Cold Spring Harbor Laboratory

2016 BANBURY CENTER

BANBURY CENTER

The Banbury Center is the small conference center at Cold Spring Harbor Laboratory, holding meetings for between 20 and 30 invited participants. Some 20 meetings are held each year on topics ranging over the spectrum of research in biology and biomedical sciences, as well as issues relating to science and healthcare policy. More than 12,000 scientists have participated in the more than 600 meetings held since the Center opened in May 1978. As of 2016, 71 Nobel laureates have taken part in Banbury Center meetings.

The Center is on a 55-acre estate on the north shore of Long Island, 40 miles east of downtown Manhattan and 5 miles from Cold Spring Harbor Laboratory. The estate was donated to the Laboratory in 1976 by Charles Sammis Robertson. What was once the estate's seven-car garage is now the Conference Room, and the Robertsons' family house is used for accommodating participants. Sammis Hall and Meier House provide additional housing so that everyone attending a Banbury Center meeting can stay on the estate.

Among the hundreds of meetings held each year in the United States, the Banbury Center meetings are unique. The small number of participants ensures that discussions, both within sessions and informal, have a major role in each meeting, and the relative isolation of the estate means that participants focus on the task at hand. Furthermore, because the expenses of participants are covered, selection of scientists is guided by the needs of the science and not dictated by whether those invited can find the money to come.

Some of the important Banbury Center meetings include:

Patenting of Life Forms. Held just one year after the famous decision in the Diamond vs. Chakrabarty case, patent lawyers and scientists met to discuss the implications of approving patenting of genetically modified bacteria. Nobel laureate Sydney Brenner was a participant.

Taxonomy, DNA, and the Barcode of Life. In the early 2000s, there was a controversial proposal to use DNA sequences as molecular "barcodes" to uniquely identify of species. Two meetings held at Banbury led to the wide acceptance of DNA barcoding and the establishment of the Consortium for the Barcode of Life project.

DNA Technology and Forensic Science. The forensic world began using DNA fingerprinting but without a good understanding of its limitations. The meeting included scientists, prosecutors, defense attorneys, and judges, and it led to the founding of the Innocence Project by Peter Neufeld and Barry Scheck.

Support for the Center has come from many sources, including companies contributing to the Cold Spring Harbor Laboratory Corporate Sponsor Program. Companies such as Pfizer, Glaxo, Janssen, Illumina, and Sanofi have funded specific meetings. The Federal Government has supported meetings through the National Institutes of Health, the National Science Foundation, and the Departments of Energy, Defense, Justice, Agriculture, and Homeland Security. Many foundations devoted to biomedical research have used the Center, including the ALS Association, the FRAXA Foundation, the Ovarian Cancer Research Fund, and the Swartz Foundation.

Cover: Discussions continue on the Conference Room deck.

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BANBURY CENTER
EXECUTIVE DIRECTOR'S REPORT

I wrote in my first Banbury Center *Annual Report* (1988):

> I have been at the Banbury Center for just over one year, and I am finding it to be as enjoyable and fascinating as I had expected. I was enthusiastic about the aims of the Banbury Center before I arrived, and my experience of the variety of topics and the enthusiasm of participants demonstrates that the Banbury Center is a unique resource for exchanging scientific information.

My experience over the 29 years since then has confirmed in every respect my early expectations. In that time, Banbury has held almost 600 meetings with approximately 12,000 participants. There have been many memorable meetings but none more significant than *DNA and Forensic Technology*, which helped in establishing the Innocence Project. Others were held at particularly auspicious moments in the development of a field: *The* Arabidopsis *Genome* and *Telomeres* in 1994, *RNA Silencing* in 2000, and many meetings on human genetic and psychiatric disorders. In particular, there were important series of meetings on the fragile X syndrome, prion disease, amyotrophic lateral sclerosis, and Lyme disease. Not all the meetings dealt with research. The Alfred P. Sloan Foundation provided many years of support for workshops introducing science journalists and congressional staff to important contemporary issues in biomedicine, and the Federal Judicial Center provided funding for a similar series of meetings for federal judges.

But, the time has come for me to step down and I am delighted to introduce Rebecca Leshan who will be taking over from me. Rebecca's background is in Molecular and Integrative Physiology. Her Ph.D. was on hypothalamic leptin receptor expression and action in the mouse with Martin Myers (University of Michigan, Ann Arbor). Rebecca did a postdoc with Donald Pfaff (The Rockefeller University). She decided to use her science background in a different field and joined the United Kingdom Government's Science & Innovation Network (UKSIN), based at British Consulate General, Cambridge, Massachusetts. UKSIN promotes U.K. science in the United States as well as fostering U.S.–U.K. collaborations and informing science policy. Her job involved writing reports and organizing meetings and seminars on a wide variety of science topics, skills that will be put to good use at Banbury.

Jan Witkowski and Rebecca Leshan

I have had a wonderful time as the Banbury director. I would never have learned about as many topics nor met such stellar scientists anywhere else. That the job was so enjoyable was also due to the support provided by many people. Since 2009, Hakon Heimer has provided advice and helped organize meetings on topics in neuroscience and mental health. It has been a pleasure to work with him and our fruitful collaboration is exemplified by the 2016 meeting on Nordic genomics and healthcare. In the Banbury Center office, Bea Toliver, Janice Tozzo, and Ellie Sidorenko did a wonderful job, and Michelle Corbeaux and Pat Iannotti continue to do so. Katya Davey and Basia Polakowski welcomed participants

Conversation at the coffee break

as hostesses at Robertson House while Barbara and Jennifer Gordon looked after participants' needs in the dining room. The Audiovisual crew from Meetings and Courses—Herb Parsons, Ed Campodonico, Bill Dickerson, Jonathan Parsons, Ken Orff, and James Whittaker—saw the transition from slides and overheads to digital and coped with all manner of emergencies. Chris McEvoy has acted as watchman as well as groundsman. The departments of Administration, Culinary Services, Facilities, and IT have all contributed to the smooth running of Banbury.

There are three people who have enabled the Banbury Center to flourish. The first, of course, is Charles Robertson, whose generosity in donating the Banbury estate to Cold Spring Harbor Laboratory is the foundation of what we have done. Jim Watson decided to use the estate as a conference center, and his advice to me over all these years has been invaluable. The Center could not have functioned at its high level without his continuing support. I am fortunate that Bruce Stillman shares Jim's enthusiasm for the Banbury program and has continued to support the Center.

2016 in Numbers

The Banbury Center continues to be a busy place. The Conference Room was used for 42 events in 2016, including Banbury Center meetings, courses from the Meetings and Courses Program, the Watson School of Biological Sciences, and CSHL scientists holding retreats at Banbury. There were 574 participants in the Banbury Center meetings, drawn from 30 states, with California, Maryland, Massachusetts, and New York leading the way. The proportion of non-U.S. participants was 18%, coming from 23 countries, the low number continuing to reflect concerns about travel expenses and may be further affected by U.S. immigration policies. Thirty percent of participants were female, a percentage that has been at this level for a number of years.

Using the chalkboard

Looking at the year's meetings, I can see some of the themes that have run through my tenure at Banbury. The Center has held many meetings on what might be called basic research, although regrettably, these have declined recently because of funding difficulties. An example from 2016 was the meeting organized by Hyman Hartman and Temple Smith. Fifty years ago, the 31st Cold Spring Harbor Symposium on Quantitative Biology was devoted to *The Genetic Code*. It was, as Crick wrote in the Symposium volume, an historic occasion. However, he was less sanguine about progress in understanding the structure of the genetic code and its origin. Crick feared that they were heading for "a very unhealthy situation, in that theory will run far ahead of useful experimental facts," as had studies on the genetic code in the 1950s. What was needed was "some way of obtaining more experimental evidence." Crick's wish for more experimental evidence has been amply fulfilled in the 50 years since that historic occasion. Participants in the 2016 Banbury meeting on *Evolution of the Translational Apparatus: Implications for the Origin and History of the Genetic Code* had a wealth of data derived from new findings on the ribosome and the aminoacyl tRNA synthetases.

Banbury has also played a role in helping the development of new fields of research. Previous examples that come to mind are DNA bar coding and RNAi. Similarly, in 2016, *Ancient DNA and Archaeology*, generously supported by the Lehrman Institute, was held to encourage interactions between archaeologists, historians, ancient DNA specialists, and geneticists. One goal was to identify questions, regions, and time periods in which DNA studies would be particularly likely to yield insights not possible with other methods. It did not altogether succeed, but analogies were drawn with the introduction of radiocarbon dating, initially the province of just a few experts. Just as the "radiocarbon revolution" provided archaeologists with an accurate timescale for the past, the "ancient DNA revolution" has the potential to show how human remains—together with their archaeological contexts—relate to present and ancient populations.

Banbury has contributed to plant science by holding annual meetings funded by the contributions of Monsanto and Pioneer Hi-Bred over the years to the Laboratory's Corporate Sponsor

Program, with contributions from other companies. The meetings have covered a wide variety of topics including plant genetics, genomics, and physiology. Crop breeders are hampered by the long time needed for traditional breeding, and the 2016 meeting on *Genomics-Enabled Accelerated Crop Breeding* examined how the new methods for manipulating genes can be used to accelerate the process. These new methods include TALENs and the CRISPR-Cas9 system. Participants reviewed the application of these techniques to a variety of crops including cassava, lettuce, soybean, and tomato. The meeting was especially timely as the U.S. Department of Agriculture had recently declared that mushrooms modified using CRISPR-Cas9 would not be considered to be genetically modified organisms.

I was fortunate to arrive at Banbury at a time when mapping human disease genes was under way, and the human genome project was about to begin. My background was in human molecular genetics, and so I began a series of meetings in that field. Psychiatric genetics was an early topic; in the first flush of enthusiasm for restriction-fragment-length polymorphism (RFLP)-linkage analysis, it was hoped that genes involved with psychiatric disorders would soon be identified. The first of the meetings was *Genetic Approaches to Schizophrenia*, and others followed through the 1990s, but it became clear that psychiatric disorders were a very difficult problem. Nevertheless, progress has been made and genetic counseling is important and useful in psychiatry, even without full knowledge of all the genes involved. The meeting *Genetic Counseling for Psychiatric Disorders: Challenges in the Genomic Era* was held to consider two questions: How can the ever-increasing understanding of the genetics of psychiatric disorders be translated into interventions that improve outcomes for patients and their families? What needs to be done to prepare for the time when exome or even whole-genome sequencing becomes the norm?

Meetings on cancer have been a feature of the Banbury Center from the early meetings on chemical carcinogenesis and environmental hazards. However, it is rather surprising, given the Laboratory's intensive research on DNA tumor viruses throughout the 1970s, that the first Banbury meeting on the molecular genetics of cancer was not held until 1984 (*SV40 Large-T Antigen*). Since then, the application of ever-more-sophisticated techniques has led to ever-increasing knowledge about the nature of cancer. In recent years, there has been an increasing emphasis on metabolic changes in tumor cells, focusing on redox pathways and targeting reactive oxygen species (ROS). This has been shown to be an effective strategy, and participants in the meeting *Making Oxidative Chemotherapy Less Toxic* reviewed the evidence for whether combination therapies may be more effective at killing cancer cells and less damaging to noncancer cells.

The first meeting of 2016 was *After UKCTOCS: Public Messaging on Screening and Early Detection for Ovarian Cancer.* UKCTOCS is the United Kingdom Collaborative Trial of Ovarian Cancer Screening study, which followed more than 200,000 women. The meeting was organized by the U.S. Ovarian Cancer Research Fund Alliance, and participants discussed the implications of the UKCTOCS findings for advising women on the use of multimodal screening for early detection of ovarian cancer. One of the questions posed to the participants was "Do we believe that the UKCTOCS data are sufficiently strong to support a recommendation for population screening for ovarian cancer?" Three questions followed, depending on the answer:

1. If yes, should the recommendation be limited to the population studied in UKCTOCS or expanded or narrowed?
2. If no, should there be an alternative recommendation? What should it be?
3. If it's uncertain, what do we tell people?

The conclusion, published as an editorial in the journal *American Family Physician*, was the answer to question 3, that using multimodal screening was not yet justified.

If genomic medicine is to be successful, we need to know how genetic variants affect an individual's health. This requires sequencing tens of thousands of individuals and then examining

their medical records to correlate their health with their genetic variants. The former, although still not trivial, is no longer an obstacle but relating genetic variants to health is a huge undertaking, requiring comprehensive and accurate medical records. Fortunately, the health systems of the Nordic countries have such records, and the title of the meeting *Studying the Genomic Variation That Underlies Health and Disease: The Unique Contribution of the Nordic Health Systems* captures the essence of the discussions. Participants discussed how the countries could work together and some of the challenges—scientific, medical, and legal—to doing so. The meeting was a great success and led to an influential report and follow-up meetings.

These meetings exemplify the type of meeting for which Banbury is particularly suitable. The Banbury setting is ideal for intense discussions of perhaps controversial topics, discussions of a form that would not be possible in larger, public meetings. Other notable meetings in this category include those on scientific fraud, DNA fingerprinting, public mistrust of immunization, and end of life issues.

Acknowledgments

I have already thanked those who have helped me over the years but there is every reason to repeat myself for those who worked hard in 2016 to keep Banbury running. Michelle Corbeau and Pat Iannotti hold the fort in the Banbury Center office while Basia Polakowski continues to welcome and look after participants in Robertson House. Participants never fail to comment on the beauty of the estate, a tribute to the hard work of Jose Covera, Joe McCoy, and Saul Covera. Culinary Services, Facilities, and the Meetings Office play key roles in the operation of the Center. The meetings would not be the success they are without the contributions of organizers and participants, the generosity of the Laboratory's Corporate Sponsors and the other donors who fund our meetings, and the Laboratory's scientists who continue to support the Center.

Jan A. Witkowski
Executive Director

1988 2017

Jan Witkowski, 30 years at Banbury, 1987–2017

BANBURY CENTER MEETINGS

Date	*Title*	*Organizer(s)*
February 7–9	After UKCTOS: Public Messaging on Screening and Early Detection for Ovarian Cancer	J. Boyd, S. DeFeo, A. Moran, M. Seiden
February 16–19	Studying the Genomic Variation That Underlies Health and Disease: The Unique Contribution of the Nordic Health Systems	O. Andreassen, N. Freimer, L. Groop, H. Heimer, A. Palotie
February 26–March 2	Communicating Science	C. Walther, S. Schedler
March 6–9	Autophagy and Cancer	E. White, R. Amaravadi, A. Kimmelman
March 15–18	STAT3 in Cancer: How Can It be Inhibited?	J. Darnell, D. Levy, G. Stark
April 29–May 1	NIMH Brain Camp VIII	B. Cuthbert, J. Chung
May 15–17	Ancient DNA and Archaeology	D. Reich, T. Higham, S. Pääbo
July 5–8	Measuring and Modeling Quantitative Sequence–Function Relationships	J.B. Kinney, D. Fowler, A. Siepel
August 21–23	Can We Make Animal Models of Human Mental Illness? A Critical Review	E. Nestler, R. McCombie, H. Heimer
September 6–8	Mammalian Brain Cell Diversity and Census	A. Beckel-Mitchener, J. Huang
September 11–14	Making Oxidative Chemotherapy Less Toxic	A. Holmgren, R. Maki, D. Tuveson
September 18–21	Diagnostic Tests for Lyme Disease: A Reassessment	J. Branda, S. Schutzer
October 16–19	Genomics-Enabled Accelerated Crop Breeding	B. Staskawicz, D. Voytas
November 1	The Lustgarten Foundation: Vitamin D Day	R. Evans, P. Sharp, D. Tuveson
November 9–11	Patenting Genes, Natural Products, and Diagnostics: Current Status and Future Prospects	K. Sonnenfeld, H. Sauer, M. Brivanlou
November 13–16	Evolution of the Translational Apparatus and Implication for the Origin of the Genetic Code	H. Hartman, T. Smith
November 30–December 2	Genetic Counseling for Psychiatric Disorders: Challenges in the Genomic Era	J. Austin, F. McMahon
December 4–7	Evolution and Revolution in Anatomic Pathology: Automation, Machine-Assisted Diagnostics, Molecular Prognostics, and Theranostics	J.M. Crawford, P. Mitra, M. Wigler
December 11–14	Developing Gene Editing as a Therapeutic Strategy	A. Wagers, C. Gersbach, J.K. Joung

BANBURY CENTER MEETINGS

After UKCTOS: Public Messaging on Screening and Early Detection for Ovarian Cancer

February 7–9

FUNDED BY **Ovarian Cancer Research Fund Alliance**

ARRANGED BY **J. Boyd,** Florida International University, Miami
S. DeFeo, Ovarian Cancer Research Fund Alliance, New York
A. Moran, Ovarian Cancer Research Fund Alliance, New York
M. Seiden, McKesson Specialty Health, The Woodlands, Texas

The United Kingdom Collaborative Trial of Ovarian Cancer Screening study (UKCTOCS) was designed to provide firm data that can be used as the basis for assessing the value of current methods of early detection of ovarian cancer. The findings were published online in *The Lancet,* December 2015, and will need to be communicated to patients, physicians, and payers, and a discussion about access and reimbursement will need to take place. The goals of this meeting were to review the findings of the UKCTOCS trial and discuss what recommendations Ovarian Cancer Research Fund Alliance might make to its constituency.

S. Skates, B. Levin, C. Chiuzan

Welcoming Remarks and Background: J.A. Witkowski, Cold Spring Harbor Laboratory, and **A. Moran,** Ovarian Cancer Research Fund Alliance, New York

Introduction and Background: J. Boyd, Florida International University, Miami
M. Seiden, McKesson Specialty Health, The Woodlands, Texas

SESSION 1: Addressing the Questions

Chairperson: I. Jacobs, University of New South Wales, Sydney, Australia

U. Menon, University College London, United Kingdom; and S. Skates, Massachusetts General Hospital, Boston: Update on the UKCTOCS trial.

S. Narod, University of Toronto, Canada: The UKCTOCS trial: A closer look.

B. Levin and C. Chiuzan, Columbia University, New York: UKCTOCS: Biostatistical perspectives.

Panel Discussion: Communicating Controversial Public Health Issues to Lay and Medical Audiences

Facilitator: M. Seiden, McKesson Specialty Health, Woodlands, Texas

Panel

M. Ebell, University of Georgia, Athens
A. Ellis, Ovarian Cancer Survivor, White Plains, New York
M. Eiken, Society of Gynecologic Oncology, International Gynecologic Cancer Society, Chicago, Illinois
R. Smith, American Cancer Society, Inc., Atlanta, Georgia
A. Moran, Ovarian Cancer Research Alliance, New York
C. Balas, Ovarian Cancer Research Fund Alliance, New York

Group Consideration of Three Major Questions

1. Do we believe that the UKCTOCS trial results prove that screening prevents deaths from ovarian cancer?

D. Barley

K. Gavin

2. Do we believe that the UKCTOCS data are sufficiently strong to support a recommendation for population screening for ovarian cancer?
3. If we support screening of a population of healthy women, do we support use of the ROCA-based algorithm and the use of Abcodia as the only legitimate screening strategy?

Continued Group Discussion

Group 1: Lay Community
Group 2: Medical Community

SESSION 2: Preparing the Communications

Studying the Genomic Variation That Underlies Health and Disease: The Unique Contribution of the Nordic Health Systems

February 16–19

FUNDED BY **The Norwegian Research Council and NordForsk**

ARRANGED BY **O. Andreassen,** University of Oslo, Norway
N. Freimer, University of California, Los Angeles
L. Groop, Lund University, Malmo, Sweden
H. Heimer, Cold Spring Harbor Laboratory
A. Palotie, Broad Institute, Cambridge, Massachusetts

This meeting examined the possible coordination of medical genomics across Nordic countries, and how best to engage the health systems of the Nordic countries in such cross-national efforts. The meeting brought together data managers, clinical leaders, policy makers, and researchers from the Nordic countries; international researchers who collaborate on projects using Nordic health records; electronic records and data privacy experts, and representatives of funding agencies. The meeting explored critical questions about the potential of combining data sets that include as many as 20 million health records. In addition to scientific questions regarding study design, participants considered legal, ethical, and logistic issues concerning cross-national and international use of health records.

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

Origin of the Meeting: H. Heimer, Cold Spring Harbor Laboratory

C. Stoltenberg, P. Njølstad

K. Hveem, A. Palotie

SESSION 1: Opportunities in Genetics/Genomics

Chairperson: O. Andreassen, University of Oslo, Norway

N. Freimer, University of California, Los Angeles: Deep phenotype data obtained over decades: Can genomics turn past investments into future health?

A. Palotie, Institute for Molecular Medicine, Helsinki, Finland: Special features of Finland for developing genome medicine.

A. Metspalu, University of Tartu, Estonia: Deep sequencing of the Estonian population sample of 2400 subjects—first results.

K. Hveem, Norwegian University of Science and Technology, Levanger, Norway: Perspective from the Nordic cohorts and registries.

A. Addington, National Institute of Mental Health, Rockville, Maryland: Perspective from the NIH.

C. Fox, Merck & Co. Inc., Boston, Massachusetts: Perspective from pharma.

SESSION 2: Opportunities in Data Mining and Informatics

Chairperson: A. Palotie, Institute for Molecular Medicine, Helsinki, Finland

J. Kaprio, University of Helsinki, Finland: Twin registries as a resource in the Nordic countries.

C. Stoltenberg, Norwegian Institute of Public Health, Olso, Norway: MOBA—The Norwegian mother, father, and child cohort: A prospective, population-based health study with nearly 300,000 participants.

S. Brunak, University of Copenhagen, Denmark: Disease trajectories and time-ordered co-morbidities.

E. Hovig, Oslo University Hospital, Norway: Perspective from the Nordic cohorts and registries.

J. Palmgren, Karolinska Institutet, Stockholm, Sweden: Infrastructure for data: Integrating health, lifestyle, and molecular information.

J. Larkin, National Institutes of Health, Bethesda, Maryland: Perspective from the NIH.

M. Sogaard, Pfizer, Inc., New York: Perspective from pharma.

SESSION 3: Opportunities for Clinical and Translational Application of Genetics and Informatics

Chairperson: J. Kaprio, University of Helsinki, Finland

L. Groop, Lund University, Malmö, Sweden: Toward precision medicine in diabetes.

O. Andreassen, University of Oslo, Norway: Neuropsychiatric disorders: Opportunities for prediction and stratification.

N. Stitziel, Washington University School of Medicine, St. Louis, Missouri: Identifying and validating therapeutic targets for cardiovascular disease.

P. Njølstad, University of Bergen, Norway: Monogenic disease: Beacons for identifying therapy-relevant novel causes of complex disorders.

C. Jaquish, National Heart, Lung, and Blood Institute, Bethesda, Maryland: NHLBI precision medicine/whole-genome

A. Jalanko

sequencing program: NHLBI TOPMed (trans-omics for precision medicine).

Q. Li, Janssen Research & Development, LLC, Raritan, New Jersey: Perspective from pharma.

SESSION 4: Breakout Groups: Proposals for Opportunities for Collaborations Across Nordic Countries, between Nordic Countries, and U.S. Investigators and Funding Agencies; Public Private Partnerships

Group 1: Genetics/Genomics, M. Daly, Leader
Group 2: Data Mining/Informatics, E. Hovig, Leader
Group 3: Clinical/Translational, J. Dillner, Leader

SESSION 5: Presentation of Reports of Breakout Groups and Discussion

Chairperson: L. Groop, Lund University, Malmö, Sweden

Group 1: Genetics/Genomics. M. Daly, Leader
Group 2: Data Mining/Informatics, E. Hovig, Leader
Group 3: Clinical/Translational, J. Dillner, Leader

SESSION 6: Developing an Outline for a Position Paper and Discussion of Next Steps

Communicating Science

February 26–March 2

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

ARRANGED BY **C Walther,** Boehringer Ingelheim Fonds, Mainz, Germany
S. Schedler, Boehringer Ingelheim Fonds, Mainz, Germany

The Boehringer Ingelheim Fonds has an international program of support for Ph.D. fellowships, and 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 2016 stay at Banbury was the ninth occasion that they have been here. At Banbury, the fellows receive intensive instruction in matters such as giving presentations and writing papers, topics usually learned by default and often poorly during graduate research.

Introductory Remarks: J.A. Witkowski, Cold Spring Harbor Laboratory

Opening Remarks and All About BIF—Part 1: C. Walther, Boehringer Ingelheim Foundation, Mainz, Germany

K. Achenbach, Boehringer Ingelheim Foundation, Mainz, Germany: Communication: Why and how?

N. LeBrasseur, DNA Medical Communications, New York: Writing techniques and how to structure papers; Writing assignment 1.

B. Tansey, Vanderbilt University, Nashville, Tennessee: Preparing and delivering a scientific talk; PowerPoint presentations, videotaped with replay and feedback.

N. LeBrasseur, DNA Medical Communications, New York: Discussion of writing assignment 1; Writing assignment 2.

N. LeBrasseur, DNA Medical Communications, New York: Image manipulation: Dos and don'ts—A short intro; Return and discussion of writing assignment 2.

J. Carlos Lopez, Roche Innovation Center: Career talk.

K. Ris-Vicari, Katie Ris-Vicari Graphic Design, Bethpage, New York: How to design figures.

C. Walther, Boehringer Ingelheim Foundation, Mainz, Germany: All about BIF: Part 2 and feedback.

Autophagy and Cancer

March 6–9

FUNDED BY **Astellas Pharma Inc., Millennium Pharmaceuticals, Inc., Merck Serono, Novartis, and Presage Biosciences, Inc.**

ARRANGED BY **E. White,** Rutgers Cancer Institute of New Jersey, Brunswick
R. Amaravadi, University of Pennsylvania, Philadelphia
A. Kimmelman, Dana-Farber Cancer Institute, Boston, Massachusetts

Autophagy is a process of cellular self-cannibalization that captures intracellular proteins and organelles and degrades them in lysosomes. Autophagy plays a critical role in human disease, including cancer, and there is evidence that autophagy can be either a tumor suppression or promotion mechanism. There remain many important unanswered questions on the role of autophagy in cancer and participants in the meeting focused on five: The role of autophagy in tumors; autophagy and nutrient sensing signaling; autophagy and metabolism; selective autophagy and nonmacroautophagy mechanisms; and translational/clinical aspects of autophagy modulation.

Introduction: J.A. Witkowski, Banbury Center, Cold Spring Harbor Laboratory

Goals and Objectives: E. White, Rutgers Cancer Institute of New Jersey, New Brunswick

K. Ryan

M. Lotze

SESSION 1: Role of Autophagy in Tumors

Chairperson: A. Kimmelman, Dana-Farber Cancer Institute, Boston, Massachusetts

J. Debnath, University of California, San Francisco: Autophagy in mouse models of breast cancer.

K. Ryan, Beatson Institute, Glasgow, United Kingdom: Pancreatic cancer autophagy.

N. Roy D'Amore, Takeda Oncology, Cambridge, Massachusetts: Atg7 and Vps34 inhibitors.

J. Moscat, Sanford Burnham Prebys Medical Discovery Institute, La Jolla, California: Control of p62 homeostasis by autophagy in cancer.

SESSION 2: Autophagy and Nutrient Sensing Signaling

Chairperson: K. Ryan, Beatson Institute, Glasgow, United Kingdom

E. White, Rutgers Cancer Institute of New Jersey, New Brunswick: Metabolic control of p53 by autophagy.

N. Cosford, Sanford Burnham Medical Research Institute, La Jolla, California: Ulk1 inhibitor development for cancer therapy.

N. Bardeesy, Massachusetts General Hospital, Boston: Lkb1 and nutrient sensing.

J.-L. Guan, University of Cincinnati, Ohio: The role of autophagy in cancer stem cells.

L. Shawver, Cleave Biosciences Burlingame, California: ERAD, UPR, and autophagy; experience with inhibitors of p97.

SESSION 3: Autophagy and Metabolism

Chairperson: E. White, Rutgers Cancer Institute of New Jersey, New Brunswick

A. Kimmelman, Dana-Farber Cancer Institute, Boston, Massachusetts: Ras and pancreatic cancer metabolism.

Y. Guo, Rutgers Cancer Institute of New Jersey, New Brunswick: Autophagy in lung cancer metabolism.

R. Perera, University of California, San Francisco: Transcriptional control of autophagy.

W. Harper, Harvard Medical School, Cambridge, Massachusetts: Autophagy networks.

M. Lotze, University of Pittsburgh, Pennsylvania: Autophagy, HMGB1/RAGE, Ras, and the tumor immune response.

R. Klinghoffer, Presage Biosciences, Seattle, Washington: Not all lysosomal inhibitors are created equal: Direct comparison of antitumor effects in canine sarcoma patients.

SESSION 4: Selective Autophagy and Nonmacroautophagy Mechanisms

Chairperson: J. Debnath, University of California, San Francisco

R. Youle, National Institutes of Health, Bethesda, Maryland: Mechanism of mitophagy.

K. Macleod, University of Chicago, Illinois: Autophagy promotes focal adhesion disassembly and cell motility of metastatic tumor cells through direct interaction of paxillin with LC3.

C. Dorsey, Eli Lilly, Indianapolis, Indiana: Targeting autophagy.

X. Jiang, Memorial Sloan Kettering Cancer Center, New York: Autophagy regulation.

J. Martinsson, Sprint Bioscience, Stockholm, Sweden: Development of selective Vps34 inhibitors.

SESSION 5: Translational/Clinical Aspects of Autophagy Modulation

Chairperson: R. Perera, University of California, San Francisco

R. Amaravadi, University of Pennsylvania, Pennsylvania: Clinical modulation of autophagy with HCQ.

J. Mehnert, Rutgers Cancer Institute of New Jersey, New Brunswick: Autophagy in melanoma.

A. Thorburn, University of Colorado, Denver: Autophagy in brain cancer.

V. Kirkin, Merck Serono, Darmstadt, Germany: How do we fill the current gap in validation of the concept of targeting autophagy in cancer?

J. Goodwin, Novartis, Cambridge, Massachusetts: Is autophagy a therapeutic target in cancer?

General Discussion and Closing Remarks

STAT3 in Cancer: How Can It Be Inhibited?

March 15–18

FUNDED BY **Boston Biomedical, Inc.**

ARRANGED BY **J. Darnell,** The Rockefeller University, New York
D. Levy, New York University School of Medicine, New York
G. Stark, Cleveland Clinic Foundation, Ohio

This meeting brought together an international group of researchers to review what is known of STAT3, its potential as a target in cancer, and what progress has been made in developing therapies. Discussions included talks on current research on the biology of STAT3 (e.g., cancer stem cells and STAT3; mitochondrial role of STAT3; STAT3 as a tumor suppressor) and current understanding of new and previously recognized targets for STAT3 inhibition. There were reports on the use of the newer anti-STAT3 compounds.

Welcoming Remarks: J.A. Witkowski, Banbury Center, and **J. Watson,** Cold Spring Harbor Laboratory

SESSION 1: Cancer Stem Cells and Natural STAT inhibitors

Chairperson: J. Darnell, The Rockefeller University, New York

I. Marie, New York University Medical Center, New York: What do loss-of-function studies teach us about the physiologic role of STAT3?

J. Rich, Lerner Research Institute, Cleveland, Ohio: STAT3 in brain tumor stem cells.

M. Venere, Ohio State University, Columbus: Converging on NF-κB to target cancer stem cells.

H. Rogoff and A. Yang, Boston Biomedical, Inc., Cambridge, Massachusetts: Targeting cancer stemness through blocking STAT3.

K. Shuai, University of California, Los Angeles: Mechanisms to inhibit STAT signaling through PIAS proteins.

G. Stark, K. Struhl

D. Levy, J. Bromberg, J. Turkson

J. Babon, Walter and Eliza Hall Institute of Medical Research, Victoria, Australia: Mimicking the action of SOCS3: A potent physiological inhibitor of STAT3 signaling.

SESSION 2: Mitochondrial Connection, Genetics, and Mutations

Chairperson: G. Stark, Cleveland Clinic Foundation, Ohio

T. Benveniste, University of Alabama, Birmingham: The role of CK2 and STAT3 in cancer: Impact on the tumor microenvironment.

G. Inghirami, Weill Cornell Medical College, New York: Activating mutations of the JAK/STAT3 pathway and T-cell transformation.

D. Levy, New York University School of Medicine, New York: The mitochondrial role of STAT3 in cancer.

J. Milner, National Institute of Allergy & Infectious Diseases, Bethesda, Maryland: Monogenic disorders due to germline mutations in STAT3 and other STATs: Lessons learned from gain, loss, and cross-talk.

J. Hart, Scripps Research Institute, La Jolla, California: Non-kinase inhibitors of STAT3.

C. Mertens, The Rockefeller University, New York: Mutations in the linker domain affect phospho STAT3 function and suggest targets for interrupting STAT3 activity.

SESSION 3: Pharmacologic Inhibitors: Old and New

Chairpersons: D. Levy, New York University School of Medicine, New York, and **J. Grandis**, University of California, San Francisco

J. McMurray, M.D. Anderson Cancer Center, Houston, Texas: Inhibition of STAT6 blocks aberrant Th2 signaling in allergic asthma.

J. Turkson, University of Hawaii Cancer Center, Honolulu: Targeting JAK/STAT signaling pathways for cancer therapy.

J. Grandis, University of California, San Francisco: A decoy oligonucleotide approach to STAT3 inhibition.

C. Li, Boston Biomedical Inc., Cambridge, Massachusetts: Clinical development of napabucasin (BB608), a first-in-class cancer stemness inhibitor that works by blocking STAT3.

C. Catapano, Institute of Oncology Research, Bellinzona, Switzerland: How to kill a cancer cell: Insights from novel small-molecule inhibitors of STAT3.

D. Placantonakis, New York University School of Medicine, New York: The overlap in basic ideas in management of glioblastoma multiforme.

P. McCoon, AstraZeneca Pharmaceuticals, Waltham, Massachusetts: Clinical biomarkers of a STAT3 antisense oligonucleotide, AZD9150, suggest an immune-modulatory role in tumors.

Y. Kanno, NIAMS, National Institutes of Health, Bethesda, Maryland: Targeting cytokine signaling by Jakinibs to control genomic switches.

D. Frank, Dana-Farber Cancer Institute, Boston, Massachusetts: Targeting the transcriptional function of STAT3: From the lab to clinical trials.

M. Jackson, Case Western Reserve University, Cleveland, Ohio: Cooperative STAT3-SMAD3 signaling drives cancer cell plasticity.

K. Struhl, Harvard Medical School, Boston, Massachusetts: Role of STAT3 and STAT3-mediated transcriptional regulatory circuits in cancer.

T. Miller, IC-MedTech, Las Vegas, Nevada: Can ROS prevent STAT3 phosphorylation?

SESSION 4: Caution and Discussion

Chairperson: J. Darnell, The Rockefeller University, New York

G. Stark, Cleveland Clinic Foundation, Ohio: Modulation of STAT3-dependent signaling by EGFR, induction of U-STAT3, and lysine methylation.

J. Bromberg, Memorial Sloan Kettering Cancer Center, New York: Targeting JAK and Stat 3 in solid tumors: Clinical and preclinical observations.

L. Kenner, Ludwig Boltzmann Institute Cancer, Vienna, Austria: IL-6/Stat3 in diagnosis and treatment of prostate cancer.

SESSION 5: General Discussion and Summary of Key Points for Further Research

J. Darnell, The Rockefeller University, New York: Thoughts and questions on the role of STAT3 in cancer.

I. Marie

J. Darnell, U. Vinkemeier

NIMH Brain Camp VIII

April 29–May 1

FUNDED BY **National Institute of Mental Health, NIH**

ARRANGED BY **B. Cuthbert,** National Institute of Mental Health, Bethesda, Maryland
J. Chung, National Institute of Mental Health, Bethesda, Maryland

Cold Spring Harbor Laboratory is renowned worldwide for its education programs, from high school level to the highest professional levels. One of the Banbury Center's contributions is 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 came as guest speakers to the meeting. The goal of the series of meetings is to develop a neuroscience curriculum that can eventually be shared with psychiatry training programs around the country.

SESSION 1

B. Cuthbert, National Institute of Mental Health, Bethesda, Maryland: Welcome and Introductions.
M. Pao, National Institute of Mental Health, Bethesda, Maryland: Brief history of the NIMH camp.
S. Hollingsworth Lisanby, National Institute of Mental Health, Bethesda, Maryland: From discovery to recovery: Transforming the practice of psychiatry through translation.

SESSION 2

A. Raznahan, National Institute of Mental Health, Bethesda, Maryland: A genetics-first approach to parsing the biology of neurodevelopmental disorders.
A. Molofsky, University of California, San Francisco: Psychiatric diseases from a glial cell perspective.
A. Etkin, Stanford University, California: Neural circuits as substrates of mental illness and targets for therapeutics.

C. Tamminga, University of Texas Southwestern Medical Center, Dallas: Psychosis as a learning and memory disorder: A dimensional approach.

J. Conn, Vanderbilt University, Nashville, Tennessee: Allosteric modulators of muscarinic acetylcholine receptors as a novel approach for treatment of schizophrenia.

SESSION 3

B. Stevens, Harvard University, Boston, Massachusetts: Pruning synaptic circuits: New mechanisms and implications in neuropsychiatric disorders.

Ancient DNA and Archaeology

May 15–17

FUNDED BY **Lehrman Institute, New York**

ARRANGED BY **D. Reich,** Harvard Medical School, Boston, Massachusetts
T. Higham, University of Oxford, United Kingdom
S. Pääbo, Max-Planck-Institute for Evolutionary Anthropology, Leipzig, Germany

Analysis of DNA extracted from ancient remains is transforming studies of the origins of modern humans, human migrations, and history, as well as related fields such as the domestication of plants and animals. The power of ancient DNA to supplement paleontological and archaeological studies may in some respects be compared with radiocarbon dating. Just as the "radiocarbon revolution" provided archaeologists with an accurate timescale for the past, the "ancient DNA revolution" has the potential to show how human remains—and by extension their archaeological contexts—relate to present and ancient populations. To realize this potential, it will be necessary over the next ten years to make DNA technologies readily accessible to archaeologists. This meeting was held to discuss how this can best be achieved.

Welcoming Remarks and Background: J.A. Witkowski, Banbury Center, Cold Spring Harbor Laboratory

E. Banffy

S. Pääbo, N. Patterson

SESSION 1: The Big Questions

S. Pääbo, Max-Planck-Institute for Evolutionary Anthropology, Leipzig, Germany: The current state of ancient DNA: What can be done and what can't.

K. Kristiansen, University of Gothenburg, Göteberg, Sweden: What can archaeology contribute to genetics and vice versa?

Discussion

Moderators: T. Higham, University of Oxford, Oxford, United Kingdom, and **D. Reich**, Harvard Medical School, Boston, Massachusetts: What can we learn with archaeogenetics? What are the big questions?

SESSION 2: Moore's Law of Ancient DNA: The 2012–2015 Methods Revolution

M. Meyer, Max-Planck-Institute for Evolutionary Anthropology, Leipzig, Germany: Going deep in time: Denisova and Sima.

R. Pinhasi, University College Dublin, Ireland: Leveraging osteology, histology, and anatomy to optimize yields.

D. Reich, Harvard Medical School, Boston, Massachusetts: Industrial scale ancient DNA.

Discussion

Moderators: J. Krause, Max-Planck-Institute for the Science of Human History, Jena, Germany, and **D. Bradley**, Trinity College Dublin, Dublin, Ireland

SESSION 3: How Can Geneticists Provide Useful Information to Archeologists?

S. Pääbo, Max-Planck-Institute for Evolutionary Anthropology, Leipzig, Germany: What could a service facility for DNA look like?

T. Higham, University of Oxford, United Kingdom: How does a state-of-the-art radiocarbon service facility work?

J. Mountain, 23andMe, Mountain View, California: How does 23andMe make genetic results comprehensible?

Discussion

Moderators: D. Reich, Harvard Medical School, Boston, Massachusetts, and **D. Meltzer,** Southern Methodist University, Dallas, Texas: How can geneticists make ancient DNA an accessible tool for archaeologists? What can genetics provide to archaeologists on a routine basis? What is archaeologically useful? What would a useful report look like? Is there a way for archaeologists and geneticists to collaborate better at the outset?

SESSION 4: How Can Archaeologists Distinguish between What's Solid and Not?

M. Meyer, Max-Planck-Institute for Evolutionary Anthropology, Leipzig, Germany: The cases of Hoyo Negro and the early Neolithic British wheat.

D. Reich, Harvard Medical School, Boston, Massachusetts: Why many published ancient DNA findings are false.

Discussion

Moderators: D. Meltzer, Southern Methodist University, Dallas, Texas, **D. Anthony**, Hartwick College, Oneonta, New York, and **K. Kristiansen**, University of Gothenburg, Göteberg, Sweden: How can archaeologists distinguish between what's solid and not? What are the questions archaeologists should routinely ask of geneticists in regard to their analyses and results?

SESSION 5: Challenge Areas: A Genetics Perspective

J. Krause, Max-Planck-Institute for the Science of Human History, Jena, Germany: Ancient pathogen genomics.

B. Shapiro

B. Shapiro, University of California, Santa Cruz: Learning about human history using megafaunal ancient DNA.

G. Larson, University of Oxford, United Kingdom: Domestication.

Discussant-Led Conversation: N. Boivin, University of Oxford, United Kingdom, **D. Fuller,** University College London, United Kingdom, and **N. Patterson,** Broad Institute, Cambridge, Massachusetts: What opportunities exist for collaboration between geneticists and archaeologists?

SESSION 6: How Can Archeologists Help Geneticists?

Moderators: E. Banffy, German Archaeological Institute, Frankfurt, Germany, **D. Anthony,** Hartwick College, Oneonta, New York, and **D. Meltzer,** Southern Methodist University, Dallas, Texas.

Topics for Consideration:

How can we improve recovery from challenging areas?

How do we address issues of sampling, conservation, and destruction of material (e.g., petrous bones)?

Can archaeologists reduce contamination on site during excavation?

How can we best frame archaeological problems in a manner testable with DNA?

Pots aren't people/climate is not a deus ex machina: How can archaeologists help geneticists avoid archaeologically naïve interpretations and explanations?

SESSION 7: How Should We Overcome the Barriers between Disciplines?

Topics for Consideration: How should we overcome the barriers between disciplines (e.g., lack of comparable training, cross-disciplinary comprehension, few common journals, and sparse interaction) and improve communication?

What steps can be taken to make interactions between archaeologists and geneticists more productive?

Should we initiate a joint community project?

Moderators: T. Higham, University of Oxford, United Kingdom, and **D. Reich**, Harvard Medical School, Boston, Massachusetts: List and review ideas of all groups. Develop an outline for a white paper or opinion piece.

Final Comments

Measuring and Modeling Quantitative Sequence–Function Relationships

July 5–8

FUNDED BY **The Simons Center for Quantitative Biology, Cold Spring Harbor Laboratory**

ARRANGED BY **J.B. Kinney,** Cold Spring Harbor Laboratory
D. Fowler, University of Washington, Seattle, Washington
A. Siepel, Cold Spring Harbor Laboratory

Understanding how DNA sequence relates to function is a fundamental problem in biology that is becoming increasingly acute as more organisms and individuals are sequenced. A variety of massively parallel assays now make it possible to measure sequence–function relationships with unprecedented resolution and quantitative precision. At the same time, advances in our theoretical understanding of sequence–function relationships have resulted in increasingly accurate models. However, current efforts are scattered across multiple disciplines including gene regulation, protein science, and evolution. This meeting gathered leading experimentalists and theorists to discuss unifying disparate approaches for studying quantitative sequence–function relationships and to delineate important outstanding problems in this emerging area of biology.

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

Open Discussion I: Introduction and Meeting Goals
Chairperson: J. Kinney, Cold Spring Harbor Laboratory

J. Kinney, A. DePace

A. Keating, J. Thornton, M. Bulyk

SESSION 1

Chairperson: G. Stormo, Washington University School of Medicine, St. Louis, Missouri

M. White, Washington University School of Medicine, St. Louis, Missouri: The not-so-simple consequence of a simple *cis*-regulatory grammar.

M. Bulyk, Harvard Medical School, Boston, Massachusetts: Survey of variation in human transcription factors reveals prevalent DNA-binding changes.

R. Gordân, Duke University School of Medicine, Durham, North Carolina: Quantitative TF-DNA-binding models explain a large fraction of gene expression variation.

M. Maurano, NYU Institute for Systems Genetics, New York: Decoding human regulatory variation: Pinpointing trait associations and functional noncoding variant.

R. Rohs, University of Southern California, Los Angeles: Quantitative modeling of TF-DNA binding: Beyond DNA shape toward biophysical features.

SESSION 2

Chairperson: B. Frey, University of Toronto, Canada

G. Stormo, Washington University School of Medicine, St. Louis, Missouri: Transcription factor specificity and cooperativity.

H. Bussemaker, Columbia University, New York: Learning protein–DNA recognition models from sparse sequencing data.

J. Kinney, Cold Spring Harbor Laboratory: Quantitative modeling of sequence–function relationships.

SESSION 3

Chairperson: A. DePace, Harvard Medical School, Boston, Massachusetts

B. Frey, University of Toronto, Canada: Bridging the genotype–phenotype gap using quantitative sequence-to-molecular phenotype models.

R. Das, Stanford University School of Medicine, California: Testing computational models of RNA structure/function.

M. Noyes, NYU Institute for Systems Genetics, New York: Capturing the low end of affinity.

SESSION 4

Chairperson: S. Kosuri, University of California, Los Angeles

F. Roth, University of Toronto, Canada: Potential for exhaustive atlases of functional missense variation for most human disease genes.

J. Thornton, University of Chicago, Illinois: Evolutionary determinants of DNA recognition in an ancient transcription factor.

A. Keating, Massachusetts Institute of Technology, Cambridge: High-throughput, quantitative analysis of protein–protein interactions.

R. Sun, University of California, Los Angeles: Quantitative viral genomics at single-nucleotide resolution.

D. Fowler, University of Washington, Seattle: Large-scale functional assessment of variants for genome interpretation.

Open Discussion II: New Technologies and Needed Resources

Chairperson: D. Fowler, University of Washington, Seattle

SESSION 5

Chairperson: R. Phillips, California Institute of Technology, Pasadena

S. Kosuri, University of California, Los Angeles: How do we design the best 10,000 reporters to differentiate hypotheses for how sequence determines function?

A. Abate, University of California, San Francisco: High-density sequence function mapping of an enzyme with droplet-based microfluidics.

J. Taipale, Karolinska Institutet, Huddinge, Sweden: Genome-wide analysis of protein–DNA interactions.

SESSION 6

Chairperson: M. Laub, Massachusetts Institute of Technology, Cambridge

S. Kosuri

R. Phillips, California Institute of Technology, Pasadena: Discovering the rules of regulation in biology's best-understood organism.

G. Tkačik, Institute of Science and Technology Austria, Klosterneuburg, Austria: Evolutionary and biophysical constraints on the regulatory sequence.

A. Walczak, Ecole Normale Supérieure, Paris, France: High-throughput measurement of antigen-antibody affinity.

SESSION 7

Chairperson: F. Roth, University of Toronto, Canada

M. Laub, Massachusetts Institute of Technology, Cambridge: Mapping the sequence space of bacterial signaling proteins.

R. Ranganathan, University of Texas Southwestern Medical Center, Dallas: The evolutionary design of proteins.

J. Bloom, Fred Hutchinson Cancer Research Center, Seattle, Washington: Using measurements in the lab to understand evolution in nature.

A. DePace, Harvard Medical School, Boston, Massachusetts: Precision and plasticity in animal transcription.

D. McCandlish, University of Pennsylvania, Philadelphia: Comprehensible models of higher-order interactions.

A. Siepel, Cold Spring Harbor Laboratory: Inference of fitness consequences for regulatory mutations.

Open Discussion III: Big Challenges and Future Directions

Chairperson: A. Siepel, Cold Spring Harbor Laboratory

Can We Make Animal Models of Human Mental Illness? A Critical Review

August 21–23

FUNDED BY **The Stanley Research Foundation**

ARRANGED BY **E. Nestler,** Icahn School of Medicine, Mount Sinai, New York
R. McCombie, Cold Spring Harbor Laboratory
H. Heimer, Cold Spring Harbor Laboratory

The use of animal models in studies of psychiatric disorders is increasingly controversial. There are arguments, on the one hand, that although imperfect, they are indispensable for research and, on the other hand, that because they are imperfect, they are at best inadequate and at worst misleading. The participants in this meeting reviewed critically and dispassionately the state of this field and covered topics such as current models and their effectiveness and how to integrate genetic and environmental factors in animal models; discussed how the new gene-editing techniques might be used in this field; assessed arguments that only primate models are valid, and discussed the implications of this approach.

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

L. Young

L. Monteggia, S. Morris

SESSION 1: Introduction to Critical Questions

Chairperson: H. Heimer, Cold Spring Harbor Laboratory

E. Nestler, Icahn School of Medicine at Mount Sinai, New York: Where have we gone wrong in the past that has limited our animal models?

S. Morris, National Institute of Mental Health, Bethesda, Maryland: Animal models of…what? The RDoC perspective.

SESSION 2: Social Processing

Chairperson: A. Grace, University of Pittsburgh, Pennsylvania

J. Crawley, MIND Institute, University of California Davis, Sacramento: Translational mouse models of autism to understand causes and discover therapeutics.

A. Mills, Cold Spring Harbor Laboratory: Modeling 16p11.2 copy-number variations.

L. Young, Emory University, Atlanta, Georgia: Oxytocin, social attachment, and empathy-related behaviors in monogamous prairie voles: Implications for autism.

L. Monteggia, University of Texas Southwestern Medical Center, Dallas: Mechanism of rapid antidepressant action.

Z.-L. Qiu, Institute of Neuroscience, Shanghai, China: The non-human primate for autism: What can we learn from monkey?

SESSION 3: Negative Valence Systems

Chairperson: B. Moghaddam, University of Pittsburgh, Pennsylvania

A. Grace, University of Pittsburgh, Pennsylvania: The MAM developmental disruption model of schizophrenia.

N. Kalin, University of Wisconsin, Madison: Translating molecular models in non-human primates to human anxiety disorders.

S. Russo, Mount Sinai School of Medicine, New York: Can we model domains of behavior relevant to personality disorders in mice?

B. Dias, Yerkes National Primate Research Center, Atlanta, Georgia: Using olfaction to study intergenerational influences of stress.

SESSION 4: Cognitive Systems

Chairperson: A. Mills, Cold Spring Harbor Laboratory

S. Haber, University of Rochester, New York: From primate anatomy to human neuroimaging: Linking circuits to psychiatric disease.

C. Kellendonk, Columbia University, New York: Using human brain imaging studies as a guide toward animal models of schizophrenia.

F. Lee, Weill Cornell Medical College, New York: Genetic mouse models of altered anxiety-related behaviors.

C. McClung, University of Pittsburgh, Pennsylvania: The Clock mutant mice: A complex model resembling bipolar disorder.

SESSION 5: Positive Valence Systems

Chairperson: C. Kellendonk, Columbia University, New York

E. Nestler, Icahn School of Medicine, Mount Sinai, New York: Reward circuitry in drug and depression models.

Y. Shaham, IRP-NIDA, Baltimore, Maryland: Incubation of drug craving after choice-based voluntary abstinence: Implications for current "gold standard" animal models of addiction.

R. Carelli, University of North Carolina, Chapel Hill: When a good taste turns bad: Modeling negative affect and natural reward devaluation by cocaine.

SESSION 6: Orthogonal Dimensions

Chairperson: S. Haber, University of Rochester, New York

Sex Differences

T. Bale, University of Pennsylvania, Philadelphia: Similar to cancer, thinking of neuropsych disease as multiple hits that may begin at the germ cell stage.

J. Becker, University of Michigan, Ann Arbor: Sex differences and rodent models of human mental illness.

Genes, Environment, Development

J. Waddington, Royal College of Surgeons, Dublin, Ireland: Closing the translational gap between animal models and the clinical reality of mental illness: The exemplar of dimensions of psychopathology, G × E and G × G interactions, in mutant mouse models of psychosis.

B. Moghaddam, University of Pittsburgh, Pennsylvania: How to integrate genetic and environmental factors in animal models.

M. Meaney, McGill University, Montreal, Canada: Gene x environment designs in animal models.

SESSION 7: Discussion Session

Chairperson: E. Nestler, Mount Sinai School of Medicine, New York

Review of important points from previous sessions.

Consensus statement or article?

C. Kellendonk, S. Haber

Mammalian Brain Cell Diversity and Census

September 6–8

FUNDED BY **National Institute of Mental Health, NIH**

ARRANGED BY **A. Beckel-Mitchener,** National Institute of Mental Health, Bethesda, Maryland
J. Huang, Cold Spring Harbor Laboratory

The objective of this meeting was to initiate discussions among international groups with common interests in identifying, classifying, and characterizing cell types in the vertebrate brain. Cells are essential components that make up the circuitry underlying complex function, and better classification of the functional cell classes that are present in the brain will yield valuable results providing an important foundation for systems-based studies. A detailed classification of the variety of cell types present will broaden our understanding of the brain and enable the manipulation of specific cells and circuits. The primary goal of the workshop was to discuss the potential for coordinating the production of broad reference cell catalogs for the vertebrate (mammalian) brain.

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

Introduction: A. Beckel-Mitchener, National Institute for Mental Health Bethesda, Maryland

G. Feng, J. Huang

W. Koroshotz, J. Eberwine

SESSION 1: Cell Type

Moderator: S. Hill, Ecole Polytechnique Fédérale de Lausanne, Geneva, Switzerland

C. Koch, Allen Institute for Brain Science, Seattle, Washington: Integrating distinct data modularities to derive cell types.

S. Linnarssen, Karolinska Institutet, Stockholm, Sweden: Cell-type discovery in mouse developing and adult nervous system.

J. Huang, Cold Spring Harbor Laboratory: Transcriptional definition of cortical GABAergic neuron types.

J. Ngai, University of California, Berkele: Illuminating cellular diversity in the nervous system.

K. Harris, University College London, United Kingdom: New algorithms for scRNA-Seq data, applied to classification of CA1 and V1 interneurons.

A. Regev, Broad Institute of MIT and Harvard, Cambridge, Massachusetts: Case studies toward a cell atlas of neurons.

SESSION 2: Connectome

Moderator: Y. Yao, National Institute of Mental Health, Rockville, Maryland

P. Osten, Cold Spring Harbor Laboratory: Tools for automated mapping of brain cell density, morphology, and connectivity.

H. Dong, University Southern California, Los Angeles: Mouse Connectome Project: Bridging macro-, meso-, and micro-scales.

E. Callaway, Salk Institute for Biological Studies, La Jolla, California: Improved monosynaptic neural circuit tracing using engineered rabies virus glycoprotein variants.

H. Zeng, Allen Institute for Brain Science, Seattle, Washington: Multiscale, integrated connectomics among cell types in local and global circuits.

SESSION 3: Technology

Moderator: J. Huang, Cold Spring Harbor Laboratory

Q. Luo, Huazhong University of Science and Technology, Wuhan, China: Visible brain-wide networks at single neuron resolution with landmarks.

J. Eberwine, University of Pennsylvania, Philadelphia: Subcellular single-neuron genomics.

K. Zhang, University of California, San Diego, La Jolla: Methods for cell-type classification, annotation, and spatial mapping.

SESSION 4: Partnership: General Discussion

Discussion Leaders: W. Koroshetz, National Institute of Neurological Disorders and Stroke, Bethesda Maryland.

S. Hill, Ecole Polytechnique Fédérale de Lausanne, Geneva, Switzerland,

C. Koch, Allen Institute for Brain Science, Seattle, Washington, and

G. Feng, Massachusetts Institute of Technology, Cambridge

SESSION 5: Big Brain

Moderator: C. Koch, Allen Institute for Brain Science, Seattle, Washington

H. Zeng

T. Shimogori, RIKEN BSI, Saitama, Japan: Gene expression atlas of marmoset brain.

G. Feng, Massachusetts Institute of Technology, Cambridge: Genome-editing in primates.

E. Lein, Allen Institute for Brain Science, Seattle, Washington: Multimodal characterization and classification of cell types in human neocortex.

A. Kriegstein, University of California, San Francisco: Origins of cell diversity in the developing human neocortex.

C. Walsh, Harvard Medical School, Boston, Massachusetts: Cell-type-specific splicing regulates neurogenesis in developing cerebral cortex.

SESSION 6: Data Integration and Visualization

Moderator: K. Harris, University College London, United Kingdom

G. Ascoli, George Mason University, Fairfax, Virginia: Draft neuron census based on axonal/dendritic locations.

M. Hawrylycz, Allen Institute For Brain Science, Seattle, Washington: Digital atlases and resources for a mammalian brain cell census.

S. Hill, Ecole Polytechnique Fédérale de Lausanne, Geneva, Switzerland: A data-driven knowledge space for single cells.

Final General Discussion

Making Oxidative Chemotherapy Less Toxic

September 11–14

FUNDED BY **Northwell Health–Cold Spring Harbor Lab Partnership**

ARRANGED BY **A. Holmgren,** Karolinska Institute, Stockholm, Sweden
R. Maki, Northwell Health Cancer Institute, Lake Success, New York
D. Tuveson, Cold Spring Harbor Laboratory

Many effective anticancer drugs are known to induce cell cycle arrest, or kill tumors by increasing oxidative pressure on the tumor through the production of reactive oxygen species (ROS). ROS function as second messengers controlling cell proliferation and differentiation in cancer cells. Tight control of ROS is critical for biological processes in normal cells for regulating gene expression and protein translation, as well as protein–protein interactions and ATP production. However, oxidizing strategies useful in oncology such as chemotherapy and radiation lack selectivity, producing dose-limiting toxicities that prevent them from reaching their full therapeutic potential. Bursts of ROS that specifically target cancer cells could prove beneficial for patients if untoward toxicity can be minimized. This meeting discussed new strategies for making oxidative and other chemotherapies less toxic.

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

SESSION 1: New Ways That Redox Regulates Cancer Cells

Chairperson: M. Espey, National Cancer Institute, Rockville, Maryland

D. Tuveson and C. Chio, Cold Spring Harbor Laboratory: NRF2 and mRNA translation.

L. Cantley, Weill Cornell Medical College, New York: ROS inhibits glycolysis.

SESSION 2: Metformin and Improved Cancer Treatments

Chairperson: D. Tuveson, Cold Spring Harbor Laboratory

K. Struhl, Harvard Medical School, Boston, Massachusetts: Can metformin permit the use of lower doses of oxidative chemotherapy?

M. Pollak, McGill University, Montreal, Quebec, Canada: Metformin and therapy.

SESSION 3: Balancing ROS Efficacy and Toxicity

Chairperson: R. Maki, Northwell Health Cancer Institute, Lake Success, New York

T. Pardee, Wake Forest Baptist Medical Center, Winston-Salem, North Carolina: Targeting the TCA cycle in cancer to increase response to therapy.

P. Roberts, G1 Therapeutics, Research Triangle Park, North Carolina: Protecting the bone marrow and immune system from cytotoxic drugs during cancer treatment.

C. Li, Boston Biomedical Inc., Cambridge, Massachusetts: STAT3 drugs in cancer.

P. Bingham, Stony Brook University, New York: Selectively targeting tumor mitochondrial metabolism synergizes with traditional oxidative chemotherapies.

General Discussion Highlighting Key Points

M. Espey, National Cancer Institute, Rockville, Maryland, and **R. Maki,** Northwell Health Cancer Institute, Lake Success, New York

SESSION 4: STAT3, Redox and Cancer

Chairperson: D. Frank, Dana-Farber Cancer Institute, Boston, Massachusetts

J. Bromberg, Memorial Sloan Kettering Cancer Center, New York: Reversing resistance to targeted therapies.

D. Frank, Dana-Farber Cancer Institute, Boston, Massachusetts: The effect of redox-active molecules on oncogenic signaling pathways.

D. Levy, New York University School of Medicine, New York, and M. Isabelle, New York University Medical Center, New York: Mitochondrial STAT3 and redox stress.

R. Pethig, The University of Edinburgh, Scotland: A summary of some studies (with Albert Szent-Györgyi) of the quenching of ascorbate/semiquinone free radicals by Ehrlich ascites tumor cells.

SESSION 5: Vitamin C, K, and Others in Cancer Therapy

Chairperson: A. Holmgren, Karolinska Institute, Stockholm, Sweden

S. Coutts, IC-MedTech, Santa Fe, New Mexico, and T. Miller, IC-MedTech, Las Vegas, Nevada: Apatone: Basic science to clinic.

J. Verrax, APB Belgian Pharmaceutical Association, Brussels, Belgium: Mechanisms involved in the anticancer properties of Apatone.

D. Neal, Summa Health, Akron, Ohio: The beginning for Apatone.

A. Holmgren, Karolinska Institute, Stockholm, Sweden: Apatone in cancer treatment: Role of replicative stress following oxidative effects on ribonucleotide reductase and its electron donors thioredoxin and glutathione.

L. Trotman, Cold Spring Harbor Laboratory: Apatone in metastatic prostate cancer.

General Discussion Highlighting Key Points

A. Holmgren, Karolinska Institute, Stockholm, Sweden

SESSION 6: Translation of Redox Therapies to the Clinic

Chairperson: G. Raptis, Northwell Health Cancer Institute, Lake Success, New York

D. Lamm, B.C.G. Oncology, P.C., Phoenix, Arizona: Urothelial carcinoma: The stepchild that could lead the way.

L.J. Hoffer, Lady Davis Institute for Medical Research, Montreal, Canada: Redox clinical trials.

T. Miller, IC-MedTech, Las Vegas, Nevada: Regulatory affairs of ROS clinical trials.

W. Isacoff, University of California, Los Angeles: Discussion of clinical trial development.

L. Cantley, J. Bromberg

D. Levy, C. Li, J. Watson

Diagnostic Tests for Lyme Disease: A Reassessment

September 18–21

FUNDED BY **Global Lyme Alliance, Greenwich, Connecticut**

ARRANGED BY **J. Branda,** Harvard University, Boston, Massachusetts
S. Schutzer, Rutgers, The State University of New Jersey, Newark

Lyme disease, caused by *Borrelia burgdorferi*, is the number one tick-borne disease in the United States and Eurasia. Accurate and unambiguous diagnosis of infections is not only important for the individual patient, but also essential for providing objective evidence of infections for subjects to be enrolled in clinical trials and to monitor the effectiveness of new therapies. The current diagnostic test was established in 1994 at the Dearborn Conference. However, new technologies for detecting microbial infections have been developed over the past 22 years, and this was an excellent time to review the current state of laboratory diagnosis of Lyme disease and to examine whether any of the more-recently developed techniques might be useful. This meeting brought experts in Lyme disease diagnostics together with experts developing tests for other emerging infections. The goal was to end the meeting with a clearer picture of what can be done to improve Lyme disease diagnosis.

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

Goals and Objectives: J. Branda, Massachusetts General Hospital, Boston
S. Schutzer, Rutgers New Jersey Medical School, Newark, New Jersey

SESSION 1: Historical Perspective and Current Approaches to Serologic Testing for Lyme Disease

Chairperson: J. Branda, Massachusetts General Hospital, Boston

A. Steere, Massachusetts General Hospital, Boston: Origin and overview of current serologic testing approach: Strengths of standard serologic testing.

R. Dattwyler, New York Medical College, New York: New-generation serologic tests.

SESSION 2: Recent Advances in Serologic Testing for Lyme disease

Chairperson: A. Steere, Massachusetts General Hospital, Boston

W. Robinson, Stanford University School of Medicine, California: Limitations of standard serologic testing; areas for improvement.

J. Branda, Massachusetts General Hospital, Boston: Variations on two-tiered testing.

M. Kintrup, Viramed Biotech AG, Planegg, Germany: Microchip platform in use for serologic testing.

SESSION 3: New Technologies and Approaches to Lyme Disease Diagnostics: Serologic Testing

Chairpersons: A. Marques, National Institute for Allergies & Infectious Diseases, Bethesda, Maryland, and **E. Fikrig,** Section of Infectious Diseases, Yale University School of Medicine, New Haven, Connecticut

M. Schriefer, Center of Disease Control and Prevention, Ft. Collins, Colorado: CDC experience with modified two-tiered testing protocols.

M. Gomes-Solecki, University of Tennessee Health Sciences Center, Memphis: Issues related to multiplexed assays, illustrated by lab-on-a-chip point of care device.

A. Steere, Massachusetts General Hospital, Boston: Detection of autoantibodies as biomarkers of *B. burgdorferi* infection.

SESSION 4: New Technologies and Approaches to Lyme Disease Diagnostics: Molecular Diagnostics

Chairpersons: M. Ilias, National Institute for Allergies and Infectious Diseases, Rockville, Maryland, and **S. Schutzer,** Rutgers New Jersey Medical School, Newark, New Jersey

T. Lowery, T2 Biosystems, Lexington, Massachusetts: High-sensitivity culture-free detection with T2MR for sepsis and Lyme disease.

T. Slezak, Lawrence Livermore National Laboratory Livermore, California: Targeted sequencing for microorganism detection.

E. Mongodin, University of Maryland, Baltimore, Maryland: Whole-genome sequencing to detect microorganisms.

L. Liotta, George Mason University, Manassas, Virginia, and S. Schutzer, Rutgers New Jersey Medical School, Newark: Sample concentration/enrichment technologies.

J. Boyle, Qiagen, Inc., Germantown, Maryland: Hot topics for further discussion.

SESSION 5: Adoption of New Diagnostic Methods for Other Infectious Diseases

Chairpersons: M. Gomes-Solecki, University of Tennessee Health Sciences Center, Memphis, and **A. Marques,** National Institute for Allergies & Infectious Diseases, Bethesda, Maryland

S. Wong, New York State Department of Health, Albany, New York: Public health diagnostic response to emerging pathogens.

M. Schriefer, Center of Disease Control and Prevention, Ft. Collins, Colorado: CDC experience with modified two-tiered testing protocols.

B. Branson, Centers for Disease Control and Prevention, Atlanta, Georgia: Adoption of new HIV testing strategies: How we did it.

SESSION 6: Pathways to Adoption of New Lyme Disease Diagnostic Approaches

Chairperson: M. Lewinski, Roche Molecular Systems, Inc., Pleasanton, California

P. Mead, Centers for Disease Control and Prevention, Atlanta, Georgia: Process for updating CDC recommendations.

K. Roth, U.S. Food and Drug Administration, Silver Spring, Maryland: FDA procedures for clearance of new tests for Lyme disease: New 2015 approach to ASRs.

B. Body, LabCorp, Burlington, North Carolina: How do regulatory issues influence the decision to adopt or develop new assays? Laboratory-developed tests versus FDA-cleared assays.

Further Discussion of Hot Topics

J. Branda, Massachusetts General Hospital, Boston, and **S. Schutzer**, Rutgers New Jersey Medical School, Newark, New Jersey

SESSION 7: Review of Highlights and Discussion about Potential White Paper

Chairpersons: J. Branda, Massachusetts General Hospital, Boston, and **S. Schutzer,** Rutgers New Jersey Medical School, Newark

M. Ilias, National Institute for Allergies & Infectious Diseases, Rockville, Maryland: New opportunities and initiatives at NIH.

Discussion of White Paper/Opinion Piece

Suggestions for Follow-Up Meetings

Genomics-Enabled Accelerated Crop Breeding

October 16–19

FUNDED BY **Monsanto Company (CSHL Corporate Sponsor Program) with additional funding from DuPont Pioneer, 2Blades Foundation, and Calyxt Inc.**

ARRANGED BY **B. Staskawicz,** University of California, Berkeley
D. Voytas, University of Minnesota, St. Paul

The application of genomics-enabled crop improvement is rapidly being adopted by both the academic and commercial sectors. The "next-generation" breeding tools are revolutionizing crop production and will also bring about profound changes in what are considered genetically modified organisms. Indeed, the United States Regulatory Agencies are currently re-evaluating how these technologies will be regulated, and recommendations will be made toward the end of 2016. Over the years, the Banbury Center has held many meetings on rapidly changing fields, providing an opportunity to take stock of what is happening and to look to future developments. This meeting set out to do the same. Participants examined topics including the development and application of genome editing tools in plants, the future convergence of breeding and multiplex genome editing in crop plants, and what the regulatory landscape of genome-edited plants will be in the future. The meeting was international in scope and participants, covering a wide range of crops, were drawn from both academia and industry.

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

Techniques of Plant Genome Engineering: Past, Present, Future
H. Puchta, Karlsruhe Institute of Technology, Karlsruhe, Germany

R. Michelmore, Y. Qi

F. Zhang (MIT)

SESSION 1: Tools

Chairperson: C. Gao, Institute of Genetics and Developmental Biology, CAS, China

A. Britt, University of California, Davis: CenH3-mediated haploid induction.

G. Gocal, Cibus, San Diego, California: Precision genome-editing tools for nontransgenic trait development.

S. Jacobsen, University of California, Los Angeles: Targeted epigenetic modification.

N. Patron, The Earlham Institute, Norwich, United Kingdom: Improving the plant genome engineering toolbox.

Y. Qi, East Carolina University, Greenville, North Carolina: Multiplexing systems for plant genome editing and transcriptional regulation.

F. Zhang, Massachusetts Institute of Technology, Cambridge: Exploring bacterial diversity for genome engineering.

SESSION 2: Implementation

Chairperson: F. Zhang, Calyxt Inc., New Brighton, Minnesota

J. Corn, University of California, Berkeley: Mechanisms to improve sequence modification at defined genomic loci.

C. Gao, Institute of Genetics and Developmental Biology, CAS, China: Developing transgene-free genome-editing technologies in wheat.

D. Voytas, University of Minnesota, St. Paul: Optimizing gene targeting in plants.

Y. Yang, Penn State University, University Park, Pennsylvania: CRISPR/Cas9-enabled multiplex genome editing and precision crop breeding.

SESSION 3: Feeding the World

Chairperson: R. Bart, Donald Danforth Plant Science Center, St. Louis, Missouri

D. Horvath, 2Blades Foundation, Evanston, Illinois: Advancing crop-breeding strategies for disease resistance.

B. Mazur, DuPont Pioneer, Wilmington, Delaware: Providing advanced breeding-enabled crops to growers globally.

SESSION 4: Applications: Editing

Chairperson: A. Hummel, KWS Gateway Research Center, St. Louis, Missouri

R. Bart, Danforth Center, St. Louis, Missouri: Genome editing in cassava.

J. Jones, The Sainsbury Laboratory, Norwich, United Kingdom: Crisping in *Arabidopsis* and tomato for discovery and crop improvement.

R. Michelmore, University of California, Davis: Genome editing in lettuce.

R. Stupar, University of Minnesota, St Paul: Opportunities and obstacles for CRISPR in soybean.

B. Staskawicz, University of California, Berkeley: Genome editing for disease resistance in crop plants.

F. Zhang, Calyxt, Inc., New Brighton, Minnesota: Genome editing for crop and food improvement.

SESSION 5: Applications: Breeding

Chairperson: R. Stupar, University of Minnesota, St. Paul

R. Buell, Michigan State University, East Lansing Polyploid and clonally propagated crops: Challenges in genomics-enabled breeding.

S. Dellaporta, Yale University, New Haven, Connecticut: Genomic and computational pipelines for plant breeding populations.

R. Dirks, Rijk Zwaan Breeding BV, Fijnaart, The Netherlands: Chromosome substitution lines and libraries: Designer chromosomes, designer breeding.

S. Soyk, Cold Spring Harbor Laboratory: Using genome editing to create novel qualitative and quantitative variation for breeding.

S. Yang, Monsanto Company, St. Louis, Missouri: Accelerating breeding with molecular methods for trait discovery and deployment.

SESSION 6: The Future

Chairpersons: D. Voytas, University of Minnesota, St. Paul, and **B. Staskawicz,** University of California, Berkeley

D. Ware, Cold Spring Harbor Laboratory: Biology enabled crop breeding.

The Lustgarten Foundation: Vitamin D Day

November 1

FUNDED BY **Stand Up to Cancer and The Lustgarten Foundation**

ARRANGED BY **R. Evans,** Salk Institute for Biological Studies, La Jolla, California
P. Sharp, Massachusetts Institute of Technology, Cambridge
D. Tuveson, Cold Spring Harbor Laboratory

Synthetic, nonmetabolized vitamin D agonists promote drug delivery and response to chemotherapy in mouse models of pancreatic cancer. The working hypothesis is that this is due to reprogrammed pancreatic stellate cells and an altered tumor microenvironment. In the first human study, a neoadjuvant trial of Gemcitabine + Abraxane + Paracalcitol showed potential activity. The mechanism of response is not clear and may involve immune cells. The purpose of this meeting was to clearly articulate the known and unknown aspects of vitamin D clinical trials that are completed or under way, such that synergy and cooperation can occur.

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

Meeting Goals: P. Sharp, Massachusetts Institute of Technology, Cambridge
R. Evans, Salk Institute for Biological Studies, La Jolla, California
D. Tuveson, Cold Spring Harbor Laboratory

V. Balachandran

E. Furth

SESSION 1: SU2C Team 1 Results of Neoadjuvant Trial

Chairperson: D. Tuveson, Cold Spring Harbor Laboratory

Clinical Data: P. O'Dwyer, University of Pennsylvania, Philadelphia, and J. Drebin, University of Pennsylvania, Philadelphia

PSC Findings:

R. Evans, Salk Institute for Biological Studies, La Jolla, California

TME Analysis:

R. Vonderheide, Abramson Cancer Center, Philadelphia, Pennsylvania, and E. Furth, University of Pennsylvania, Philadelphia

SESSION 2: Other Vitamin D Approaches

Chairperson: D. Tuveson, Cold Spring Harbor Laboratory

"Grand Slam"

D. Von Hoff, Translational Genomics Research Institute, Phoenix, Arizona, and E. Borazanci, HonorHealth Research Institute, Scottsdale, Arizona: GAC + Paracalcitol + anti-PD1.

Convergence Team

J. Drebin, University of Pennsylvania, Philadelphia, and J. Wolchok, Memorial Sloan Kettering Cancer Center, New York: Anti-PD1 + vitamin D.

B. Vogelstein

LF Planned Trial in Stage-4 PDA

B. Wolpin, Dana-Farber Cancer Institute, Boston, Massachusetts: Paracalcitol + chemotherapy.

SESSION 3: Discuss Strategy to Expand Efforts

Chairperson: P. Sharp, Salk Institute for Biological Studies, La Jolla, California

Preclinical: Led by R. Evans and M. Truitt, Salk Institute for Biological Studies, La Jolla, California

Clinical: Led by P. O'Dwyer and J. Drebin, University of Pennsylvania, Philadelphia

D. Von Hoff, Translational Genomics Research Institute, Phoenix, Arizona, and R. Vonderheide, Abramson Cancer Center, Philadelphia, Pennsylvania: Neoadjuvant, adjuvant, advanced: First line versus second line; ImmunoTx.

SESSION 4: Plan for Future Trials (Milestones)

Chairpersons: D. Tuveson, Cold Spring Harbor Laboratory, and **P. Sharp,** Salk Institute for Biological Studies, La Jolla, California

SESSION 5: Assembly of a Vitamin D Task Force to Report Quarterly to SU2C/Lustgarten Foundation

Patenting Genes, Natural Products, and Diagnostics: Current Status and Future Prospects

November 9–11

FUNDED BY **Genentech, Inc., King & Spalding, LLP, DRI Capital Inc., McDonnell Boehnen Hulbert and Berghoff LLP, and Biotechnology Innovation Organization**

ARRANGED BY **K. Sonnenfeld,** King & Spalding LLP, New York
H. Sauer, Biotechnology Innovation Organization, Washington, D.C.
M. Brivanlou, King & Spalding LLP, New York

The Supreme Court's decisions in Mayo, Myriad, and Alice, and their broad interpretation by the USPTO, have significantly limited the subject matter eligible for patent protection related to diagnostic processes and preparations of naturally occurring substances and materials. Patent protection for subject matter that has been patentable for more than 100 years is now in question. The Federal Circuit itself has stated that it feels bound by the Supreme Court precedent to invalidate patents directed to commercially important discoveries used to create novel and nonobvious diagnostics. Furthermore, these actions have also created a growing anomaly in U.S. patent law, where biotech inventions that are patentable in most other industrialized countries are being denied patent protection in the United States, with attendant effects on trade and the cross-border flow of innovation. It is an appropriate time to examine whether well-intentioned Supreme Court decisions and their implementation by the USPTO have "overshot" their goals and given rise to an overcorrection in the law that is inconsistent with good trade and innovation policy.

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

Introduction: K. Sonnenfeld, King & Spalding, New York
M. Brivanlou, King & Spalding, New York
H. Sauer, Biotechnology Innovation Organization, Washington, D.C.

S. Knowles

SESSION 1: Where Have We Been? What We Have Gained? What We Have Lost?

Chairperson: K. Sonnenfeld, King & Spalding, New York

S. Knowles, Knowles Intellectual Property Strategies, Atlanta, Georgia: Framing the issues.

K. Noonan, McDonnell Boehnen Hulbert & Berghoff LLP, Chicago, Illinois: Is it time for Perestroika in U.S. Patent Law?

M. Moran, U.S. Patent and Trademark Office, Alexandria, Virginia: Evolution of USPTO eligibility guidance in the life sciences.

SESSION 2: The Law: How Did We Get Here? How Have the Courts and USPTO Reacted? How Will the Law Evolve?

Chairperson: I. Pleasure, Genentech, South San Francisco, California

K. Sonnenfeld, King & Spalding, New York: The expansion of Funk Brothers.

F. Chapinal, PharmaMar, Madrid, Spain: Under what circumstances can naturally occurring substances be patent-eligible?

K. Dow, Johnson & Johnson, Spring House, Pennsylvania: Patenting of method of treatment claims.

C. Coburn, Genentech Inc., South San Francisco, California: Therapeutic antibodies after Myriad.

J. Haley, Jr., Ropes and Gray LLP, New York: Claims that USPTO has issued in last 2–3 years to genes, natural products and diagnostics, and rationale.

SESSION 3: International Perspective: How Does Patentability of Genes, Natural Products, and Diagnostics Differ Abroad? What Can We Learn from the Comparison?

Chairperson: M. Brivanlou, King & Spalding, New York

H. Rainer-Jaenichen, Vossius & Partner, Munich, Germany: Limits to patentability of biotech and pharmaceutical inventions in the EPO.

J. Cherry, FPA Patent Attorneys, Melbourne, Australia: Myriad in Australia: The informational approach of the High Court.

G. Lewis, JA Kemp, London, United Kingdom: Patentable subject matter at the EPO with focus on antibodies and partner diagnostics.

C. Salsberg, Novartis, Washington, D.C.: International impact of U.S. Patent eligibility law.

J. Haley, Jr., Ropes and Gray LLP, New York: Reflections on the 1981 Banbury Center meeting.

H. Rainer-Jaenichen

T. Rea

SESSION 4: Policy: How Does the Patentability of Genes, Natural Products, and Diagnostics Impact Innovation, Investment, and Competition?

Chairperson: H. Sauer, Biotechnology Innovation Organization, Washington, D.C.

T. Rea, Crowell & Moring LLP, Washington, D.C.: Observations on recent studies and where we are today.

P. Alloway, DRI Capital Inc., Toronto, Canada: Challenges of investing in an antipatent environment.

D. Kappos, Cravath, Swaine & Moore LLP, New York: Approaches for cleaning up the 101 mess: Policy and practical.

SESSION 5: Panel Discussion: Where Do We Go from Here? What, If Any, Reforms Should be Made? How Could We Effect Them?

Moderator: G. Elliot, Retired USPTO, Alexandria, Virginia

NEED TALKS??

R. Dreyfuss, New York University of Law, New York

R. Armitage, Consultant, IP Strategy & Policy, Marco Island, Florida

S. Michel, Google Inc., Washington, D.C.

H. Sauer, Biotechnology Innovation Organization, Washington, D.C.

SESSION 6: Review and Summary

Chairpersons: K. Sonnenfeld and M. Brivanlou, King & Spalding LLP, New York, and **H. Sauer,** Biotechnology Innovation Organization, Washington, D.C.

Evolution of the Translational Apparatus and Implication for the Origin of the Genetic Code

November 13–16

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

ARRANGED BY **H. Hartman,** Massachusetts Institute of Technology, Cambridge
T. Smith, Boston University, Massachusetts

The origin of the genetic code is one of the great challenges of biology. In the 50 years since the 1966 Cold Spring Harbor Laboratory Symposium on "The Genetic Code," there have been revolutionary advances in our understanding of the relationship between the genetic code and proteins and the insights this provides on how the genetic code has the form it does. The main evidence covered in this meeting was the origin and evolution of the translational apparatus, focusing on the ribosome, the aminoacyl-tRNA synthetases, and their tRNAs. Under the assumption that the origin of the Code can be separated from the origin of life, participants also reviewed the pre-code biosynthesis of the monomers (e.g., the amino acids, lipids, sugars, nucleotides, and their early polymerization). The meeting concluded with discussions of the significance of these findings for our understanding of the origin and history of the Genetic Code.

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

Opening Remarks: T. Smith, Boston University, Massachusetts

M. Yarus, T. Steitz

K. Musier-Forsyth

SESSION 1: Ribosomal RNA Implications

H. Noller, University of California, Santa Cruz: The ribosome: Overview and origin.
T. Steitz, Yale University New Haven, Connecticut: What the ribosomal RNA structure tells us.
L. Williams, Georgia Institute of Technology, Atlanta: Evolution of the ribosome before LUCA.
A.S. Petrov, Georgia Institute of Technology, Atlanta: The LSU is from Mars, the SSU is from Venus.

SESSION 2: Early Peptide and RNAs from Pieces

A. Lupas, Max-Planck-Institute for Developmental Biology, Tubingen, Germany: Ribosomal proteins as documents of the transition from (poly)peptides to folded proteins.
L. Jaeger, University of California, Santa Barbara: RNA self-assembly, RNA structural evolution, and RNA nanomachines.
M. Yarus, University of Colorado, Boulder: Molecularity/catalysis/utility (MCU) theory and the primordial genetic system.

SESSION 3: Ribosomal Proteins

T. Smith, Boston University, Massachusetts: Protein taxonomic block structure.
G. Fox, University of Houston, Texas: Ribosome origins and subsequent evolution.

SESSION 4: Aminoacyl tRNA Synthetases

D. Soll, Yale University, New Haven, Connecticut: The evolution of genetic code deviants.
D. Moras, Institut Génétique Biologie Moléculaire Cellulaire, Illkirch, France: Specific structural features of class II synthetases.
L.R. de Pouplana, Institute for Research in Biomedicine, Barcelona, Spain: Functional limits of the genetic code.
K. Musier-Forsyth, Ohio State University, Columbus: Prolyl-tRNA synthetases: Aminoacylation and editing.
A. Torres-Larios, National Autonomous University of Mexico: Why two Glycyl-tRNA synthetases?

SESSION 5: tRNA Evolution

T. Steitz, Yale University, New Haven, Connecticut: Structure of CCA adding enzyme.
L. Aravind, National Center for Biotechnology Information, Bethesda, Maryland: The deep evolutionary links between cyclic nucleotide synthetases and nucleic acid polymerases.
C. Francklyn, University of Vermont, Burlington: Minihelices and the operational code.
M. Di Giulio, Institute Biosciences & Bioresources, CNR, Naples, Italy: The origin of the tRNA molecule.

SESSION 6: Origins

H. Jakubowski, Rutgers University, New Jersey Medical School, Newark: Thioester chemistry and the origin of coded peptide synthesis.
D. Segre, Boston University, Massachusetts: Richness and implications of a prephosphate metabolism.

SESSION 7: What Are the Implications for Our Understanding of the Origin and Evolution of the Genetic Code?

H. Hartman, Massachusetts Institute of Technology, Cambridge: Summary and thoughts on the evolution of the genetic code.

Genetic Counseling for Psychiatric Disorders: Challenges in the Genomic Era

November 30–December 2

FUNDED BY **International Society of Psychiatric Genetics, Tennessee, National Society of Genetic Counselors, Illinois, Institute of Neurosciences, Mental Health and Addiction, University of British Columbia, Vancouver, and Cold Spring Harbor Laboratory**

ARRANGED BY **J. Austin,** University of British Columbia, Vancouver, Canada
F. McMahon, National Institute of Mental Health, Bethesda, Maryland

There is considerable misunderstanding of the term genetic counseling; in particular, it is often conflated with genetic testing and is often thought of as any simple interaction between a healthcare provider and a patient where genetic risk or testing is discussed. In fact, genetic counseling is a specialist healthcare discipline that involves helping clients to "understand and adapt to the medical, psychological, and familial implications of genetic contributions to disease." Fundamental questions remain regarding how best to use genetic counseling—and genetic testing—in psychiatry. Some of these questions were tackled by participants in this Banbury meeting with the aim of developing a framework to guide future developments in psychiatric genetic counseling.

Welcoming Remarks and Background: J.A. Witkowski, Banbury Center, Cold Spring Harbor Laboratory

Introduction: J. Austin, University of British Columbia, Vancouver, Canada
F. McMahon, National Institutes of Health, Bethesda, Maryland

SESSION 1: Use of Genetic Testing to Predict Risk for Psychiatric Disorders

D. Ledbetter, Geisinger Health System, Danville, Pennsylvania: Routine genetic diagnostic testing and prenatal diagnosis for psychiatric disorders.

C. Janssens, Emory University, Atlanta, Georgia: How predictive is our DNA? An overview of everything from Mendelian to polygenic diseases and traits.

J. Smoller, Massachusetts General Hospital, Boston: Implications of pleiotropy and/or issues in returning research results.

D. Alexis Carrere, McMaster University, Hamilton, Ontario, Canada: Direct-to-consumer genetic testing for bipolar disorder: Findings from the impact of personal genomics (PGen) study.

SESSION 2: Psychiatric Genetic Counseling, International Perspectives on Current Practice

E. Morris, University of British Columbia, Vancouver, Canada: Clinical applications of psychiatric genetics: Updates from Vancouver, B.C.

K. McGhee, Bournemouth University, Poole, United Kingdom: Bridging the gap between research and patient. Implementing PsyGC: The UK perspective.

R. Moldovan, Babes-Bolyai University, Cluj-Napoca, Romania: Evidence-based genetic counseling for psychiatric disorders.

F. Degenhardt, University of Bonn, Germany: Perspective from a clinical geneticist.

S. Hartz, Washington University Medical Center, St. Louis, Missouri: Pragmatic approaches to translate genetic findings into clinical care.

B. Biesecker, National Human Genome Research Institute, Bethesda, Maryland: Families rich with psychiatric disorders: Navigating communication, privacy, and a "need to know."

SESSION 3: Psychopharmacogenomics in the Clinic

J. Biernacka, Mayo Clinic, Rochester, Minnesota: Psychiatric pharmacogenomics.

J. Kennedy, Centre for Addiction and Mental Health, Ontario, Canada: Pharmacogenetic testing is becoming widely accepted: What are the issues?

A. Malhotra, Zucker Hillside Hospital, Glen Oaks, New York: Pharmacogenetics in psychiatry.

SESSION 4: Looking Forward/Next Steps

Questions for Break-Out Groups:

- What needs to be done to make genomic testing useful in the psychiatric clinic?
- What is the proper role of genetic counseling in psychiatric care? Consider relationships between psychiatrists and genetic counselors.
- What is the role(s) of professional societies in promoting the effective use of genetic testing and counseling, educating professionals, setting the research agenda as it relates to psychiatric genetics?

SESSION 5: Reports from Break-Out Groups, Summary, and Next Steps

Evolution and Revolution in Anatomic Pathology: Automation, Machine-Assisted Diagnostics, Molecular Prognostics, and Theranostics

December 4–7

FUNDED BY **Northwell Health–Cold Spring Harbor Laboratory Partnership**

ARRANGED BY **J.M. Crawford,** Northwell Health, Lake Success, New York
P. Mitra, Cold Spring Harbor Laboratory
M. Wigler, Cold Spring Harbor Laboratory

Revolutionary advances in machine intelligence, robotics, and genomics have taken place that should fundamentally improve the efficiency and quality of patient care through automated diagnostic algorithms and personalized medicine. However, implementing these new technologies will not be easy, and key hurdles to be overcome include closing nonautomated gaps in anatomic pathology; linking machine-learning to medical decision-making; data standardization and curation; and preparing for regulatory oversight and approval. The goal of the meeting was to facilitate this change by bringing together the different groups involved (scientists and engineers, medical professionals and leaders, FDA regulators, payers and insurance companies, and industry) to review two broad themes: enabling technologies, and how to integrate the information from these technologies into the practice of medicine.

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

SESSION 1: Defining the Challenge for Anatomic Pathology

Chairperson: J. Crawford, Hofstra Northwell School of Medicine, Hempstead, New York

U. Balis, University of Michigan, Ann Arbor, and J. Tomaszewski, University of Buffalo, New York: Anatomic pathology as quantitative evidence for medicine: Defining the transformation that must occur for anatomic pathology.

B. Bastian, University of California, San Francisco: Tissue-based molecular diagnostics: State-of-the-art methods for analyzing the molecular evolution of cancers—From precursor identification of biomarkers to assisting in diagnosis and staging.

SESSION 2: Anatomic Pathology as Structural Molecular Diagnostics

Chairperson: K. Roth, Columbia University, New York

M. Loda, Dana-Farber Cancer Institute, Boston, Massachusetts: Anatomic pathology as molecular diagnostics: Comparing formalin-fixed paraffin-embedded versus 2D/3D molecular data.

R. Levenson, University of California, Davis: Data integrity and interoperability: Examining standards for generation of quantitative data from anatomic pathology and requirements for data transmission.

SESSION 3: Examining the Regulatory and Preanalytical Environment

Chairperson: R. Michel, The Dark Report, Spicewood, Texas

B. Gallas, U.S. Food and Drug Administration, Silver Springs, Maryland, and C. Compton, Arizona State University, Tucson, Arizona: Mitotic counting reproducibility/feature study with pathologists preanalytical processing: The biospecimen quality initiative.

SESSION 4: Expanding the Analytic Value of Anatomic Pathology

Chairperson: T. Chang, Hofstra Northwell School of Medicine, Hempstead, New York

J. Gilbertson, Massachusetts General Hospital, Boston: Informatics as empowerment for pathology to examine the informatics context for anatomic pathology.

T. Fuchs, Memorial Sloan Kettering Cancer Center, New York: Informatics as the pivot point for human diagnostics: To examine the broader perspectives of healthcare information.

M. Wigler, Cold Spring Harbor Laboratory: Cellular informatics: To examine the power of single-cell analysis and spatial data.

P. Mitra, M. Wigler

R. Levenson, J. Crawford

SESSION 5: Examining the Power of Digital Analytics 1

Chairperson: Y. Yagi, Memorial Sloan Kettering Cancer Center, New York

B. Perkins, Human Longevity, Inc., San Diego, California: The digital human: Looking to the bluest part of the sky.

M. Sivaprakasan, India Institute of Technology, Madras, India, and J. Joseph, Healthcare Technologies Innovation Center, Madras, India: The international context for automating pathology.

SESSION 6: Examining the Power of Digital Analytics 2

Chairperson: M. Lloyd, Inspirata, Inc., Tampa, Florida

P. Mitra, Cold Spring Harbor Laboratory: High-throughput histology pipeline and informatics.

Y. Yagi, Memorial Sloan Kettering Cancer Center, New York: Validating technologies for anatomic pathology.

SESSION 7: Technological Advances That Need to Occur: Machine Learning, Automation, Digital Imaging, Genomics, Biomarkers

Chairperson: R. Levenson, University of California, Davis: Moderated discussion.

SESSION 8: Nontechnological Events That Need to Occur: Regulatory, Payers, Clinical Workflow, Education of Pathologists

Chairperson: S. Cohen, Rutgers University–New Jersey Medical Center, New Brunswick: Moderated discussion.

SESSION 9: Identifying Hurdles, Making a Plan to Advance the Field

Chairpersons: P. Mitra, Cold Spring Harbor Laboratories, and **U. Balis,** University of Michigan, Ann Arbor: Moderated discussion.

SESSION 10: Implementing Banbury Outcomes after Banbury: White Paper Outline and Plan

Chairperson: J. Crawford, Hofstra Northwell School of Medicine, Hempstead, New York: Moderated discussion.

Developing Gene Editing as a Therapeutic Strategy

December 11–14

FUNDED BY **Genentech, with additional funding from Pfizer and Cold Spring Harbor Laboratory Corporate Sponsor Program**

ARRANGED BY **A. Wagers,** Harvard University, Cambridge, Massachusetts
C. Gersbach, Duke University, Durham, North Carolina
J.K. Joung, Harvard Medical School, Charlestown, Massachusetts

Targeted genome editing has emerged as an exciting potential clinical strategy for many human diseases. New and ever-improving strategies for modifying mammalian genomes raise the imminent possibility that disease-causing mutations may be therapeutically recoded to provide permanent, long-term recovery of function. Yet, key challenges remain for realizing the full potential of genome editing in human patients. This meeting on genome editing brought together key leaders in this rapidly evolving field to discuss strategies to both anticipate and overcome challenges to clinical gene editing. Specific topics included the identification of disorders amenable to such approaches; the challenges of in vivo versus ex vivo genome editing; strategies for delivery of gene editing effectors to target cells; the influence of the immune response; approaches for increasing specificity and minimizing possible genotoxicity; and clinical and regulatory issues as informed by prior experience with other forms of gene therapy.

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

Introduction and Goals of Meeting: A. Wagers, C. Gersbach, and J.K. Joung

SESSION 1: Technologies

Chairperson: C. Gersbach, Duke University, Durham, North Carolina

J.K. Joung, Harvard Medical School, Charlestown, Massachusetts: Defining and minimizing off-target effects of CRISPR-Cas nucleases.

F. Zhang, Massachusetts Institute of Technology, Cambridge: Therapeutic genome editing: Prospects and challenges.

A. Scharenberg, Seattle Children's Research Institute, Washington: Challenges for in vivo genome editing: Immunologic barriers to delivery of recombination templates.

D. Schaffer, University of California, Berkeley: Directed evolution of novel viral gene delivery vehicles for therapeutic gene delivery and genome editing.

K. Suzuki, Salk Institute for Biological Studies, La Jolla, California: In vivo genome editing via CRISPR-Cas9-mediated homology-independent targeted integration.

SESSION 2: T Cells

Chairperson: C. Dunbar, National Heart, Lung, and Blood Institute, Bethesda, Maryland

C. June, University of Pennsylvania, Philadelphia: Using synthetic biology to generate smarter T cells.

M. Sadelain, Memorial Sloan Kettering Cancer Center, New York: CAR T-cell editing for cancer immunotherapy.

Y. Zhao, Abramson Family Cancer Research Institute, Philadelphia, Pennsylvania: Use CRISPR/CAS9 gene editing to improve adoptive T-cell immunotherapy for cancer.

SESSION 3: Human Stem Cells

Chairperson: A. Wagers, Harvard University, Cambridge, Massachusetts

P. Cannon, Keck School of Medicine of University of Southern California, Los Angeles: Genome editing for HIV.

C. Dunbar, National Heart, Lung & Blood Institute, Bethesda, Maryland: Use of non-human primate models to optimize the safety and efficacy of hematopoietic stem cell gene editing.
D. Kohn, University of California, Los Angeles: Gene editing in human hematopoietic stem cells.
D. Bauer, Harvard University, Boston, Massachusetts: Genome editing for the hemoglobin disorders.

SESSION 4: In Vivo Genome Editing

Chairperson: M. Sadelain, Memorial Sloan Kettering Cancer Center, New York

J. Wilson, University of Pennsylvania, Philadelphia: Challenges of in vivo genome editing with viral vectors.
A. Wagers, Harvard University, Cambridge, Massachusetts: Therapeutic gene editing in skeletal muscle and muscle stem cells.
C. Gersbach, Duke University, Durham, North Carolina: Genome editing for Duchenne muscular dystrophy.
D. Duan, University of Missouri Health, Columbia, Missouri: Large mammal translation.

SESSION 5: Industry Perspective

Chairperson: J.K. Joung, Harvard Medical School, Charlestown, Massachusetts

M. Holmes, Sangamo BioSciences, Inc., Richmond, California: Genome editing in primary human cells and organs: Toward the goal of engineering genetic cures.
M. Certo, bluebird bio, Cambridge, Massachusetts: Developing megaTALs for therapeutic genome editing.
C. Albright, Editas Medicine, Cambridge, Massachusetts: Advancing CRISPR medicines.
T. Barnes, Intellia Therapeutics, Inc., Cambridge, Massachusetts: Translating CRISPR/Cas9 genome editing into therapeutic reality.
S. Lundberg, CRISPR Therapeutics, Cambridge, Massachusetts: Gene editing to treat β-thalassemia and sickle cell disease.

Concluding Remarks

J. Witkowski, A. Wagers, C. June

D. Kohn, C. Dunbar

BANBURY CENTER GRANTS

Grantor	*Program*	*Duration of Grant*	*2016 Funding*
FEDERAL SUPPORT			
National Institute of Mental Health, National Institutes of Health	NIMH Brain Camp VIII	2016	$21,280
National Institute of Mental Health, National Institutes of Health	Mammalian Brain Cell Diversity and Census	2016	35,000
NONFEDERAL SUPPORT			
Astellas Pharma Inc.	Autophagy and Cancer	2016	19,985
AstraZeneca	STAT3 in Cancer: How Can It Be Inhibited?	2016	1,495
Biotechnology Innovation Organization	Patenting Genes, Natural Products, and Diagnostics: Current Status and Future Prospects	2016	5,000
Boehringer Ingelheim Foundation	Communicating Science	2016	66,481
Boston Biomedical, Inc.	STAT3 in Cancer: How Can It Be Inhibited?	2016	63,337
Calyxt Inc.	Genomics-Enabled Accelerated Crop Breeding	2016	5,000
Cold Spring Harbor Corporate Sponsor Program	Genomics-Enabled Accelerated Crop Breeding	2016	35,666
Cold Spring Harbor Corporate Sponsor Program	Evolution of the Translational Apparatus and Implication for the Origin of the Genetic Code	2016	46,100
DRI Capital	Patenting Genes, Natural Products, and Diagnostics: Current Status and Future Prospects	2016	5,000
DuPont Pioneer	Genomics-Enabled Accelerated Crop Breeding	2016	5,000
Genentech	Patenting Genes, Natural Products, and Diagnostics: Current Status and Future Prospects	2016	30,000
Genentech	Developing Gene Editing as Therapeutic Strategy	2016	10,000
Global Lyme Alliance	Diagnostic Tests for Lyme Disease: A Reassessment	2016	48,599
International Society of Psychiatric Genetics	Genetic Counseling for Psychiatric Disorders: Challenges in the Genomic Era	2016	10,000
Institute of Neurosciences, Mental Health and Addiction, University of British Columbia	Genetic Counseling for Psychiatric Disorders: Challenges in the Genomic Era	2016	3,133
King & Spalding, LLP	Patenting Genes, Natural Products, and Diagnostics: Current Status and Future Prospects	2016	5,000
Lehrman Institute	Ancient DNA and Archaeology	2016	47,397
The Lustgarten Foundation	The Lustgarten Foundation Scientific Meeting/Vitamin D	2016	26,556
McDonnell Boehnen Hulbert and Berghoff LLP	Patenting Genes, Natural Products, and Diagnostics: Current Status and Future Prospects	2016	5,000
Merck Serono	Autophagy and Cancer	2016	15,000
Millennium Pharmaceuticals, Inc.	Autophagy and Cancer	2016	5,000
National Society of Genetic Counselors	Genetic Counseling for Psychiatric Disorders: Challenges in the Genomic Era	2016	10,000
NordForsk	Studying the Genomic Variation that Underlies Health and Disease: The Unique Contribution of the Nordic Health Systems	2016	27,475
Northwell Health–Cold Spring Harbor Lab Partnership	Making Oxidative Chemotherapy Less Toxic	2016	46,901
Northwell Health–Cold Spring Harbor Lab Partnership	Evolution and Revolution in Anatomic Pathology: Automation, Machine-Assisted Diagnostics, Molecular Prognostics, and Theranostics	2016	46,156
The Norwegian Research Council	Studying the Genomic Variation That Underlies Health and Disease: The Unique Contribution of the Nordic Health Systems	2016	26,742
Novartis	Autophagy and Cancer	2016	5,000
Ovarian Cancer Research Fund Alliance	After UKCTOS: Public Messaging on Screening and Early Detection for Ovarian Cancer	2016	36,467

BANBURY CENTER GRANTS (*Continued*)

Grantor	*Program*	*Duration of Grant*	*2016 Funding*
Pfizer	Developing Gene Editing as Therapeutic Strategy	2016	$10,000
Presage Biosciences, Inc.	Autophagy and Cancer	2016	2,500
The Simons Center for Quantitative Biology	Measuring and Modeling Quantitative Sequence-Function Relationships	2016	56,686
Stand Up to Cancer	The Lustgarten Foundation Vitamin D Day	2016	2,829
The Stanley Research Foundation	Can We Make Animal Models of Human Mental Illness? A Critical Review	2016	36,216
2Blades Foundation	Genomics-Enabled Accelerated Crop Breeding	2016	5,000

Banbury Center

Jan A. Witkowski, Executive Director
Michelle Corbeau, Executive Assistant
Patricia Iannotti, Secretary
Barbara Polakowski, Hostess
Jose Pena Corvera, Grounds Foreman
Saul Pena Corvera, Groundskeeper
Joseph McCoy, Groundskeeper
Riley McKenna, Groundskeeper (from 10/3/2016)

Cold Spring Harbor Laboratory

Jamie C. Nicholls, Chairman
Bruce Stillman, President & Chief Executive Officer
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