, environmental, and genetic) to be analyzed. Report of breakout group A and full group discussion.
Report of breakout group B and full group discussion.

SESSION 2: Obtaining, Storing, and Displaying the Data
Concurrent meeting of breakout groups led by C. Pikaard (Group A) and R. Martienssen (Group B)

Group A: Data sets and tools needed.
Group B: Data collection (coordination, standards, and analysis), data storage, data display, and availability.
Report of breakout group A and full group discussion.
Report of breakout group B and full group discussion.

SESSION 3: Plan of Action
Concurrent meeting of breakout groups led by D. Wagner (Group A) and R. Martienssen (Group B)

Group A: Engaging the community.
Group B: Governance structure for an International EPIC consortium.
Report of breakout group A.
Report of breakout group B.
Full group discussion of the White paper draft: Contents, authors.
Next steps for EPIC, future meetings, and engaging the funding agencies for an international cooperative effort.

L. Dennis

E. Richards, C. Pikaard

V. Chandler

Myc and the Pathway to Cancer

November 6–9

FUNDED BY **Cold Spring Harbor Laboratory Corporate Sponsor Program**

ARRANGED BY **C. Dang,** University of Pennsylvania, Philadelphia
R. Eisenman, Fred Hutchinson Cancer Research Center, Seattle, Washington

Myc was discovered 30 years ago and was recognized as being a key player in cancer development. Although a great deal has been learned about Myc interactions and functions, we still lack a detailed understanding of how Myc activity influences normal versus cancer cell behavior. Specific topics covered at the meeting included the regulation of *myc* gene transcription, the role of Myc in normal and tumor stem cells, transcriptional and nontranscriptional activities of Myc, and functions of the extended Myc network (including Mlx and Mondo proteins). Participants included experts in cancer models who provided perspective concerning potential roles of Myc in different tumor systems. The meeting explored ways through which *myc*, as a pivotal oncogene in human cancers, and its associated pathways can provide targets for the development of therapies.

Welcoming Remarks: **J.A. Witkowski,** Banbury Center, Cold Spring Harbor Laboratory, New York
Introductory Remarks: **R. Eisenman,** Fred Hutchinson Cancer Research Center, Seattle, Washington

SESSION 1: Myc Transcriptional Activities
Chairperson: C. Dang, University of Pennsylvania, Philadelphia

R. Young, Whitehead Institute, Boston, Massachusetts: Control of gene expression by c-Myc.

S. Hann, Vanderbilt University, Nashville, Tennessee: ARF inhibition of c-Myc transcriptional domain ubiquitylation controls c-Myc-mediated apoptosis.

M. Cole, Dartmouth University, Lebanon, New Hampshire: A new mechanism for Myc-mediated repression.

SESSION 2: Regulation of Myc Abundance
Chairperson: S. Hann, Vanderbilt University, Nashville, Tennessee

D. Levens, National Cancer Institute, Bethesda, Maryland: How a simplified model of Myc function requires and explains the complexity of the c-Myc promoter.

J. Bradner, Dana-Farber Cancer Institute, Boston, Massachusetts: Chemical inhibition of Myc expression and function.

R. Sears, Oregon Health & Science University, Portland, Oregon: Phosphorylation and proline isomerization events that regulate c-Myc DNA binding, oncogenetic activity, and protein stability.
W. Tansey, Vanderbilt University, Nashville, Tennessee: Regulation of Myc by the ubiquitin-proteasome system.
J. Freedman, GlaxoSmithKline, Collegeville, Pennsylvania: Regulation of Myc through bromodomain modulation (ready for patient testing).

SESSION 3: Myc Regulation of Cell Physiology
Chairperson: L. Penn, University of Toronto, Ontario, Canada

G. McArthur, Peter MacCallum Cancer Centre, East Melbourne, Victoria, Australia: Inhibition of RNA polymerase I as a therapeutic strategy for cancer-specific activation of p53 in Myc-driven malignancy.
L. Johnston, Columbia University, New York: Myc, p53, and metabolism: A *Drosophila* model for premalignancy.
C. Dang, University of Pennsylvania, Philadelphia: Regulation of cancer cell metabolism by Myc and therapeutic targets.
D. Ayer, University of Utah, Salt Lake City: Nutrient sensing by MondoA:M1x complexes.

SESSION 3 (*continued*): Myc Regulation of Cell Physiology
Chairperson: M. Cole, Dartmouth University, Lebanon, New Hampshire

S. McMahon, Thomas Jefferson University, Philadelphia, Pennsylvania: Control of the survival/apoptosis decision by Myc.
B. Amati, Italian Institute of Technology, Milan, Italy: Targeting the ATR-Chk1 pathway in Myc-induced lymphoma.
S. Dalton, University of Georgia, Athens: Myc in pluripotency and reprogramming.

SESSION 4: Myc-regulated Targets and Pathways
Chairperson: C. Sherr, St. Jude Children's Research Hospital, Memphis, Tennessee

J. Sedivy, Brown University, Providence, Rhode Island: Role of Myc in aging: The best of two worlds.
S. Lowe, Memorial Sloan-Kettering Cancer Center, New York: Characterizing tumor maintenance genes using mouse models and RNAi.
L. Staudt, National Cancer Institute, Bethesda, Maryland: Pathogenetic pathways and treatment strategies from a Burkitt lymphoma genome project.
M. Henriksson, Karolinska Institutet, Stockholm, Sweden: MYCN and neuroblastoma differentiation.
D. Felsher, Stanford University, California: Multiscale modeling of Myc-associated oncogene addiction.

SESSION 5: Tumorigenesis and Therapeutic Approaches
Chairperson: M. Roussel, St. Jude Children's Research Hospital, Memphis, Tennessee

L. Penn, University of Toronto, Ontario, Canada: Strategies to target Myc as an effective anticancer therapeutic: Understanding posttranslational modifications as a point of Myc regulation.
M. Eilers, University of Würzburg, Germany: Synthetic lethal interactions with deregulated Myc or genome-wide analyses of Myc and miz1-binding sites
M. Ptashne, Memorial Sloan-Kettering Cancer Center, New York: Epigenetic switches are easier to construct in eukaryotes than in prokaryotes.

SESSION 5 (*continued*): Tumorigenesis and Therapeutic Approaches
Chairperson: M. Eilers, University of Würzburg, Germany

T. Look, Dana Farber Cancer Institute, Massachusetts: Apoptotic response in MycN-overexpressing sympathoadrenal cells is blocked by activated ALK, leading to neuroblastoma.
C. Grandori, Fred Hutchinson Cancer Research Center, Seattle, Washington: Identification of therapeutic targets for Myc-driven cancers by functional genomics.
R. Eisenman, Fred Hutchinson Cancer Research Center, Seattle, Washington: A point mutation in Myc generates a tumor-prone phenotype.
M. Roussel, St. Jude Children's Research Hospital, Memphis, Tennessee: Myc proteins in pediatric medulloblastoma.
C. Vakoc, Cold Spring Harbor Laboratory: RNAi screening to identify epigenetic vulnerabilities in acute myeloid leukemia.

Concluding Remarks and General Discussion: R. Eisenman, Fred Hutchinson Cancer Research Center, Seattle, Washington, and **C. Dang,** University of Pennsylvania, Philadelphia

Transmissible Amyloidoses

November 29–December 2

FUNDED BY **The Cold Spring Harbor Laboratory Corporate Sponsor Program**

ARRANGED BY **J. Collinge,** University College London, United Kingdom
D. Goldgaber, SUNY Stony Brook, New York

After succeeding in demonstrating the transmission of kuru and Creutzfeldt–Jacob disease (CJD) in the late 1960s, Carleton Gajdusek suspected that other late-onset diseases of the brain might also be transmissible. In the 1970s, he inoculated hundreds of animals with brain tissues of patients with Alzheimer's disease, multiple sclerosis, Parkinson's disease, and other diseases and kept them under observation for many years, some of them for decades. Using the same criteria that worked for kuru and CJD, namely, clinical symptoms and gross pathological changes in the brain, he found not a single case of transmission. In the 1990s, however, data began to accumulate that Alzheimer's disease amyloidosis can be transmitted to primates, and transmission of β-amyloid to transgenic mice was demonstrated. The time was clearly right for a critical review of the data on transmission of the amyloidoses, the mechanisms involved, and the implications for human health.

D. Goldgaber, J. Collinge

Welcoming Remarks: **J.A. Witkowski,** Banbury Center, Cold Spring Harbor Laboratory, New York
Introductory Remarks: **D. Goldgaber,** SUNY Stony Brook, New York

SESSION 1: Mammalian and Yeast Prions and Their Properties
Chairperson: J. Collinge, University College London, United Kingdom

J. Collinge, University College London, United Kingdom: Mammalian prion propagation, strains, and transmission barriers.
B. Caughey, NIAID Rocky Mountain Laboratories, Hamilton, Montana: Structure and detection of prions.
I. Vorberg, Deutsches Zentrum für Neurodegenerative Erkrankugen, Bonn Germany: Propagation of yeast prions in mammalian cells.
R. Wickner, National Institute of Diabetes and Digestive and Kidney Diseases, Bethesda, Maryland: Yeast prion disease amyloid structure can explain prion strains.
C. Weissmann, Scripps Research Institute, Jupiter, Florida: Mutation of prions.

J. Buxbaum, C. Weissmann

D. Eisenberg, I. Vorberg

SESSION 2: Mechanisms of Protein Misfolding/Aggregation and Structure of Amyloids
Chairperson: A. Horwich, Yale University School of Medicine, New Haven, Connecticut

R. Tycko, National Institute of Diabetes and Digestive and Kidney Disease, Bethesda, Maryland: In vitro vs. vivo β-amyloid fibril structures: Propagation of amyloid structures in vitro.

D. Eisenberg, University of California, Los Angeles: Are structural polymorphisms the basis of prion strains?

R. Morimoto, Northwestern University, Evanston, Illinois: Transmission of protein aggregates in *C. elegans.*

SESSION 3: Alzheimer's Disease and Tauopathies
Chairperson: D. Goldgaber, SUNY Stony Brook, New York

D. Goldgaber, SUNY Stony Brook, New York: Historical perspective and review of archived NIH primate transmission series.

A. Nicoll, UCL Institute of Neurology, London, United Kingdom: Review of archived attempted transmission of Alzheimer pathology to transgenic mice.

L. Walker, Emory University, Atlanta, Georgia: Seeded induction of β-amyloid deposition in transgenic rodents.

M. Jucker, University of Tübingen, Germany: Characterization of β-amyloid-inducing seed.

M. Goedert, MRC Laboratory of Molecular Biology, Cambridge, United Kingdom: Prion-like properties of assembled Tau.

C. Soto, University of Texas Medical School, Houston: Transmission of Alzheimer's disease and type-2 diabetes.

M. Diamond, Washington University in St. Louis, Missouri: Propagation of protein misfolding in neurodegenerative diseases.

General Discussion

SESSION 4: Cellular Spread and Pathogenesis: Prion-like Mechanisms
Chairperson: J. Buxbaum, Scripps Research Institute, La Jolla, California

A. Bertolotti, MRC Laboratory of Molecular Biology, Cambridge, United Kingdom: Prion-like propagation of mutant SOD1 misfolding.

S.-J. Lee, Konkuk University, Seoul, Korea: Transmission of synucleinopathies and neuroinflammation via extracellular α-synuclein.

K. Luk, University of Pennsylvania School of Medicine, Philadelphia: α-synuclein transmission in synucleinopathies.

T. Outeiro, University Medizin Göttingen, Germany: Intra- and extracellular effects of α-synuclein oligomers: Implications for transmission.

General Discussion

SESSION 5: Transmissibility of other Amyloidoses
Chairperson: D. Eisenberg, University of California, Los Angeles

J. Watts, University of California, San Francisco: Bioluminescence imaging of induced protein deposition in transgenic mice.

J. Buxbaum, Scripps Research Institute, La Jolla, California: Amyloid–amyloid interactions.

K. Higuchi, Shinshu University School of Medicine, Matsumoto, Japan: Transmission of amyloidoses in mouse and cheetah: Implications in human systemic amyloidoses.

P. Westermark, Uppsala University, Sweden: Transmission of systemic amyloidosis/dissemination of deposits in systemic amyloidoses.

General Discussion

L. Walker, M. Jucker

Evolution of Neural Circuits and Behavior

December 7–9

FUNDED BY **Marie Robertson Memorial Fund**

ARRANGED BY **K. Honegger,** Cold Spring Harbor Laboratory, New York
S. Shea, Cold Spring Harbor Laboratory, New York

Nervous systems have evolved under unique sets of selective pressures driving adaptive changes, and thus, their structure and function reflect the organism's environment. The ultimate expression of these forces on the brain is diversity of behavior. Empirical studies of the interaction among environment, neural processing, and behavior have largely consisted of neuroethological, comparative, and molecular genetic approaches. Participants in the meeting discussed how the synthesis of these complementary approaches might enrich our understanding of nervous system function and further aid in the interpretation of experimental findings across animal phyla.


D. Chklovskii

Welcoming Remarks: **J.A. Witkowski,** Banbury Center, Cold Spring Harbor Laboratory, New York
Introductory Remarks: **K. Honegger,** Cold Spring Harbor Laboratory, New York

SESSION 1: Fundamental Constraints of the Evolution of Neural Circuits
Chairperson: D. Chklovskii, Janelia Farm/HHMI, Ashburn, Virginia

S. Grant, University of Edinburgh, United Kingdom: Synapse evolution.
D. Chklovskii, Janelia Farm/HHMI, Ashburn, Virginia: Do more neurons make you smarter? A sensory processing perspective.
J. Niven, University of Cambridge, United Kingdom: Energetic and biophysical constraints on neural circuits.
P. Katz, Georgia State University, Atlanta: Homology and homoplasy in neural circuits underlying behavior.

SESSION 2: Molecular Genetics and the Evolution of Neural Circuits
Chairperson: J. Dubnau, Cold Spring Harbor Laboratory

D. Stern, Howard Hughes Medical Institute, Ashburn, Virginia: Tools and approaches for studying the evolutionary genetics of behavior in closely related *Drosophila* species.
J. Huang, Cold Spring Harbor Laboratory: Chandelier cell: An entry point to cortical circuit organization, assembly, and evolution.
J. Dubnau, Cold Spring Harbor Laboratory: A microRNA–dopamine receptor genetic module in distinct neural circuits for olfactory arousal and olfactory memory.

SESSION 3: Comparative Neuroanatomy
Chairperson: H. Karten, University of California, San Diego

S. Farris, West Virginia University, Morgantown: Evolution of structural and functional novelty in insect mushroom bodies.
C. Ragsdale, University of Chicago, Illinois: Sensory, motor, and memory circuitries in the octopus CNS.
M. Hale, University of Chicago, Illinois: Biomechanical and neural analysis of the evolution of motor systems.
H. Karten, University of California, San Diego: Cells, circuits, and systems: Natural selection and conservation among amniotes.

SESSION 4: Comparative Physiology
Chairperson: H. Zakon, University of Texas, Austin

E. Fortune, The Johns Hopkins University, Baltimore, Maryland: Evolution of neural circuits for cooperative behaviors.
N. Sawtell, Columbia University, New York: Mechanisms for predicting sensory events in cerebellum-like circuits.
H. Zakon, University of Texas, Austin: Electric fish are green: Conserving energy and recycling ion channels.
D. Soares, University of Maryland, College Park: Sensory specialization and adaptation in cavefishes.
D. Kelley, Columbia University, New York: Evolution of songs and their neural circuits in *Xenopus*.
C. Fernando, University of Sussex, Brighton, United Kingdom: Darwinian neurodynamics.

General Discussion and Summary: S. Shea, Cold Spring Harbor Laboratory

M. Hale

H. Zakon

Psychiatric Genomics

December 11–14

FUNDED BY **The Stanley Research Foundation**

ARRANGED BY **W.R. McCombie,** Cold Spring Harbor Laboratory, New York
M. Owen, Cardiff University, United Kingdom

The first Banbury Center meeting on molecular human genetics was held in 1982 at a time when restriction-fragment-length polymorphisms (RFLPs) linked to human genetic diseases were first being sought and a complete human gene had yet to be sequenced. How times have changed! And yet it is still difficult to find the genes underlying psychiatric and other complex disorders. However, new high-through-put DNA sequencing techniques have made, or are about to make, it possible to sequence the whole exomes and genomes of large numbers of individuals. This will provide opportunities to develop new gene-hunting strategies for complex genetic disorders. This meeting brought together experts to critically assess current strategies and to outline how genome-scale sequencing can be used most effectively and efficiently.

Welcoming Remarks: **J.A. Witkowski,** Banbury Center, Cold Spring Harbor Laboratory, New York
Introductory Remarks: **W.R. McCombie,** Cold Spring Harbor Laboratory, New York

SESSION 1: Common Variants
Chairperson: D. Goldstein, Duke University, Durham, North Carolina

O. Andreassen, Oslo University Hospital, Norway: LD-based annotation enrichment reveals new schizophrenia genes.

P. Gejman, North Shore University Health System–Research Institute, Evanston, Illinois: Genome-wide gene expression study of a schizophrenia GWAS data set.

S. Leal, Baylor College of Medicine, Houston, Texas: Quantifying missing heritability and estimating genetic effects for complex traits due to rare variants.

M. Noethen, University of Bonn, Germany: NCAN in psychiatric disorders: From genetic association to mouse model.

A. Corvin, St. James Hospital, Dublin, Ireland: Schizophrenia redefined: The promise of genomics.

M. Daly, Massachusetts General Hospital, Boston: Autism sequencing?

SESSION 2: Phenotype
Chairperson: D. Goldstein, Duke University, Durham, North Carolina

K. Kendler, Virginia Commonwealth University, Richmond: Genetics and psychiatric nosology in the genomics era.

D. Blackwood, University of Edinburgh, United Kingdom: Phenotypic spectrum of DISC1 variation.

M. Owen, Cardiff University, United Kingdom: Rethinking psychiatric phenotypes.

K. Mitchell, Trinity College, Dublin, Ireland: Rare mutations, oligogenic interactions and endophenotypes.

P. Thomson, University of Edinburgh Centre for Molecular Medicine, United Kingdom: Next-generation sequencing of the *DISC1* (*disrupted in schizophrenia 1*) locus.

SESSION 3: Rare Variants
Chairperson: W.R. McCombie, Cold Spring Harbor Laboratory, New York

W. Byerley, University of California, San Francisco: Whole-genome sequencing of multiplex bipolar pedigrees.

C.T. Caskey, Baylor College of Medicine, Houston, Texas: Whole-genome sequencing of families with multiple affected individuals with schizophrenia.

E. Eichler, University of Washington, Seattle: New mutations and autism.

D. Goldstein, Duke University, Durham, North Carolina: Finding schizophrenia risk factors in sequence data.

M.-C. King, University of Washington School of Medicine, Seattle: Discovering the (many) genes responsible for schizophrenia: Strategies based on genomic sequencing.

J. Lupski, Baylor College of Medicine, Houston, Texas: Reciprocal CNV, mirror image phenotypes and neuropsychiatric traits.

S. McCarroll, Harvard Medical School, Boston, Massachusetts: What constitutes sufficient evidence that a gene actually related to schizophrenia?

F. McMahon, National Institute of Mental Health, Bethesda, Maryland: Sequencing members of virtual pedigrees drawn from inbred founder populations.

M. O'Donovan, Cardiff University School of Medicine, United Kingdom: Synaptic genes and de novo mutations.

A. Need, Duke University, Durham, North Carolina: Next-generation sequencing of 170 schizophrenia patients.

A. Palotie, Wellcome Trust Sanger Institute, Cambridge, United Kingdom: Identification of low-frequency variants in the neurodevelopmental studies of the UK10K project.

J. Potash, University of Iowa, Iowa City: Whole-exome sequencing in bipolar disorder.

S. Purcell, Massachusetts General Hospital, Boston: Exome sequencing in schizophrenia.

G.A. Rouleau, CHU Sainte-Justine, Montreal, Canada: De novo mutations in psychiatric diseases.

M. Wigler, Cold Spring Harbor Laboratory: Role of de novo mutation in autism.

SESSION 4: What's Next?
Chairperson: M. Owen, Cardiff University, United Kingdom

F. Henn, Cold Spring Harbor Laboratory: Problems, circuits, genes, and models: An agnostic's thoughts on psychiatric genetics.

T. Lehner, National Institute of Mental Health, Bethesda, Maryland: The neuropsychiatric disease consortium.

W.R. McCombie, Cold Spring Harbor Laboratory: Case controls or family studies, and where do we have to go next to understand rare variants.

D. Weinberger, National Institute of Mental Health, Bethesda, Maryland: From gene to brain circuits and back.

Y. Berstein

M.C. King

C.T. Caskey

BANBURY CENTER GRANTS

Grantor	*Program*	*Duration of Grant*	*2011 Funding*
FEDERAL SUPPORT			
Defense Threat Reduction Agency Department of Defense	Scientific and Technological Barriers to Global Real-Time Risk Assessment of Vector-Borne Infections	2011	$ 34,929
NIH–National Institute of Mental Health	The 3rd Annual NIMH-Sponsored Brain Camp	2011	41,325
National Science Foundation	The Future of Plant Genome Sequencing and Analysis	2011	34,196
NONFEDERAL SUPPORT			
Boehringer Ingelheim Fonds	Science: Get it across!	2011	65,472
CFIDS Association	Strategic Research Initiative for CFS	2011	33,397
Cold Spring Harbor Laboratory Corporate Sponsor Program	Genotype to Phenotype: Deriving Biological Knowledge from Large Genomic Datasets	2011	42,051
Cold Spring Harbor Laboratory Corporate Sponsor Program	Transmissible Amyloidoses	2011	41,078
Cold Spring Harbor Laboratory Corporate Sponsor Program	Myc and the Pathway to Cancer	2011	45,337
Cold Spring Harbor Laboratory–Pioneer/DuPont Collaborative Research Program	Dosage, Epigenetics, and the Biology of Hybridization and Hybrids	2011	51,155
Epigenomics of Plants International Consortium	Board Meeting	2011	17,384
FEBS Journal	FEBS Journal Editorial Board Meeting	2011	10,020
The Gatsby Charitable Foundation	Neuronal Response Variability and Cortical Computation	2011	15,000
Hazen Polsky Foundation	Curing Melanoma and Other Cancers by Targeted Therapies	2011	50,000
Individual participants	The Future of Biomarker Discovery and Biobanks in Cancer Diagnosis, Prognosis, and Therapy	2011	2,610
Individual participants	Scientific and Technological Barriers to Global Real-Time Risk Assessment of Vector-Borne Infections	2011	15,665
John Wiley & Sons Ltd	FEBS Journal Editorial Board Meeting	2011	1,695
The Lehrman Institute	DNA and the History of Mankind	2011	170,245
Leukemia & Lymphoma Society	SCOR Retreat	2011	7,235
Marie Robertson Research Fund	Evolution of Neural Circuits and Behavior	2011	20,000
Melanoma Research Alliance	Curing Melanoma and Other Cancers by Targeted Therapies	2011	50,000
Oliver Grace Fund	Antibiotic Resistance: Past, Present, Future	2011	46,970
Oliver Grace Cancer Fund	Metformin and Neoplasia	2011	51,121
Sanofi-Aventis TSU-Aging	Translation of Cellular and Molecular Mechanisms of Aging to Geriatric Disorders	2011	44,817
The Swartz Foundation	Neuronal Response Variability and Cortical Computation	2011	43,266
The Stanley Research Foundation	Psychiatric Genomics	2011	63,607
SWOG	The Future of Biomarker Discovery and Biobanks in Cancer Diagnosis, Prognosis and Therapy	2011	30,943
Time for Lyme, Inc.	Lyme Disease in the Proteomics-Genomics Era	2011	41,304

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Joseph McCoy, Groundskeeper