

Environmental Mutagenesis and Genomics Society

57th Virtual Annual Meeting, October 12-14, 2026

Advancing Exposure Science: From Mechanisms to Risk

Monday, October 12, 2026

10:00 to 11:45 am **Symposium 1: From Flames to Genes: Identifying Epigenetic Modifications as a Potential Mechanism linking occupational Exposures to Adverse Health Outcomes in First-Responders**

Chairs: Luke Montrose, PhD (*Colorado State University*)

Abstract: 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.

Speakers: Olorunfemi Adetona, PhD (*The Ohio State University*)
When Strength Meets Smoke: Assessing the Molecular Toll of Wildland Firefighting on Respiratory Health

Jaclyn Goodrich, PhD (*University of Michigan*)
Epigenetics and Wildland Firefighting

Timothy Jenkins, PhD (*Brigham Young University*)
Air pollutants, occupational exposures, and the sperm epigenome: impacts on fertility and offspring health

10:00 to 11:45 am **Symposium 2: Beyond DNA: Role of RNA in Genome Integrity and Mutagenesis**

Chairs: Kyle Miller, PhD (*Emory University*), and Ning Tsao, PhD (*Washington University*)

Abstract: 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.

Speakers: Nima Mosammaparast, PhD (*Washington University*)
RNA damage: the canary in the coal mine?

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Li Lan, PhD (*Duke University*)

The m5C RNA modification in R-loops acts as an off switch for homologous recombination and Alt-NHEJ

Blerta Xhemalce, PhD (*Emory University*)

RNA modifications in R-loops and DNA damage responses

11:45 to 12:00 pm **Break**

12:00 to 1:30 pm **Poster Session 1: DNA Repair**

Selected from abstract submissions.

12:00 to 1:30 pm **Poster Session 2: Genotox**

Selected from abstract submissions.

1:30 to 2:00 pm **Lunch Break**

2:00 to 3:00 pm **Keynote Lecture 1**

Chris Mason, PhD (*Cornell University*)

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

3:00 to 3:15 pm **Break**

3:15 to 4:45 pm **Platform Session 1: DNA Repair**

Selected from abstract submissions.

3:15 to 4:45 pm **Platform Session 2: New Approach Methodologies and Emerging Biomarkers for Genotoxicity Assessment**

Selected from abstract submissions.

4:45 to 5:00 pm **Break**

5:00 to 6:00 pm **EMGS Young Investigator Spotlight**

Tess Leuthner (*Indiana University*)

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

Tyler Weaver (*University of Virginia School of Medicine*)

Mechanisms of Chromatin-Based Single-Strand Break Repair

6:00 to 6:15 pm **Break**

6:15 to 7:00 pm **Business Meeting**

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10:00 to 11:45 am **Symposium 3: Diverse Approaches in Error-Corrected Next-Generation Sequencing-Innovations and Applications in Genetic Toxicology**

Chairs: Shaofei Zhang, PhD (*Pfizer, Inc*), Nimrat Chatterjee, PhD (*University of Vermont*), and Natalia Cestari Moreno, PhD (*University of Kansas*)

Abstract: 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 on 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.

Speakers: Christopher Bradley, PhD (*Mutagentech, Inc*)
SMM-seq (Single-Molecule Mutation Sequencing) for the Detection of Ultra-Rare Somatic Mutations and Structural Variants

Javier Revollo, PhD (*US FDA*)
Advancing HiFi Sequencing for Sensitive Detection of Mutations in Genetic Toxicology

Azeet Narayan, PhD (*Broad Institute*)
One Read, Two Strands: Reinventing Duplex Sequencing with CODEC for Ultra-Sensitive Mutation Detection

10:00 to 11:45 am **Symposium 4: Converging on NAM: Building Scientific Confidence in the Regulatory Application of Genotoxicity New Approach Methods (NAMs)**

Chairs: Andreas Zeller, PhD (*Roche*), and Steve Bryce, PhD (*Litron Laboratories*)

Abstract: 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

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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.

Speakers: Nadine Stoker, PhD (*Washington University*)
A Digital Pathology Artificial Intelligence (AI) Readout for Single Cell Apoptosis Evaluation in Organoids and Tissues

Clive Roper, PhD (*Duke University*)
Successful use of NAMs in regulatory applications, some case studies with a focus on inhalation toxicology; learnings for genetic toxicology

Caroline Hilmi, PhD (*Bayer CropScience*)
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

Levi Winkelman, PhD (*Leiden University*)
A Meta-Analysis on in Vitro Genotoxicity Data for DNA-Alkylating Agents

11:45 to 12:00 pm *Break*

12:00 to 1:30 pm **Poster Session 3: EPI-GDS**
Selected from abstract submissions.

12:00 to 1:30 pm **Poster Session 4: DNA Repair – Replication**
Selected from abstract submissions.

1:30 to 2:00 pm *Lunch Break*

2:00 to 3:00 pm **Alexander Hollander Award Lecture**
Barbara Parsons, PhD (*National Center for Toxicological Research, Food & Drug Administration*)
Clonal Expansion of Cancer Driver Gene Mutants as a New Approach Methodology for Carcinogenicity Testing

3:00 to 3:15 pm *Break*

3:15 to 4:45 pm **Student Led Session: AI and Visualization**
Selected from abstract submissions.

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4:45 to 5:00 pm **Break**

5:00 to 6:45 pm **Symposium 5: Developmental Exposures and Germ Cell Health: Mechanisms, Multigenerational Effects, and Mitigation Strategies**

Chairs: Jill Escher (*Escher Fund for Autism*), Brandon Pearson, PhD (*Oregon State University*), and Gurugowtham Ulaganathan, (*Duke University*)

Abstract: 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.

Speakers: Patrick Allard, PhD (*University of California Los Angeles*)
Role of metabolite-epigenetic pathways in guiding reproductive toxicity

Wei Yan, PhD (*Washington State University*)
Paternal Metabolic Reversal Remodels Sperm RNA Profiles and Ameliorates Intergenerational Metabolic Disorder in Mice

Satoshi Namekawa, PhD (*University of California, Davis*)
Epigenetic Programming in the Parental Germlines and Epigenetic Inheritance

5:00 to 6:45 pm **Symposium 6: In Vitro Assessment of Nitrosamine Mutagenicity Beyond Hazard ID**

Chairs: Zhanna Sobol, PhD (Merck & Co., Inc.), and Raechel Puglisi, PhD (*Health and Environmental Sciences Institute*)

Abstract: 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. Ascertaining the carcinogenic potential and distinguishing between high- and low-potency nitrosamines has been an important focus of researchers in recent years. 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. According to ICH M7 guidelines, in vivo studies are necessary to confirm positive Ames results. However, as the predictivity of the Ames assay has been questioned, researchers have tested many NDSRIs negative in Ames in vivo to support non-mutagenic classification. Moreover, well-known mutagenic and carcinogenic small nitrosamines were tested using the TGR assay and error-corrected next-generation sequencing (ecNGS). Due to the lack of carcinogenicity studies for NDSRIs, investigations are being conducted to determine how potency

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ranking of in vivo positive NDSRIs using the BMDL approach could support the calculation of an acceptable intake (AI). Additionally, researchers are evaluating the applicability of the Less than Lifetime (LTL) approach. In the area of mutagenic impurities, a new approach aiming to classify NDSRIs into mutagenic potencies based on their structural features has been initiated. This approach enables the control of NDSRIs to AIs derived from QSAR/QM modeling.

Speakers: Zhanna Sobol, PhD (*Merck & Co., Inc.*)

Intro to the Challenges of Nitrosamine Risk Assessment and the Importance of In Vitro Tools

Steve Bryce, PhD (*Litron Laboratories*)

Assessment of Mechanism and Potency in the MultiFlow Assay with S9

Qiangen Wu, PhD (*FDA-NCTR*)

Metabolic Activation and DNA Adduct Formation of Complex Nitrosamines

Wen Sun, PhD (*Pfizer*)

Optimization of the HepaRG 3D Culture Model for Detecting Mutagenic Nitrosamines Using Error-Corrected Sequencing

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Wednesday, October 14, 2026

10:00 to 11:45 am Symposium 7: Cell-free and Exosomal DNA in Environmental Genotoxin Exposure

Chairs: Mike Kemp, PhD (*Wright State University*) and
Alex Carpenter, PhD (*Wright State University*)

Abstract: 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 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.

Speakers: Marcus Cooke, PhD (*University of South Florida*)
Nucleic Acid Adductomics: A Tool to Dissect Exposome?

Aadel Chaudhuri, PhD (*Mayo Clinic*)
Beyond Mutations: Cell-Free DNA for Noninvasive Profiling of Cancer and the Tumor Microenvironment

Trevor Pugh (*University of Toronto*)
Illuminating the Cancer Journey With Cell-Free Whole Genome Sequencing

10:00 to 11:45 am Symposium 8: Sex Differences in the Response to Mutagens

Chairs: Isabelle Miousse, PhD (*University of Arkansas for Medical Sciences*), Erica Briggs, PhD (*Litron Laboratories*), and Raechel Puglisi, PhD (*Health and Environmental Sciences Institute*)

Abstract: 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

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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.

Speakers: Gregory Holmes-Hampton, PhD (*Uniformed Services University of the Health Sciences*)
Sex as a Factor in Murine Radiation Research

Berna Ozdemir, PhD (*Insel Gruppe*)
Same Genome, Different Risks: How Sex Affects Mutagen Response

Dana Dolinoy, PhD (*University of Michigan*)
Lead and Phthalate Genomic Imprinting by Sex

11:45 to 12:00 pm **Break**

12:00 to 1:30 pm **Poster Session 5: Mutagenic Mechanisms and Assessments**
Selected from abstract submissions.

12:00 to 1:30 pm **Poster Session 6: DNA Damage and Repair**
Selected from abstract submissions.

2:00 to 3:00 pm **Keynote Lecture 2**
Allan Balmain, PhD, FRS (*University of California, San Francisco*)
TBD

3:00 to 3:15 pm **Break**

3:15 to 4:45 pm **Platform Session 3: DNA Damage Responses at Replication Forks and Telomeres**
Selected from abstract submissions.

3:15 to 4:45 pm **Platform Session 4: Multiomic Approaches to Characterizing Genome Architecture, Sequence Variation, and Mutational Instability**
Selected from abstract submissions.

4:45 to 5:00 pm **Break**

5:00 to 6:00 pm **EMGS Award Lecture**
Paul Doetsch, PhD (*National Institute of Environmental Health Sciences*)
Engaging Mutagenesis and DNA Repair from Outside the Box: Examples from Four Decades of Search and Discovery

6:00 to 6:15 pm **Break**

6:15 to 7:00 pm **EMGS Awards Ceremony**