Capturing RNA Sequence and Transcript Diversity, From Technology Innovation to Clinical Application

Virtual Event

Speaker and Executive Committee Biographies

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Speakers

Chris Burge

Chris Burge, Ph.D. is a Professor of Biology at MIT and Director of MIT's Computational and Systems Biology Ph.D. Program. He is also an extramural member of the Koch Institute for Integrative Cancer Research and an Associate Member of the Broad Institute of MIT and Harvard. He completed his BS and Ph.D. degrees at Stanford where he worked in the research group of Samuel Karlin,Ph.D., to develop the GENSCAN algorithm for de novo gene prediction from genomic sequence. He did postdoctoral work in the lab of Phillip Sharp, Ph.D., at MIT from 1997-1999 where he studied RNA splicing and molecular evolution. His laboratory has developed a number of computational methods for understanding gene regulation, including RESCUE-ESE for identification of splicing regulatory elements, TargetScan for microRNA target prediction (with the David Bartel lab), and MISO for inference of exon and isoform abundance from RNA-Seq data (with Edo Airoldi). The lab has contributed to the understanding of splicing regulatory elements, RNA-binding proteins (RBPs), microRNA targeting, and alternative RNA processing in health and disease. His lab's current research focuses on large-scale quantitative analysis of protein-RNA affinity, integrative analysis of RBP function, and the effects of pre-mRNA splicing on gene expression, using a combination of high-throughput and targeted molecular approaches in combination with computational methods. His awards include the Overton Prize for Computational Biology in 2001, the Technology Review Young Innovator's Award in 2002, a Searle Scholar Award in 2003 and the Schering-Plough Research Institute Award in 2007 and is the author of over 120 publications relating to post-transcriptional gene regulation, molecular evolution, and computational genomics.

Brenton Graveley

Brenton Graveley, Ph.D., is Chair of the Department of Genetics and Genome Sciences, the Health Net, Inc. Chair in Genetics and Developmental Biology, and Associate Director of the Institute for Systems Genomics. He has studied RNA biology throughout his entire career and is a recognized leader in the field of alternative splicing. He has been a lead investigator of the ENCODE and modENCODE projects. He performed his undergraduate studies at the University of Colorado, Boulder with David Prescott, his graduate studies at the University of Vermont with Greg Gilmartin, and his postdoctoral studies at Harvard University with Tom Maniatis. He joined UConn Health as an Assistant Professor in the Department of Genetics and Developmental Biology in 1999. He was a member of the Board of Directors of the RNA Society, editor of the journal RNA, a member of the National Advisory Council for Human Genome Research and is a member of the Connecticut Academy of Science and Engineering.

Jeannie T Lee

Jeannie T Lee, MD, Ph.D., is the Philip A. Sharp, Ph.D., Endowed Chair in Molecular Biology, Professor of Genetics (and Pathology) at Harvard Medical School, and Vice Chair of the Department of Molecular Biology at the Massachusetts General Hospital. Lee specializes in the study of epigenetic regulation by long noncoding RNAs and uses X-chromosome inactivation as a model system. She is a Member of the National Academy of Sciences, a Harrington Rare Disease Scholar of the Harrington Discovery Institute, a recipient of the Lurie Prize from the Foundation for the National Institutes of Health, an awardee of the Centennial Prize from the Genetics Society of America, the 2010 Molecular Biology Prize and the 2020 Cozzarelli Prize from the National Academy of Sciences, U.S.A, and a Fellow of the American Association for the Advancement of Science. Lee was also named a Distinguished Graduate of the University of Pennsylvania School of Medicine and an Investigator of the Howard Hughes Medical Institute. From 2013-2018, she co-launched the Epigenetics Initiative at Harvard Medical School and served as its co-Director. Serving on the Board of Directors of the Genetics Society of America (GSA), Lee spearheaded the TAGC (The All-Genetics) Conference in 2016. As GSA's President, Lee established a Strategic Plan and a Development strategy for the society in 2018. She received her A.B. in Biochemistry and Molecular Biology from Harvard University and obtained MD-Ph.D. degrees from the University of Pennsylvania School of Medicine. Lee then carried out postdoctoral work at the Whitehead Institute & MIT and became Chief Resident of Clinical Pathology at the Massachusetts General Hospital prior to joining the Faculty at Harvard Medical School.

Yunsun Nam

Yunsun Nam, Ph.D., is an Associate Professor in the Departments of Biochemistry and Biophysics at the University of Texas Southwestern Medical Center and a Southwestern Medical Foundation Scholar in Biomedical Research. Her undergraduate degree was in Biochemical Sciences, from Harvard College. She received her Ph.D. in Biological Chemistry and Molecular Pharmacology at Harvard Medical School, for her work on the structure and function of intracellular Notch and its activation of transcription complexes. Her postdoctoral work continued the mechanistic investigation of nucleic acid/protein complexes, focusing on Lin28 and let-7 microRNAs. For postdoctoral training, she received the Damon Runyon Cancer Research Fellowship and the Charles A. King Trust Fellowship. As an independent investigator, she was awarded Pew Biomedical Scholarship, Packard Fellowship, and Kavli fellowship. The Nam lab has been focusing on studying how RNA sequence and structure contribute to proper communication with proteins. Her group uses structural biology, biochemistry, and cell biology to study mechanisms of processing and modifications of RNAs, especially those relevant to cancer. Her group has elucidated core mechanisms of microRNA processing by Microprocessor including revealing a cryo-electron microscopy structure of the processing machinery in action. The Nam lab is continuing to investigate the regulatory pathways of small RNAs involving helicases, heme, and other modulatory factors. Further, her group has expanded the study to determine how various modification enzymes recognize and catalyze chemistry on RNAs.

Anna Pyle

Anna Marie Pyle, Ph.D., is the Sterling Professor of Molecular, Cellular and Developmental Biology and Professor of Chemistry at Yale University. She has been a Howard Hughes Medical Institute Investigator since 1997. Her research group specializes in structure and function of large RNA molecules and RNA remodeling enzymes. The Pyle laboratory uses a diverse set of biochemical and biophysical techniques, including crystallography and chemical probing, to understand the structural complexity of RNA architecture. She pioneered the study of RNA helicase enzymes and other RNA-stimulated ATPases that serve as translocases, RNA remodeling enzymes, folding cofactors and signaling enzymes in the cell. Her experimental work is complemented by efforts to develop new computational tools for modeling, analyzing and predicting RNA structure. She teaches the undergraduate Molecular Biology course at Yale, where she also leads initiatives to rebuild basic science infrastructure. At Brookhaven National labs, she is the vice-chair of the Science and Technology Steering Committee and on Beamline Advisory Teams at the NSLSII light source. Pyle has been elected president of the RNA Society and she previously served as chair of the MSFA Study Section, permanent member on the MSFE and MGB Study Sections at the National Institutes of Health. She has also organized numerous meetings, including Gordon Conferences, FASEB, Keystone and Telluride Meetings. She is the Co-Editor of Methods in Enzymology and serves on the Editorial Boards of eLife and the Journal of Molecular Biology. Pyle is a member of the American Academy of Arts and Sciences and has received two awards from the Blavatnik Fund for Innovation. She is also a fellow of the American Association for the Advancement of Science. Pyle received her Ph.D. in Chemistry from Columbia University in 1990and was a postdoctoral fellow in the laboratory of Thomas Cech.

Meni Wanunu

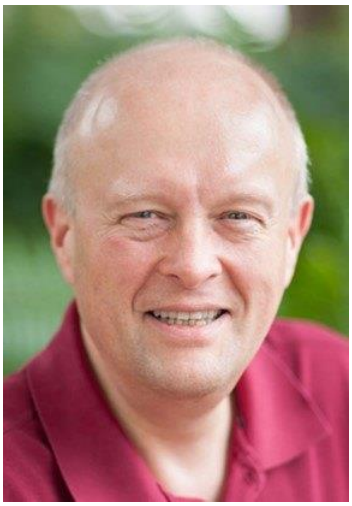
Meni Wanunu, Ph.D., is an Associate Professor in the Department of Physics at Northeastern University. Since 2017 he has served as the graduate program director at the Physics Department, and he Co-Directs Northeastern's Kostas Advanced Nano-Characterization Facility (KANCF) at Burlington MA, which specializes at atomic-resolution electron-based imaging. Wanunu is also an advisory board member at the Harvard University Center for Nanoscale Systems. He develops single-molecule methods powered by nanotechnology that address a range of challenges in biophysics and biomedical engineering in his laboratory. He is an active member of the single-molecule biophysics community, and research in his group seeks to develop novel single-molecule methods for quantifying biomolecular sequence, structure, and dynamics. In addition, he is developing nanomaterials for applications such as water purification and desalination. Wanunu has been devoted to training dozens of individuals with diverse gender, ethnic, and research backgrounds of all levels (from high school to postdoctoral associates), and currently serves on the Diversity and Inclusion Committee at the Department of Physics. He is a regular panelist for the NIH and NSF and is an academic editor of PLoS One and Journal of Nanobiotechnology.

Executive Committee Members

Vivian Cheung

Vivian G. Cheung, Ph.D., is an RNA biologist and child neurologist. She is the Frederick G.L. Huetwell Professor of Pediatrics at the University of Michigan. Cheung has a long-standing interest in gene regulation and neurogenetic disorders. Her group showed that expression levels of human genes can be studied as quantitative traits. This enabled the mapping of gene regulators without a priori knowledge of the underlying regulatory mechanisms and facilitated the identification of regulatory variants that affect disease susceptibility. This project on the genetics of human gene expression has led her group to a surprising finding of differences between RNA and its corresponding DNA sequences beyond the known RNA editing mechanisms; they referred to these as RNA-DNA sequence Differences, RDDs. Her research then revealed that RNA is modified soon after synthesis and that nucleic acid structures such as R-loops expose the RNA to modification enzymes. As a physician-scientist, Cheung takes the knowledge gained from her basic research to expand the mechanistic understanding of neurological diseases. She elucidated the molecular basis of a juvenile-onset amyotrophic lateral sclerosis due to mutations in the RNA/DNA helicase senataxin. Her group found that the patients have fewer R-loops and therefore defects in gene regulation including in the motor neurons. Additionally, her group has recently discovered a noncoding RNA whose sequence and structure regulate the expression of apolipoprotein E and is a modifier of Alzheimer's Disease. Cheung's work has shown the import of RNA sequence and structure in the regulation of cell function. She is deeply aware that the understanding of the regulatory role of RNA cannot be realized until the RNA sequences with all the modifications are known. She is committed to obtaining the complete RNA sequence with all the modifications. Cheung is a recipient of the Curt Stern Award from the American Society of Human Genetics. She is a member of the National Academy of Medicine. She served as the President of the American Society for Clinical Investigation in 2016. She is one of the founders of the Physician-Scientist Support Foundation. Cheung is a determined advocate for a diverse biomedical workforce. Her students and trainees have won prestigious awards including the Rhodes scholarship and the Harold Amos Medical Development Award.

Peter Dedon



Peter Dedon, MD, Ph.D., is the Singapore Professor in the Department of Biological Engineering at MIT and the Lead Principal Investigator in the Singapore-MIT Alliance for Research and Technology Antimicrobial Drug Resistance IRG. With a research program that applies chemical approaches to nucleic acid biology, his group has developed a variety of analytical and informatic platforms for basic and translational research in epigenetics, epitranscriptomics, and genetic toxicology in infectious disease and cancer. One platform coordinates new sequencing technologies, comparative genomics, and mass spectrometry to discover novel epigenetic marks, such as phosphorothioate, hypoxanthine, and 7-deazaguanine modifications in bacterial and bacteriophage genomes in the human microbiome. In the realm of the epitranscriptome – the dozens of modified ribonucleosides in all forms of RNA – his team has developed and applied systems-level analytics to discover a mechanism of translational regulation of gene expression in bacteria, parasites, mammalian cells and humans. This response mechanism coordinates stress-specific reprogramming of 40-50 different tRNA modifications with alternative genetic information consisting of biased used of synonymous codons in families of stress response genes. The net result is selective translation of codon-based gene families essential for survival or phenotypic change. Pete and colleagues are leveraging these discoveries to develop new enzymatic tools for biotechnology, new methods for industrial microbiology and protein production, and novel antimicrobial agents and biological therapeutics.

Brenton Graveley

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Blanton Tolbert

Blanton S. Tolbert, Ph.D., is the Rudolph and Susan Rense Professor of Chemistry at Case Western Reserve University (CWRU). He is also a member of the Center for RNA Science and Therapeutics and the Case Comprehensive Cancer Center (Case CCC). Tolbert is the Inaugural Vice Dean of Diversity, Equity and Inclusive Excellence at the CWRU School of Medicine and the Associate Director of DEI at Case CCC. He leads a diverse research group that studies biochemical mechanisms by which RNA and Retroviruses replicate within the cellular environment. His group leverages their fundamental understanding of the molecular biology of these viruses, specifically structural mechanisms of host-viral RNA interactions, to identify novel targets for therapeutic intervention. Tolbert is a Principal Investigator on several NIH grants including the Nuclear Gene Expression Project of the U54 Center for HIV RNA Studies. Tolbert is the acting Chairperson of the NIH Office of AIDS Research Advisory Council. He is also a member of the NIH HVCD study section and the Burroughs Welcome Fund Postdoctoral Enrichment Program (PDEP) Advisory Board. He is an editorial board member of the Journal of Biological Chemistry and Microbiology and Molecular Biology Reviews.