

10:00am

10:00 – 11:45am

Symposium 1: From Flames to Genes: Identifying Epigenetic Modifications as a Potential Mechanism linking occupational Exposures to Adverse Health Outcomes in First-Responders

Chair: PhD Luke Montrose

Firefighters are at an increased risk of cancer due to their occupational chemical exposures. Cancer remains the major cause of death among firefighters, with 9% higher risk of developing several types of cancers and 14% higher rate of mortality from their cancer compared to the general public. This symposium highlights the forefront of research on the epigenetic impacts of occupational exposure, focusing on its implications for both immediate and heritable health outcomes. It aims to explore how occupational exposures can lead to significant and lasting changes in the epigenome, posing risks not only to those directly exposed but also potentially affecting germ cells and future generations. The symposium will showcase innovative tools and methodologies including genomics, epigenomics, and transcriptomics, that elucidate the mechanisms by which these environmental stressors alter gene expression and epigenetic patterns. By presenting advancements in technologies such as high-throughput sequencing methods (Illumina arrays, nanopore approaches, etc.) and sophisticated bioinformatic analyses, the symposium seeks to bridge the gap between mechanistic insights and practical applications to mitigate the health risks associated with occupational exposure. This session will foster discussions on translating these findings into actionable strategies to address real-world environmental health challenges and hereditary risk factors associated with occupational exposures. This symposium will also bring awareness to scientist experts in genomics, epigenomics, and transcriptomics, a severely understudy-population with higher risk of cancer development and mortality rate.

10:00 – 10:25am | S01

When Strength Meets Smoke: Assessing the Molecular Toll of Wildland Firefighting on Respiratory Health

Olorunfemi Adetona¹¹ The Ohio State University

10:25 – 10:50am | S02

Epigenetics and Wildland Firefighting

Jaclyn Goodrich¹¹ University of Michigan

11:15 – 11:30am | S04

Firefighters' Occupational Exposures: Impact on Genomic Integrity and DNA Repair Capacity

Sneh Toprani¹¹ Harvard T H Chan School of Public Health

11:30 – 11:45am | S05

Persistent transcriptomic changes following repeated exposure to wood smoke in non-human primate airway epithelial cells

Evan Holmes¹¹ California National Primate Research Center

10:50 – 11:15am | S03

Air pollutants, occupational exposures, and the sperm epigenome: impacts on fertility and offspring health

Tim Jenkins¹¹ Brigham Young University

10:00 – 11:45am

Symposium 2: Beyond DNA: Role of RNA in Genome Integrity and Mutagenesis

Chairs: PhD Kyle Miller, Ning Tsao

Emerging evidence has identified an important but poorly understood role for RNA in genome protection mechanisms. This includes not only RNAs that associate with DNA damaged loci in cells but also damage directly to RNA that can elicit a cellular response to mutagens. RNA modifications provide another layer of regulation, with several identified to date to function in mutagenesis and genome integrity pathways, including during DNA repair. This symposium will bring together experts in this emerging field to discuss recent advancements and future directions for identifying and studying RNA in processes that maintain genome stability and function.

10:20 – 10:40am | S07

Function of the m5C RNA Modification in R-Loops

Li Lan¹¹ Duke University

10:40 – 11:00am | S08

RNA Acetylation Couples R-Loop Processing to Inflammation

Blerta Xhemalçe¹¹ Emory University School of Medicine

Session continues on next page

11:00 - 11:15am | S09

RNA Damage on R-loops is Prevented by DNA Polymerase η in Human Cancer Cells

Herene Saint-Clair¹

¹ Florida International University

11:15 - 11:30am | S10

Transcript RNA Serves as a Template for Pol ζ -Dependent DSB Repair

Alessandra Brambati¹

¹ University of Colorado – Anschutz Medical Campus

11:30 - 11:45am | S11

PARP1 Links DNA Damage to Translation Arrest

Remi Buisson¹

¹ University of California Irvine

10:00 - 10:20am | S06

ASC-1 Defines a Unifying Ubiquitin-Dependent Quality Control Principle for Stalled Ribonucleoprotein Machines

Nima Mosammaparast¹

¹ Washington University in St. Louis

11:45am

11:45am - 12:00pm

Break

12:00pm

12:00 - 1:30pm

Poster Session 1: DNA Repair

Chair: PhD Kyle Miller

12:00 - 12:05pm | PS01

NEIL1 Control of Mitochondria-Related Gene Expression and Isoform Usage

Magan Pittman^{1,2}

¹ Mitchell Cancer Institute, University of South Alabama Health, ² Department of Biochemistry and Molecular Biology

12:05 - 12:10pm | PS02

Non-Canonical Activity of DNA Glycosylase NTHL1 Forming DNA-Protein Crosslink

Yukitomo Arao¹

¹ NIEHS

12:10 - 12:15pm | PS03, Standard Best Abstract Award Winner

Mechanisms of APE1 Substrate Specificity During BER Proofreading

Chantal Kontor^{1,2}

¹ Fox Chase Cancer Center, ² Drexel University College of Medicine

12:15 - 12:20pm | PS04

Formaldehyde-Induced Lesions Promote R-loop Formation and Mutagenesis in Yeast

Charlotte McGuinness¹

¹ Medical University of South Carolina

12:20 - 12:25pm | PS05, Standard Best Abstract Award Winner

The Mechanisms by Which Ribonucleotides Within Telomeres Disrupt Stability

Justin Ling¹

¹ University of Kansas Medical Center

12:25 - 12:30pm | PS06, Standard Best Abstract Award Winner

Investigating the Mechanisms of the Replication Stress Response to Telomeric Oxidative Damage

Theresa Heidenreich^{1,2}

¹ University of Pittsburgh, ² UPMC Hillman Cancer Center

12:30 - 12:35pm | PS07

Resolution of R-Loops by Mph1 and Regulation by Top3-Rmi1 Complex

Grace Waterman¹

¹ Department of Chemistry, North Carolina State University

Session continues on next page

12:35 - 12:40pm | PS08

Targeting antioxidant enzymes to telomeres reduces oxidative damage and improves cell survival after oxidative stress

Gannon McDonough¹

¹ Department of Pharmacology and Chemical Biology, University of Pittsburgh School of Medicine

12:40 - 12:45pm | PS09

Manganese Induces Oxidative RNA Damage on R-Loops of a Long Noncoding RNA in Human Cancer Cells

Thalia Oliveros¹

¹ Florida International University

12:45 - 12:50pm | PS10

Mechanisms of PARP1 Mediated Resolution of R-loops and Their Impact on Genome Stability

Jennifer Rakowski^{1,2}

¹ Department of Pharmacology and Chemical Biology, University of Pittsburgh School of Medicine, ² UPMC Hillman Cancer Center

12:50 - 12:55pm | PS11, Standard Best Abstract Award Winner

Impact of nucleotide metabolism on telomerase mediated telomere synthesis in cancers

Samantha Sanford¹

¹ University of Pittsburgh

12:55 - 1:00pm | PS12

Structural Effects of Genomic Ribonucleotides on TRF1 and TRF2 Binding to Telomeres

Anzhou He¹

¹ University of Kansas Medical Center

1:00 - 1:05pm | PS13

Modeling the Competition Between Transcription Factors and DNA Repair Enzymes for Recognition of DNA Mismatches

Anthony Lau¹

¹ UMass Chan Medical School

12:00 - 1:30pm

Poster Session 2: Genotox

Chairs: Hailey Levi, Stefan Pfuhler

12:00 - 12:05pm | PS14

Miniaturized Ames Tests for Nitrosamine Mutagenicity Screening: A Systematic Cross-Platform Validation of Ames MPF and the 6-well Agar Plate Format

Csaba Boglari¹

¹ Xenometrix

12:20 - 12:25pm | PS18

In-vivo Model to Study Dietary Effects of Dietary Genistein on MLL-AF9 Translocations Analogous to Leukemia

Molly White¹

¹ University of North Carolina at Charlotte

12:45 - 12:50pm | PS23

Molecular insights into the distinct modulation of human thioredoxin reductase-1 by brevetoxin-2 and brevenal

Eman Taher¹

¹ Florida International University

12:40 - 12:45pm | PS22

Sub-Chronic, Low Dose Exposure to Dihydroxyacetone Induces DNA Damage, Mitochondrial ROS Production, and Metabolic Changes

Hailey Levi¹

¹ University of Alabama at Birmingham

1:10 - 1:15pm | PS28

Characterizing Biological Effects of Firefighter Uniforms Residues from a Variety of Fire Incidents Types

Aris Polyzos¹

¹ Lawrence Berkeley National Lab

12:30 - 12:35pm | PS20

Error-corrected sequencing reveals population differences in cancer driver mutation burden in normal breast tissue

Kelly Harris¹

¹ National Center for Toxicological Research

12:15 - 12:20pm | PS17

Are the Ames and In Vitro Micronucleus Assays Sufficient for Reliable Genotoxicity Screening of Botanical Extracts?

Stephanie Smith-Roe¹

¹ NIEHS

12:10 - 12:15pm | PS16, AGT SIG Best Abstract Award Winner

High Quercetin Diet Induces DNA Damage and Inter-Chromosomal Recombination in Reproductive Organs

Lorraine Iacob¹

¹ University of North Carolina at Charlotte

1:00 - 1:05pm | PS26

Dynamic Interaction of Brevetoxins with Human Thioredoxin Reductase

Oscar Delgado¹

¹ Florida International University

12:50 - 12:55pm | PS24

Update on Nitrosamine Studies

Rosalie Elespuru¹

¹ US FDA, retired

12:25 - 12:30pm | PS19

Multimodal phenotyping of mutation-induced metabolic alterations and histopathology in ocular and tumor-bearing mouse tissues using novel label-free Multi-Laser imaging.

Natnail Tsehay¹

¹ University of Western Ontario

12:05 - 12:10pm | PS15, Standard Best Abstract Award Winner

Establishment of a Chromatin Dynamics-Based Assessment Framework for Non-Genotoxic Carcinogens

Keigo Yamakita¹

¹ Department of Biology

12:35 - 12:40pm | PS21

Determining Risk of Dietary and Environmental Compounds to Induce Translocations Analogous to Human Leukemia

Emilee Trivette¹

¹ University of North Carolina at Charlotte

12:55 - 1:00pm | PS25

Brominated Azo Dyes are Mutagenic in the Bacterial Reverse Mutation Test, but show Dye-Specific Effects in the Peripheral Blood Micronucleus Assay

Xinwen Zhang¹

¹ NIEHS

1:05 - 1:10pm | PS27

How do A-549 tumor cells with reduced antioxidant defense respond to chronic exposure to metals?

Carlos Ryu Pérez Akiyama¹

¹ Instituto de Investigaciones Biomédicas, Universidad Nacional Autónoma de México

1:30pm

1:30 - 2:00pm

Lunch Break

2:00pm

2:00 - 3:00pm

Keynote Lecture: Dr. Chris Mason

2:00 - 3:00pm | K01

Single-Molecule Mapping of Genetic and Epigenetic Radiation Responses From Spaceflight

Christopher Mason¹

¹ Weill Cornell Medicine

3:00pm

3:00 - 3:15pm

Break

3:15pm

3:15 - 4:45pm

Platform 1: DNA Repair

Chairs: Wentao Li, Peng Mao, Lindsay Volk

3:15 - 3:30pm | P01, Standard Best Abstract Award Winner

DNA Repair Capacity and Developmental Stage Shape NDMA-Induced Genotoxicity, Clonal Expansion, and Early Tumorigenesis

Lindsay Volk¹

¹ MIT

3:30 - 3:45pm | P02

Phosphorylation of Yeast Elf1 Facilitates TFIIH Recruitment in Transcription-Coupled Nucleotide Excision Repair

Vedanth Bellad Shivashankar¹

¹ Department of Molecular Biosciences, University of South Florida

3:45 - 4:00pm | P03

A Tool for Genome-wide Induction of 8-oxoguanine to Study DNA Biology and Genome Stability

Aninda Dey¹

¹ University of Kansas Medical Center

4:00 - 4:15pm | P04, Standard Best Abstract Award Winner

Aberrant PCNA Interactions by DNMT1 Promotes Replication Stress and Mutagenesis Independently of DNA Methylation

Jullian Perren¹

¹ Emory University

4:15 - 4:30pm | P05

Temozolomide Increases RNA Methylation in Glioblastoma

Brandon Ho¹

¹ University of California San Diego

4:30 - 4:45pm | P06

TARGETING DNA REPAIR "SCARS" IN THE CANCER GENOME USING CRISPR

Vanessa Quevedo Barrios¹

¹ University of Michigan

3:15 - 4:45pm

Platform 2: New Approach Methodologies and Emerging Biomarkers for Genotoxicity Assessment

Chairs: Hailey Levi, Xilin Li

3:15 - 3:30pm | P07

Human Liver MPS: A Paradigm Shift in Genotoxicity Testing for Drug Development

Ammer Khawam¹

¹ CRL

3:30 - 3:45pm | P08

Human iPSC-Derived Liver Organoids as an In Vitro Platform for Metabolism-Mediated Genotoxicity Assessment

Ryosuke Morozumi¹

¹ National Institute of Health Sciences

3:45 - 4:00pm | P09

Chromatin-Based DNA Damage Response Analysis for Biologically Relevant Detection of Genotoxicity

Katsuyoshi Horibata¹

¹ Division of Genome Safety Science, National Institute of Health Sciences

4:00 - 4:15pm | P10, GRAPH SIG Best Abstract Award Winner

Sub-chronic Dihydroxyacetone Activates PTEN/AKT/MYC Signaling to Drive Pro-tumorigenic Transformation in Human Bronchial Epithelial Cells

Nayonika Mukherjee¹

¹ Department of Pathology, Heersink School of Medicine, University of Alabama at Birmingham

Session continues on next page

4:15 - 4:30pm | P11

Characterizing common loss-of-function genes and their potential utility in assessing population variability and chemical susceptibility in vitro

CHAN HEE KIM^{1,2}

¹ University of Florida, ² California State University, Northridge

4:30 - 4:45pm | P12

Dose-Dependent Clonal Selection of Cancer-Associated Gene Mutations in MutaMouse Lung Tissue Following 180-Day Benzo[b]fluoranthene Exposure

Meagan Myers¹

¹ National Center for Toxicological Research

4:45pm

4:45 - 5:00pm

Break

5:00pm

5:00 - 6:00pm

EMGS Young Investigator Spotlight

5:00 - 5:30pm | Y01

Genetic Architecture of Susceptibility to PFAS Revealed by Pooled-population Sequencing in *Caenorhabditis elegans*

Tess Leuthner¹

¹ Indiana University

5:30 - 6:00pm | Y02

Mechanisms of Chromatin-Based Single-Strand Break Repair

Tyler Weaver¹

¹ University of Virginia School of Medicine

6:00pm

6:00 - 6:15pm

Break

6:15pm

6:15 - 7:00pm

Business Meeting

No more sessions on Monday 12 October 2026

Tuesday 13 October 2026

10:00am

10:00 - 11:45am

Symposium 3: Diverse Approaches in Error-Corrected Next-Generation Sequencing-Innovations and Applications in Genetic Toxicology

Chairs: PhD Nimrat Chatterjee, PhD Natalia Cestari Moreno, PhD Shaofei Zhang | Sponsors: MutagenTech

Recent advancements in error-corrected next-generation sequencing (ecNGS) have the potential to revolutionize genetic toxicology by providing exceptional accuracy in detecting low-frequency mutations through the minimization of sequencing and PCR errors. These advancements address the limitations of traditional sequencing methods, enabling more precise and reliable mutation analysis. In vivo applications of ecNGS have proven effective in identifying both spontaneous and chemically induced mutations across various tissues in wild-type animals, serving as an ideal alternative to traditional TGR assays that rely on artificial reporter genes in genetically engineered animals. In vitro applications of ecNGS have broadened its utility, enabling the detection of mutations in human-derived cells with metabolic capabilities, such as HepaRG cells in both 2D and 3D models. These models provide a more accurate representation of human biology, enhancing the relevance and applicability of ecNGS in genetic toxicology. Furthermore, the versatility of ecNGS methods allows them to be tailored to specific applications, whether in vivo or in vitro. For instance, some methods are optimized for detecting ultra-low-frequency mutations in targeted genomic loci, while others excel in analyzing mutations and structural variants at a genome-wide scale. The adaptability ensures that ecNGS technologies can address a broad spectrum of toxicological challenges. This symposium will highlight the diversity of ecNGS methods and emphasize the latest developments and applications, promoting the regulatory adoption of ecNGS in genetic toxicology.

10:50 - 11:15am | S14

One Read, Two Strands: Reinventing Duplex Sequencing with CODEC for Ultra-Sensitive Mutation Detection

Azeet Narayan^{1,2}

¹ Broad Institute of MIT and Harvard, ² Broad Clinical Labs

Session continues on next page

10:25 - 10:50am | S13

Advancing HiFi Sequencing for Sensitive Detection of Mutations in Genetic Toxicology

Javier Revollo¹

¹ Food and Drug Administration

11:15 - 11:30am | S15, MMA SIG Best Abstract Award Winner

Assessment of Nitrosamine Drug Substance-Related Impurities (NDSRIs): Mutagenic Potency in 3D HepaRG Spheroids

Ji-Eun Seo¹

¹ US FDA, National Center for Toxicological Research

11:30 - 11:45am | S16

Measuring DNA Repair to Understand Mechanisms of Disease and Improve Public Health

Zachary Nage¹

¹ Harvard School of Public Health

10:00 - 10:25am | S12

SMM-seq (Single-Molecule Mutation Sequencing) for the Detection of Ultra-Rare Somatic Mutations and Structural Variants

Christopher Bradley¹

¹ Mutagentech, Inc.

10:00 - 11:45am

Symposium 4: Converging on NAM: Building scientific confidence in the regulatory application of genotoxicity New Approach Methods (NAMs)

Chairs: PhD Steve Bryce, Andreas Zeller | Sponsors: Frontage Laboratories

Traditional regulatory assessments involve the evaluation of genotoxicity data from a standard test battery of in vivo and in vitro assays, many of which have been in use for several decades. The long history of their use has provided tremendous knowledge and experience with such endpoints, however the current test battery is not well aligned with the evolving vision of higher-throughput, human-relevant mechanistic assays to inform risk assessment. New approach methodologies (NAMs), commonly defined as approaches that are not in intact animals, are valuable when assessing mode of action and elucidating molecular mechanisms of genotoxicity. Genotoxicity NAMs are now being commonly used for higher-throughput screening, to predict the outcome of GLP compliant assays, or to investigate potentially artefactual positive test results obtained from mammalian cell genotoxicity tests. However, the work to incorporate these NAMs into standard genotoxicity testing paradigms is ongoing. Although it is well recognized that genotoxicity NAMs can provide important mechanistic characterization of the genotoxic response, in order to build scientific confidence in their applicability for routine regulatory assessment of genotoxic substances it is important to continue foundational work to compare NAM outcomes with standard in vivo assay results, as well as to investigate their utility for quantitative prediction of a NAM-based point-of-departure. In this symposium, we will bring together international experts from government and industry to work on the shared challenges and vision of building scientific confidence in the regulatory application of genotoxicity NAMs.

10:50 - 11:15am | S17

A Digital Pathology Artificial Intelligence (AI) Readout for Single Cell Apoptosis Evaluation in Organoids and Tissues

Nadine Stokar-Regenscheit¹

¹ Roche Pharma Research and Early Development, Pathology and Applied Safety Sciences, Roche Innovation Center Basel, F. Hoffmann-La Roche Ltd

10:00 - 10:25am | S18

A Case Study on the Use of an Integrated Approach for Testing and Assessment for Refining Inhalation Risk Assessment from a Point of Contact Toxicity.

Clive Roper¹

¹ Roper Toxicology Consulting Limited

10:25 - 10:50am | S19

Genotoxicity Assessment in Agrochemicals: Integrating NAMs and Mechanistic Insights

Caroline Hilmi¹

¹ BAYER

11:15 - 11:40am | S20

A Meta-Analysis on in Vitro Genotoxicity Data for DNA-Alkylating Agents

Levi Winkelman¹

¹ Leiden University, Leiden Academic Centre for Drug Research, Division of Cell Systems & Drug Safety

11:45am

11:45am - 12:00pm

Break

12:00 - 1:30pm

Poster Session 3: EPI-GDS

Chairs: Pini Perera, Madelin Stueck

12:00 - 12:05pm | PS29

Loss of TET1 Intensifies Diesel Exhaust Particle-Induced Th17 InflammationTrishla Mehta¹¹ UC Davis

12:05 - 12:10pm | PS30

Hyper-Methylation Near the Human Mutation Hotspots Increased the Z-DNA-Associated Genetic InstabilityGuliang Wang¹¹ The University of Texas at Austin

12:10 - 12:15pm | PS31, EPI SIG Best Abstract Award Winner

Sex-Stratified piRNA Expression Analysis Reveals Shared Functional Impacts of Perinatal Lead Exposure in Murine HeartsKimberley Sala-Hamrick¹¹ University of Michigan School of Public Health

12:15 - 12:20pm | PS32

Novel CRISPR/dCas9-Mediated Frataxin Gene-Targeted Histone Demethylation Systems Modulate GAA Repeat Instability in Friedreich's AtaxiaSteven Vo¹¹ Florida International University

12:20 - 12:25pm | PS33, Standard Best Abstract Award Winner

Structural insights into frataxin gene-targeted histone H3K27 demethylase KDM6B substrate recognition on heterochromatin in Friedreich's ataxiaLucas Bertolami¹¹ Florida International University

12:25 - 12:30pm | PS35

PyGenePanel: Tailoring Error-Corrected Sequencing Panels to Investigate Genomic Context and MutagenesisAnnette Dodge^{1,2}¹ University of Ottawa, ² Health Canada

12:30 - 12:35pm | PS36, Standard Best Abstract Award Winner

SOFMut: A Sequence-Omics Fusion Framework for Mutation risk predictionShan Jiang¹¹ Department of Environmental Health Science, College of Public Health, University of Georgia

12:35 - 12:40pm | PS37

Machine Learning Analysis of Host-Environment Genomic and Proteomic Signatures Reveals Information Beyond Phylogeny in H3N2 Influenza A VirusMadelin Stueck¹¹ School of Computer Science, University of Guelph

12:40 - 12:45pm | PS38

Evaluation of Brevetoxin on Neural Proteomic Profile and the Effects of Mercaptan-Based Cysteamine Derivatives on Brevetoxin Binding and Induced Muscle CytotoxicityMayra Tabares-Beltran¹¹ Florida International University

12:45 - 12:50pm | PS39

Reducing Cross-Species Alignment Artifacts in Targeted Duplex Sequencing Using Orthologous Decoy ReferencePage McKinzie¹¹ US Food and Drug Administration/National Center for Toxicological Research

12:50 - 12:55pm | PS40

KmeX: A Computational Toolbox for Visualizing and Quantifying Variations in Genomic SignatureNiousha Sadjadi¹¹ University of Waterloo

12:55 - 1:00pm | PS41

Profiling the *Chlorocebus sabaeus* Genome for Aflatoxin Resistance and Sensitivity Reveals a Major Role of Mitochondrial Function in Conferring AFB1 ResistanceMichael Fasullo¹¹ University at Albany

1:00 - 1:05pm | PS42

Temporal and Compartmental Extracellular Release of miRNA Biomarkers in an In Vitro-Based Model of Renal Injury

Andrea Sanchez-Navarro¹

¹ National Institutes of Diabetes and Digestive Kidney Diseases, National Institutes of Health

12:00 - 1:30pm

Poster Session 4: DNA Repair - Replication

Chair: Justin Ling

12:00 - 12:05pm | PS43

Elucidating the Role of RFWD3-Modulated Ubiquitinated RPA in DNA Damage Response Pathways

Jonathan Weinstein¹

¹ Pennsylvania State University

12:05 - 12:10pm | PS44

Molecular Basis of DNA Damage Recognition and Repair by DNA Polymerase Lambda in Chromatin

Abigayle Vito¹

¹ University of Kansas Medical Center

12:10 - 12:15pm | PS45

Investigating the non-catalytic role of DNA Polymerase Epsilon in the initiation of DNA replication

Rohan Harollikar¹

¹ University of Pittsburgh

12:15 - 12:20pm | PS46

The role of cancer associated variants of DNA Polymerase epsilon in replication initiation

Naga Raviteja Chavata^{1,2}

¹ University of Pittsburgh, ² Tallinn university of Technology

12:20 - 12:25pm | PS47

REV1 promotes tolerance of aberrant DNA re-replication

Naveen Kothandaraman¹

¹ University of Vermont

12:25 - 12:30pm | PS48

Investigating Rad6(Rad18)₂ Interactions with PCNA at Non-Canonical Sites During DNA Translesion Synthesis

Tyler Wenzel¹

¹ Pennsylvania State University

12:30 - 12:35pm | PS49

Exploring Human DNA Polymerase δ Lesion Bypass Activities

Jessica Scheer¹

¹ Penn State University

12:35 - 12:40pm | PS50

Genotoxic Effects of Synthetic Food Dye Exposure in Fanconi Anemia Patients

Mrunmai Niljekar¹

¹ Rutgers Cancer Institute

12:40 - 12:45pm | PS51

RAD54L Promotes Mitomycin C-Induced Nascent DNA Degradation and Radial Formation in FANC-Deficient Cells

Jennifer Mason¹

¹ Clemson University

12:45 - 12:50pm | PS52, Standard Best Abstract Award Winner

Self-Assembly and ATP-Dependent Activation of Human Rad51 Filaments

Grace Young¹

¹ Penn State

12:50 - 12:55pm | PS54

Role of Fork Remodeling Translocases SMARCA1 and ZRANB3 in Stalled Replication Fork Repair.

Chayan Bhattacharya¹

¹ NIEHS

1:30pm	1:30 - 2:00pm Lunch Break
2:00pm	2:00 - 3:00pm Hollaender Award Lecture 2:00 - 3:00pm A01 Clonal Expansion of Cancer Driver Gene Mutants as a New Approach Methodology for Carcinogenicity Testing <u>Barbara Parsons</u>¹ ¹ National Center for Toxicological Research, US FDA
3:00pm	3:00 - 3:15pm Break
3:15pm	3:15 - 4:45pm Student Led Session: AI and Visualization 4:11 - 4:23pm 157 KmeX: A Computational Toolbox for Visualizing and Quantifying Variations in Genomic Signature <u>Niousha Sadjadi</u>¹ ¹ University of Waterloo 3:35 - 3:47pm 156 SOFMut: A Sequence–Omics Fusion Framework for Mutation risk prediction <u>Shan Jiang</u>¹ ¹ Department of Environmental Health Science, College of Public Health, University of Georgia 3:59 - 4:11pm 158 Using AI to Discover and Visualize Extreme-Environment DNA Motifs <u>Monireh Safari</u>¹ ¹ University of Waterloo 3:47 - 3:59pm 160 Phylogenetic Eigenvector Decomposition as a Tool for Disentangling Host-Associated Signal from Shared Ancestry in Genomic Machine Learning: An H3N2 Influenza Case Study <u>Madelin Stueck</u>¹ ¹ Department of Computer Science, University of Guelph 3:15 - 3:35pm 161 Opportunities and Limitations of AI as a Scientific Tool <u>Gerald Quon</u>¹ ¹ University of California, Davis 4:23 - 4:35pm 162 From Research Code to a Reproducible R Package: Lessons from Developing MutSeqR <u>Annette Dodge</u>^{1,2} ¹ Department of Biology, University of Ottawa, ² Environmental Health Science and Research Bureau, Health Canada
4:45pm	4:45 - 5:00pm Break
5:00pm	5:00 - 6:45pm Symposium 5: Developmental Exposures and Germ Cell Health: Mechanisms, Multigenerational Effects, and Mitigation Strategies Chairs: PhD Jill Escher, Brandon Pearson, Gurugowtham Ulaganathan Developmental exposures to environmental toxins, lifestyle factors, and pharmacological agents during critical times of germ cell development can have profound effects on offspring reproductive health. Emerging evidence highlights how these exposures alter germ cell epigenetics, disrupt meiosis, and impair fertility with consequences that may extend through multiple generations. This symposium will feature the latest work on mechanisms by which developmental exposures impact germ cell health, the potential for multigenerational effects, and the implications for human reproductive health. Here we will feature experts in reproductive toxicology, epigenetics, and environmental health to foster a multidisciplinary dialogue on identifying the risks, understanding mechanisms, and developing strategies to mitigate the long-term repercussions of developmental exposures on reproductive health.

Session continues on next page

5:50 - 6:15pm | S23

Epigenetic Programming in the Parental Germlines and Epigenetic Inheritance

Satoshi Namekawa¹

¹ UC Davis

5:25 - 5:50pm | S22

Paternal Metabolic Reversal Remodels Sperm RNA Profiles and Ameliorates Intergenerational Metabolic Disorder in Mice

Wei Yan¹

¹ Washington State University

5:00 - 5:25pm | S21

Role of Metabolo-Epigenetic Pathways in Guiding Reproductive Toxicity

Patrick Allard¹

¹ UCLA

6:15 - 6:30pm | S24, GCHE SIG Best Abstract Award Winner

De Novo Mutations Arising at Meiosis Have Non-Random Associations with Heterozygosity Identified Using J-Statistic Spatial Association Tools

Joseph Butler¹

¹ University of Western Ontario

6:30 - 6:45pm | S25

Perinatal Atrazine Exposure Alters Expression of Steroid Receptors and DNA Methylation Machinery in Testis

Neelam Pandey¹

¹ ICMR - NIRRCH

5:00 - 6:45pm

Symposium 6: In Vitro Assessment of Nitrosamine Mutagenicity Beyond Hazard ID

Chairs: PhD Raechel Puglisi, PhD Zhanna Sobol

Nitrosamines are a group of mutagenic impurities that vary widely in structure, encompassing both small molecules and complex drug-related nitrosamines and ranging from Cohort of Concern compounds to weak mutagens or to non-mutagens. Hazards Identification (Hazard ID) and genotoxicity risk assessment of nitrosamines have been the subject of intensive research, leading to new insights into this class of mutagenic impurities. Many insights about potency of simple and complex nitrosamines have been gained from thorough in vivo investigations using transgenic rodent (TGR) models and error-corrected sequencing. In addition to developing a risk assessment paradigm using in vivo studies, in vitro approaches have proven to be valuable tools to provide mechanistic insights into potency and thereby risk assessment for nitrosamines. This symposium will delve into some of the in vitro studies that go beyond hazard ID and provide risk assessment insights that may eventually minimize the need for in vivo studies.

5:25 - 5:50pm | S27

Translating Enhanced Metabolic Activation into a Quantitative Mammalian NAM for Nitrosamines

Steven Bryce¹

¹ Litron

5:50 - 6:15pm | S28

Metabolic Activation and DNA Adduct Formation of Complex Nitrosamines: *N*-Nitroso-sertraline as an Example

Qiangen Wu¹

¹ National Center for Toxicological Research, US Food and Drug Administration

6:15 - 6:40pm | S29

Optimizing HepaRG-Based Approaches for Nitrosamine Genotoxicity Assessment: Applications in DNA Damage Response and Mutagenicity Testing

Wen Sun¹

¹ Pfizer

No more sessions on Tuesday 13 October 2026

Wednesday 14 October 2026

10:00am

10:00 - 11:45am

Symposium 7: Cell-free and Exosomal DNA in Environmental Genotoxin Exposure

Chairs: PhD Alexandra Carpenter, PhD Michael Kemp

Cell-free DNA present in biofluids is increasingly being utilized for both the diagnosis of different disease states and to guide treatment strategies. DNA found in these liquid biopsies originates from nuclei and mitochondria of diverse cell types and can be released as chromatin fragments, as NETs, or in association with extracellular vesicles. The release of this DNA is impacted by exposures to various stressors and DNA repair processes and is often associated with cell death. FDA approved uses for cell-free

Session continues on next page

DNA include monitoring of fetal health via maternal blood draw, detection of cancer, and monitoring of tumor mutational signatures. Research in the field has also demonstrated that cell-free DNA sampling can observe epigenetic changes in disease, predict cancer relapse, and identify nucleases responsible for fragmentation of cell-free DNA that can contribute to autoimmune disorders. Lastly, though cellular DNA is known to contain DNA adducts following exposure to various DNA damaging environmental genotoxins, the presence of DNA lesions on cell-free DNA has not been extensively explored. This symposium will therefore explore the origins of cell-free DNA, mechanisms of chromatin fragmentation in the extracellular space, the diagnostic and therapeutic use of these DNAs in liquid biopsies, and the impact that environmental genotoxins may have on the abundance and functional properties of these extracellular DNA species.

10:00 - 10:25am | S30

Nucleic Acid Adductomics: A Tool to Dissect Exposome?

Marcus Cooke¹

¹ University of South Florida

10:50 - 11:15am | S32

Illuminating the Cancer Journey With Cell-Free Whole Genome Sequencing

Trevor Pugh^{1,2}

¹ Princess Margaret Cancer Centre, University Health Network, ² Ontario Institute for Cancer Research

11:15 - 11:30am | S33

***Staphylococcus aureus* induced oxidative stress causes fragmentation and extracellular release of nuclear DNA fragments from mouse and human airway epithelial cells**

Kayla Law¹

¹ University of Minnesota

11:30 - 11:45am | S34

Circulating cell-free DNA as a biomarker of environmentally induced tissue injury and molecular damage

Olga Tselousova¹

¹ Bashkir State Medical University

10:25 - 10:50am | S31

Beyond Mutations: Cell-Free DNA for Noninvasive Profiling of Cancer and the Tumor Microenvironment

Aadel Chaudhuri¹

¹ Mayo Clinic

10:00 - 11:45am

Symposium 8: Sex differences in the response to mutagens

Chairs: PhD Isabelle Miousse, PhD Raechel Puglisi

Historically, biomedical research, including genetic toxicology, has predominantly focused on male subjects. This bias extended beyond animal models to human studies, which primarily involved men until the mid-1990s. To this day, many countries do not have requirements for the inclusion of female animals in research, and of women in clinical trials. Even in the United States where such requirements do exist, women represent only around 42% of subjects in recent clinical trials. Furthermore, some genetic toxicology guidelines do not require the inclusion of both sexes. These practices have often overlooked sex as a key variable that can contribute to an individual's response to environmental mutagens. Recently, requirements have shifted to consider Sex as a Biological Variable (SABV), driving studies to include both sexes and assess sex-based differences. Specifically, sex has emerged as a significant factor in the metabolism and susceptibility to environmental mutagens. These differences may arise from variations in the activity of DNA repair pathways, hormone expression, and metabolic processes. Such sex-based disparities are both widespread and complex, highlighting the need for further investigation. This session will bring together experts from diverse disciplines to explore sex-influenced mechanisms in mutagen sensitivity, highlighting key differences in pathways and processes and their broader implications.

10:00 - 10:25am | S35

Sex as a Factor in Murine Radiation Research and Medical Countermeasure Development

Gregory Holmes-Hampton¹

¹ Armed Forces Radiobiology Research Institute

10:25 - 10:50am | S36

Sex and Gender Differences in Environmental Carcinogen Exposure and Cancer Risk

Berna Özdemir¹

¹ University Hospital Bern, Department of Medical Oncology

10:50 - 11:15am | S37

Sex-Specific Functional and Epigenetic Effects of Lead (Pb) Exposure on the Heart

Laurie Svoboda¹

¹ University of Michigan

11:15 - 11:30am | S38

Exposure to Emerging Contaminants: Differential Response Between Female and Male *Drosophila Melanogaster*

Adriana Muñoz-Hernández¹

¹ Laboratorio de Genética y Toxicología Ambiental-Banco de Moscas, Facultad de Ciencias, UNAM

11:30 - 11:45am | S39, GDS SIG Best Abstract Award Winner

Single-Cell Somatic Copy-Number Alteration Profiling Across Lifespan Reveals a Sex-Divergent Clock-Like Aging Signature

Bingru Feng¹

¹ Texas A&M Institute of Biosciences and Technology

11:45am

11:45am - 12:00pm

Break

12:00pm

12:00 - 1:30pm

Poster Session 5: Mutagenic Mechanisms and Assessments

Chair: Ana Cheong

12:00 - 12:05pm | PS55

Deposition of Microplastics Associated With Heavy Metals in Human Lungs of Smokers: Implications of Adsorption and Mobilization of Metals via Microplastics-Mediated Lung Damage

Irfan Rahman¹

¹ University of Rochester

12:05 - 12:10pm | PS56

Adaptive Laboratory Evolution Highlights Hidden Actors in Redox Stress Response

Natalya Degtyareva¹

¹ NIEHS

12:10 - 12:15pm | PS57

ATF2 Signaling as a Mechanistic Node in Radiation-Induced Esophageal Carcinogenesis

Manas Yogendra Agrawal¹

¹ Department of Health Physics and Diagnostic Sciences, School of Integrated Health Sciences, University of Nevada, Las Vegas

12:15 - 12:20pm | PS58

Impact of Cell-Cycle Progression on Transcription-Associated Mutagenesis

Aimi Yoshida¹

¹ Division of Genome Safety Science, National Institute of Health Sciences

12:20 - 12:25pm | PS59

Methylglyoxal-Induced Mutagenesis Through Various Repair Pathways

Kierra Marshall¹

¹ Medical University of South Carolina

12:25 - 12:30pm | PS60

Investigating the Role of Oxidative Stress in DNA Damage Induced by Natural Compounds

Rashad Badr¹

¹ University of North Carolina at Charlotte

12:30 - 12:35pm | PS62

Non-Canonical Functions of REV1 Drive Viral Pathogenesis and Cancer Therapy Resistance

Nimrat Chatterjee¹

¹ University of Vermont

12:35 - 12:40pm | PS63, Standard Best Abstract Award Winner

Exploring REV7-dependent therapeutic vulnerabilities to suppress cancer resistance

Madison Guyette¹

¹ University of Vermont

12:40 - 12:45pm | PS64, Standard Best Abstract Award Winner

Novel mechanisms of Autophagy-dependent resistance in REV1-depleted cells

Sombodhi Bhattacharya¹

¹ Department of Microbiology and Molecular genetics, Larner college of medicine, University of Vermont

12:45 - 12:50pm | PS65

Pol V (rumAB) genomic position is important for ICE R391 transfer

Douglas Lyra de Holanda Fonseca¹

¹ NIH/NICHD

Session continues on next page

12:50 - 12:55pm | PS66

Regulation of G-quadruplex structures in ribosomal DNA and nucleolar function

Kelly McGhee¹

¹ UNC Charlotte

12:55 - 1:00pm | PS67

Duplex Sequencing to investigate hypermutability in E. coli

Niketa Bhawsinghka¹

¹ National Institute of Environmental Health Sciences

1:00 - 1:05pm | PS68

Genetic heterogeneity associated with breast cancer and lung metastasis: A scoping review

Nishita Pillai¹

¹ Department of Biology, Western University

1:05 - 1:10pm | PS61

Differential Targeting of Pubertal Mammary Tissue Structures by Genotoxicants and Estrogens in Early Carcinogenesis

Jennifer Kay¹

¹ Silent Spring Institute

12:00 - 1:30pm

Poster Session 6: DNA Damage and Repair

Chair: Elijah Newcomb

12:00 - 12:05pm | PS70

Cell-Free DNA (cfDNA) Release From Human Keratinocytes Is Modulated by Exposure to Solar-Simulating UV Radiation and Photosensitizing Drugs

Michael Kemp^{1,2}

¹ Wright State University, ² Dayton VA Medical Center

12:05 - 12:10pm | PS71

Investigating the Impact of ATF2 Knockout on Cellular Response to Radiation in Human HAP1 Cells

Ghazal Darfarin¹

¹ Department of Health Physics and Diagnostic Sciences, University of Nevada, Las Vegas,

12:10 - 12:15pm | PS73, Standard Best Abstract Award Winner

High-Resolution Mapping of Transcriptional Restart Dynamics Following UV-Induced Genotoxic Stress

Noga Gluska¹

¹ Department of Microbiology and Molecular Genetics, The Institute for Medical Research Israel-Canada, The Faculty of Medicine, The Hebrew University of Jerusalem

12:15 - 12:20pm | PS74

Low-Dose Radiation Induces Persistent Phenotypic and Transcriptional Changes in Human Mammary Organoids

Ada Antypiuk¹

¹ University of Nevada Las Vegas

12:20 - 12:25pm | PS75

Repurposing an Antidiabetic Drug in Gastrointestinal Acute Radiation Syndrome

Isabelle Miousse¹

¹ University of Arkansas for Medical Sciences

12:25 - 12:30pm | PS76, Standard Best Abstract Award Winner

Transport and Response to Cell-Free Cyclobutane Pyrimidine Dimers Using Synthetic Nucleoside Tools

M Carpenter¹

¹ Duquesne University

12:30 - 12:35pm | PS77

Proximal Poly(ADP-Ribose)-Associated Protein Complexes in Response to DNA Damage

Robert Sobol¹

¹ Brown University

12:35 - 12:40pm | PS78, Standard Best Abstract Award Winner

Structural basis of end processing in the nucleosome by polynucleotide kinase/phosphatase

Daniel Boesch¹

¹ University of Virginia

12:40 - 12:45pm | PS79, Standard Best Abstract Award Winner

ATR Inhibition Sensitizes Cancer Cells to Telomere Replication Stress

Alex Garbouchian¹

¹ University of Kansas Cancer Center

12:45 - 12:50pm | PS80, Standard Best Abstract Award Winner

Architecture of the human HIRA complex reveals a pathway for H3.3 nucleosome assembly

Nicole Hoitsma^{1,2}

¹ CU Boulder, ² HHMI

12:50 - 12:55pm | PS81, DNA Repair SIG Best Abstract Award Winner

CRISPR/dCas9-Mediated Frataxin Gene-Targeted Histone Demethylation Upregulates Frataxin Gene Expression by Contracting GAA Repeat in Friedreich's Ataxia

Sutirtha Sengupta¹

¹ Florida International University

1:30pm

1:30 - 2:00pm

Lunch

2:00pm

2:00 - 3:00pm

Keynote Lecture: Dr. Allan Balmain

K02

Genetic and environmental effects on cell-cell competition and clonal selection

Allan Balmain¹

¹ University of California, San Francisco

3:00pm

3:00 - 3:15pm

Break

3:15pm

3:15 - 4:45pm

Platform 3: DNA Damage Responses at Replication Forks and Telomeres

Chairs: Marta Markiewicz-Potoczny, Jennifer Mason

3:15 - 3:26pm | P13

Single-Strand DNA Breaks Induce Distinct Double-Strand Break Repair Outcomes Following Collapse of Single Versus Convergent Replication Forks

James Dewar¹

¹ Vanderbilt University School of Medicine

3:26 - 3:37pm | P14, Standard Best Abstract Award Winner

Uncovering the Role of RPA in APE1-Mediated DNA Damage Search and Recognition at Replication Forks

Peyton Oden¹

¹ University of Kansas Medical Center

3:37 - 3:48pm | P15, Standard Best Abstract Award Winner

DHX36 Helicase Binds Various DNA Damage Lesions Generated During DNA Repair and Replication

Elijah Newcomb¹

¹ University of Kansas Medical Center

3:48 - 3:59pm | P16

DNA Repair Dependency Mapping of the Human TLS Polymerases

Peter Stirling¹

¹ BC Cancer Research Institute

3:59 - 4:10pm | P17

Defining the Role of the Fanconi Anemia Pathway in DNA-Protein Crosslink Repair and Repair Pathway Choice

Rajula Elango Alleva¹

¹ National Institutes of Environmental Health Sciences

4:10 - 4:21pm | P18

Modulation of the long non-coding RNA TERRA by telomeric 8-oxoguanine damage in ALT+ cancer cells

Mariarosaria De Rosa^{1,2}

¹ University of Nebraska Medical Center, Eppley Institute & Buffett Cancer Center, ² University of Pittsburgh Hillman Cancer Center

Session continues on next page

4:21 - 4:32pm | P19, Standard Best Abstract Award Winner

Investigating Noncanonical Roles for Nucleotide Excision Repair Proteins in Repairing 8-oxoGuanine at Telomeres

Libby Childs¹

¹ University of Pittsburgh

4:32 - 4:43pm | P20

Oxidative DNA Lesions Within the *KRAS* Promoter G-Quadruplex Modulate Repair Activity and Expression

Carson Cohen^{1,2}

¹ Temple University, ² Fox Chase Cancer Center

3:15 - 4:45pm

Platform 4: Multiomic Approaches to Characterizing Genome Architecture, Sequence Variation, and Mutational Instability

Chairs: Christina Castellani, Annette Dodge

3:15 - 3:30pm | P21

HiFi-Runner: A Reproducible PacBio HiFi WGS Pipeline and GUI for Cross-Pedigree and Cross-Tissue Comparisons in Variant Discovery and Mutation Analysis

Maximilian Cope¹

¹ Western University

3:30 - 3:45pm | P22

Fiber seq: Linking DNA Methylation to Chromatin Accessibility with Single-Molecule Long-Read Multiomics

Keith Maier¹

¹ EpiCypher, Inc.

3:45 - 4:00pm | P23

Characterization of Hairpin Loops and Cruciforms Across 118,019 Genomes Spanning the Tree of Life

Nikol Chantzi^{1,2}

¹ The University of Texas at Austin, ² The Pennsylvania State University College of Medicine

4:00 - 4:15pm | P24

Environment-Linked k-mer Signatures in Eukaryotic Genomes: A Phylogeny-Aware Computational Framework Across Three Kingdoms

Monireh Safari¹

¹ University of Waterloo

4:15 - 4:30pm | P25

RNA Integrity of a Long Non-coding RNA Modulates Genome Instability

Mustapha Olatunji¹

¹ Florida International University

4:30 - 4:45pm | P26

Long-Read, Whole-Genome Sequencing for Comparison of Paired Tumor Genetic Heterogeneity and Metastasis Clonal Expansion to Identify Mutation Drivers of Metastasis

Kathleen Hill¹

¹ Western University

4:45pm

4:45 - 5:00pm

Break

5:00pm

5:00 - 6:00pm

EMGS Award Lecture

5:00 - 6:00pm | A02

Engaging Mutagenesis and DNA Repair from Outside the Box: Examples from Four Decades of Search and Discovery

Paul Doetsch¹

¹ National Institute of Environmental Health Sciences

6:00pm

6:00 - 6:15pm

Break

No more sessions on Wednesday 14 October 2026