National Institute of Standards and Technology
U.S. Department of Commerce

NIST Genome Editing Workshop

Speaker Bios

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Laurakay Bruhn, Ph.D.

Section Manager, Biological Chemistry, Agilent

Laurakay Bruhn is Section Manager of Biological Chemistry in Agilent Research Labs and manages programs and projects aimed at developing technology breakthroughs in nucleic acid synthesis, gene editing and control, proteomics and metabolomics as well as other efforts related to developing new technologies for the life sciences research to diagnostics continuum. The group she leads has leveraged a novel RNA oligo synthesis chemistry developed at Agilent to invent new ways to use chemical modifications in guide RNAs to enhance the activity and specificity of CRISPR systems.

After receiving her Ph.D. in Molecular Biology from University of Oregon and a Postdoctoral Fellowship studying gene regulation at UCSF she joined Hewlett-Packard Laboratories in 1996 where she worked on an inter-disciplinary team of scientists that developed Hewlett-Packard's first DNA microarray products. She joined Agilent Technologies as part of Agilent Laboratories when the company was formed in 1999 and became a manager in 2000. She has 18 years experience leading inter-disciplinary teams of chemists, biochemists, molecular and cellular biologists, and computational biologists innovating sample manipulation and measurement solutions to advance the next generation of research and diagnostics in key areas such as cancer, developmental disorders, cardiovascular disease, stem cell research, and synthetic biology.

John Elliott, Ph.D.

Leader NIST Cell Systems Science Group

Dr. John T Elliott is the group leader of Cell Systems Science Group at NIST. His current focus is on measurement assurance strategies for ensuring comparability and quality in cell-based assays. Wet lab activities include identifying and monitoring sources of variability in biological assays, development of in-house cell reference materials and recently, the design of automation instruments to facilitate robustness testing in biological assays. He serves as a co-chair of the ASTM F04.46 Subcommittee on Standards for Cell Signaling and participates in standards development for ASTM F04 Tissue Engineered Medical Products (TEMPS) and ISO TC276 Biotechnology committees.

Chris Fuller, Ph.D.

VP Informatics, Caribou Biosciences, Inc.

As the Vice President of Informatics, Chris leads the informatics and software efforts at Caribou Biosciences. He has a background managing diverse teams in developing instrumentation, medical devices, software, and microfluidic systems. Prior to joining Caribou in 2014, he held research and leadership positions in consulting, startup, and established company environments, including Signature Bioscience, MDS Sciex, and Triple Ring Technologies. He led the development of the CellKey instrument for MDS Sciex from its inception through to product launch. Chris is an inventor of multiple patents and patent applications. He received his B.S. and M.S. degrees in Electrical Engineering from the Georgia Institute of Technology and a Ph.D. in Bioinformatics from the University of California, San Francisco.

Keith Jones, Ph.D.

Senior Vice President of Product Development, Mission Bio

Keith W. Jones is an accomplished R&D Executive with over 25 years of industrial experience in the research and development of molecular assays for genetic analysis. He has served as VP and SVP for Mission Bio, Affymetrix, Verinata and Illumina leading teams to conceive, developing, and launch complex genetic assays with demonstrated clinical utility. Currently, he is the SVP, Strategic Initiatives at Mission Bio where he actively engages the scientific community to understand how Mission Bio's technology could fit into the research, development or diagnostic plans they are exploring. He is the author of more than 50 peer-reviewed publications and 20 patents and received a Ph.D. in Pharmacology from Stanford University and two B.S. degrees in Chemistry and Biology from the University of California, Irvine.

Anna Kwilas, Ph.D.

Biologist, FDA Center for Biologics Evaluation and Research (CBER)

Dr. Kwilas received her Ph.D. in Biomedical Science from The Ohio State University in 2010 with an emphasis in Molecular Virology & Gene Therapy and Translational Science. She performed her graduate research at The Research Institute at Nationwide Children's Hospital examining the potential application of respiratory syncytial virus as a gene therapy vector for the treatment of cystic fibrosis.

Dr. Kwilas performed her post-doctoral research at the National Cancer Institute investigating the efficacy of modified vaccinia virus Ankara and adenovirus-based cancer vaccines alone and in combination with other approved and investigational cancer therapeutics.

Dr. Kwilas received the Interagency Oncology Task Force Fellowship in 2015. She began conducting research at FDA involving the generation of safer vector producing cells with the use of CRISPR/Cas9 genome editing technology and participating in gene therapy product CMC review. Since May 2016, Dr. Kwilas has been a full-time gene therapy CMC reviewer at the FDA.

Andy Larrea, Ph.D.

Sr. Manager Field Business Development, Pacific Biosciences

Dr. Andy Larrea received his PhD in 2008 from the University of Miami. His work at UM focused on DNA damage repair. After a short post-doc at the NIEHS/NIH using NGS to dissect the human replication fork, he moved to Pacific Biosciences. He joined PacBio in 2010, initially in the support team as a member of the Field Applications Scientists before moving into Sales. In 2017 he joined the Business Development team where he works on identifying new applications for long read sequencing.

Eric Lin, Ph.D.

Director, Material Measurement Laboratory, NIST

Dr. Eric Lin is Director of the Material Measurement Laboratory (MML) at the National Institute of Standards and Technology (NIST). Lin joined NIST as an NRC-NIST postdoctoral associate in 1996, and joined the permanent staff in 1998. In 2002, he became the Leader of the Electronics Group, where he established world class research programs in semiconductor electronics processing, nanoscale materials, and organic electronics. In 2012, he became Chief of the Materials Science and Engineering Division, formed by the merger of the Polymers and the Metallurgy Divisions. Lin's work has supported important technology areas including advanced manufacturing and advanced electronics, as well as the multi-agency Materials Genome Initiative. He has been active in several cross-NIST programs, serving on the NIST Incentive Awards Panel, the NIST-on-a-Chip Committee, and the NIST Strategic Computing Initiative Committee.

His contributions have been recognized with the Presidential Early Career Award for Scientists and Engineers (PECASE), the Department of Commerce Silver Medal, and the William P. Slichter Award. He is active in professional organizations including the American Institute of Chemical Engineers, the American Physical Society, the American Chemical Society, and the Materials Research Society. He received a B.S.E. from Princeton University in 1991 (summa cum laude) and Masters and Ph.D. degrees from Stanford in 1992 and 1996, respectively, all in chemical engineering.

Samantha Maragh, Ph.D.

Leader, NIST Genome Editing Program

Dr. Samantha Maragh Leads the Genome Editing Program at the National Institute of Standards and Technology (NIST). This program has a primary focus on measurements and assay qualification to support genome editing applications with emphasis on gene therapy applications. Included in this program is the newly launched NIST Genome Editing Consortium, which is a public-private partnership to bring together government, industry and academia to address shared pre-competitive technical measurement and standards challenges within the genome editing community. Samantha also participates on representing the U.S. as a technical expert to the International Standards Organizations Technical Committee on Biotechnology (ISO TC 276). She is currently a U.S. liaison representing the interests and expertise of the U.S. on standards relating to nucleic acids measurements. Samantha received her B.S. in Cellular and

Molecular Biology from Loyola University, M.S. in Biotechnology from Johns Hopkins University, and her Ph.D. in Human Genetics & Molecular Biology from the Johns Hopkins School of Medicine.

Roberto Nitsch, Ph.D.

Associate Director, Drug Safety and Metabolism, AstraZeneca

Roberto Nitsch graduated in Medical Biotechnology from the University of Naples (Italy) where he also obtained his PhD in Molecular Genetics. With an initial research focus on genetic and epigenetic regulation of thyroid gland differentiation, he later moved to Josef Penninger's lab (IMBA, Vienna) where he studied mouse genetics and cancer biology. He started being interested in recessive genetics and soon after CRISPR/Cas9 was discovered, he shifted focus towards genome engineering. He joined AstraZeneca in 2014 as Senior Research Scientist in Discovery Sciences in the Precise Genome Editing team. He became responsible for in vivo applications of CRISPR to the generation of translatable mouse models for drug discovery with focus on oncology models. In 2017 he became Associate Director in the New Modalities group in Clinical Pharmacology and Safety Science department as responsible for the safety of CRISPR applications in the Therapeutic Genome Editing project. Today Roberto is a leader in gene therapy safety, discussing with European and North American health authorities and being the representative for AstraZeneca at the international consortium driven by the NIST (National Institute of Standards and Technology).

Mary Perry, Ph.D.

Program Leader, NIH Office of Strategic Coordination

Since 2007, Dr. Mary Ellen Perry has been a program leader in the Office of Strategic Coordination, overseeing the development, implementation and assessment of several cutting-edge programs. Prior to joining the Office of the Director, Dr. Perry was a program director for the National Cancer Institute (NCI), where she oversaw a grant portfolio focused on research in aspects of molecular biology of particular relevance to cancer. Until 2016, Dr. Perry also maintained a laboratory at the NCI, employing genetically engineered mice to explore the relationship between development and cancer. Her background in cancer research is founded on a Ph.D. in biochemistry from the University of North Carolina and post-doctoral fellowships at Princeton University and the Imperial Cancer Research Fund, London (now part of Cancer Research, UK). For seven years, she led a cancer research laboratory at the University of Wisconsin-Madison, where she succeeded in winning two NIH grants, publishing several papers, and training five Ph.D. students, two of whom are now professors.

Luca Pinello, Ph.D.

Investigator, MGH/Harvard Medical School

Luca is an Assistant Professor at Massachusetts General Hospital and Harvard Medical School. He received his BA,MA and Ph.D. in Computer Science and Mathematics from the University of Palermo in Italy. He had the good fortune to be part of the "omics" revolution and the opportunity to work on many computationally-challenging problems since he was an undergraduate student. During his postdoctoral research at Dana-Farber Cancer Institute/Harvard School of Public Health, he studied the role of

chromatin structure in gene regulation and developed computational methods for single cell analysis and epigenomics. He has a background in computer science and extensive experience in machine learning, data mining and web technologies. His research program uses computational approaches to systematically analyze the sources of variation that affect gene regulation: epigenetic variation, genetic variation and (single-cell) gene expression variability. He is actively involved in the single-cell community and he is part of the Human Cell Atlas initiative, proposing computational strategies to model gene expression variability, its relationship with chromatin accessibility and DNA methylation, and to reconstruct developmental trajectories (http://stream.pinellolab.org). He fully embraced the revolution in functional genomics made possible by the novel genome editing approaches such as CRISPR/Cas9. He developed computational tools to quantify and visualize the outcome of genome editing experiments, that are nowadays the standard the facto for the community (http://crispresso2.pinellolab.org). He also a subgroup coordinator for the NIST Consortium on Genome Editing. His contributions center on defining standards for data obtained from genome editing experiments. In his free time, he likes to hike, play his guitar and roast green coffee.

Garrett Rettig, Ph.D.

Director of Molecular Genetics Product Development, IDT

Garrett has been in the Molecular Genetics Research department at Integrated DNA Technologies for the past 10 years. During that time, he has been a lead scientist on various RNA knockdown projects – particularly high-throughput screening of siRNAs and chemical modifications thereof. Recently, he has focused on improving methods and developing new technologies for CRISPR-mediated genome editing – specifically in the detection of off-target editing events via next-generation sequencing.

Brett Robb, Ph.D.

Scientific Director, RNA & Genome Editing, New England Biolabs

G. Brett Robb is the Scientific Director of RNA and Genome Editing Research at New England Biolabs. His work at NEB focuses on discovery, development and commercialization of enzyme technologies to support RNA synthesis, RNA analysis, and genome editing workflows. An RNA molecular biologist by training, Brett's prior work explored mechanisms of RNA interference and post-transcriptional control of gene expression.

Shengdar Tsai, Ph.D.

Assistant Member, Dept. of Hematology St. Jude Children's Hospital

Dr. Tsai is an Assistant Member in the Department of Hematology at St. Jude Children's Research Hospital. His lab focuses on genome editing technologies for therapeutics, with a special interest in editing human HSCs for treatment of hemoglobinopathies and T-cells for cancer immunotherapy. Previously, he has developed methods for high-throughput genome editing with TALENs, and for defining and improving the genome-wide specificity of CRISPR-Cas nucleases. Dr. Tsai completed a postdoctoral fellowship at Massachusetts General Hospital & Harvard Medical School, Ph.D. in Functional Genomics and M.S. in Bioinformatics from North Carolina State University, and B.S. from the University of Michigan.

Renee Wegrzyn, Ph.D.

Program Manager, DARPA Biological Technologies Office

Dr. Renee Wegrzyn joined DARPA as a Program Manager in 2016, where she applies the tools of genome engineering and synthetic biology to support biosecurity, enable flexible biomanufacturing, and outpace infectious disease. Her portfolio includes the Living Foundries, Safe Genes, and PREPARE programs. Safe Genes aims to deliver novel biological capabilities to facilitate the safe and expedient pursuit of advanced genome editing applications, while also providing the tools and methodologies to mitigate the risk of unintentional consequences or intentional misuse of these technologies. PREPARE (Preemptive Expression of Protective Alleles and Response Elements) is focused applying the tools of genome engineering to create potent, transient, and reversible medical countermeasures to combat biological, chemical, and radiological threats to public health and national security. Living Foundries seeks to transform biology into an engineering practice by developing the tools, technologies, methodologies, and infrastructure to prototype and scale engineered microbes that can produce molecules that are of value for government and commercial use.

Prior to joining DARPA as a PM, Dr. Wegrzyn worked in the private sector, where she led teams that provided scientific and strategic support in the areas of biodefense, biosecurity, and biotechnical innovation to DARPA and other federal and private institutions. She is a former Fellow of the UPMC

Justin Zook, Ph.D.

Leader NIST Genome in a Bottle Consortium

Dr. Justin Zook leads the Human Genomics Team at the National Institute of Standards and Technology and is co-leading the Genome in a Bottle Consortium's work developing authoritatively characterized human genomes to benchmark sequencing methods. He developed methods to compare and integrate whole genome DNA sequencing data from multiple platforms and sequencing runs to characterize the first whole human genome Reference Material. He is now leading the GIAB Analysis Team work combining short, linked, and long read sequencing technologies to characterize structural variation and challenging regions of the genome. He is an Informatics Representative to the Association for Molecular Pathology Clinical Practice Committee. In addition, he was Chair of the Global Alliance for Genomics and Health Benchmarking Team, which recently published best practices for benchmarking genome sequencing results.