

## 2025 Spring Symposium: Emerging Frontiers in Cancer Genetics

### Day One: April 8, 2025

---

#### **9:00am – 10:00am: Deciphering Noncoding Regulation**

- 9:00am – 9:10am      *Decoding CDH1: the hidden role of regulatory noncoding sequences in hereditary diffuse gastric cancer*  
Celina São José, Instituto de Investigação e Inovação em Saúde (i3S)
- 9:15am – 9:25am      *Modulation of Oncogenic Regulatory Networks by Exosomal miRNAs in Patients with Non-Small Cell Lung Cancers*  
Abeer Hassanin, Texas A&M Health
- 9:30am – 9:40am      *Reannotation of cancer mutations based on expressed RNA transcripts reveals novel functional non-coding mutations in melanoma*  
Xander Janssens, KU Leuven
- 9:45am – 9:55am      *Genome-Wide Mapping of Regulatory Elements and Clusters of Non-Coding Somatic Mutations in Liver Cancer Genomes*  
Todd Johnson, RIKEN Center for Integrative Medical Sciences (IMS)

#### **10:00am – 11:00am: Genomics-Aided Precision Oncology**

- 10:00am – 10:10am      *Integrated multi-omics drive precision cancer care for pediatric CNS tumors: An institutional study of 582 tumors*  
Derek Wong, Children's Hospital of Philadelphia
- 10:15am – 10:25am      *Pathways to precision cancer care: integrating genetic services into a nationwide cancer program at scale*  
Scott Topper, Color Health
- 10:30am – 10:40am      *Precision Oncology Workflow Modifications in a Community Cancer Center Led to Greater Adoption of Genetic Counseling Referral and Testing in Patients Diagnosed with Ovarian Cancer*  
Sourat Darabi, Precision Medicine
- 10:45am – 10:55am      *Defining actionable co-mutations and mutually exclusive genes in NF1-altered sporadic breast cancer*  
Mehrshid Faraji Zonooz, Van Andel Institute

### **11:00am – 12:00pm: Refining Variant Classification in Cancer**

- 11:00am – 11:10am     *Integrating Germline and Somatic Data to Resolve Variants of Uncertain Significance (VUS) in Colorectal Cancer (CRC) Patients who Self-Identified as Hispanic/Latino*  
Jonathan (Yonatan) Amzaleg, City of Hope
- 11:15am - 11:25am     *Development and application of MUTYH-specific ACMG/AMP variant classification criteria*  
Emily Nadeau, University of Vermont
- 11:30am – 11:40am     *Saturation genome editing based functional evaluation and clinical classification of BRCA2 single nucleotide variants*  
Fergus Couch, Mayo Clinic
- 11:45am – 11:55am     *Identifying patterns in testing and prevalence of gBRCA mutations among women with breast cancer who underwent hereditary cancer germline testing. A cross-sectional observational study*  
Rakesh Pinninti, Basavatarakam Indo-American Cancer Hospital and Research Institute

## Day Two: April 9, 2025

---

### **9:00am – 10:00am: Cancer Versus the Immune System**

- 9:00am – 9:10am      *AlphaMissense pathogenicity scores predict response to immunotherapy and enhances the predictive capability of tumor mutational burden*  
David Adeleke, North Dakota State University
- 9:15am – 9:25am      *Genetic regulation of TERT splicing contributes to reduced or elevated cancer risk by altering cellular replicative potential*  
Oscar Florez-Vargas, National Cancer Institute
- 9:30am – 9:45am      *Immune surveillance and cancer risk*  
Miriam Saffern, Icahn School of Medicine at Mount Sinai
- 9:45am – 10:00am      *Identification of Gene Fusions Using RNA-Seq in a Large Cohort of CLL Tumors*  
Numrah Fadra, Mayo Clinic

### **10:00am – 11:00am: Innovations in Cancer Genomics and Prediction**

- 10:00am – 10:10am      *Synergistic effect of microRNA enhances target specificity with reduced cellular toxicity: A potential tool in cancer therapeutics*  
Raghunath Chatterjee, Indian Statistical Institute
- 10:15am – 10:25am      *Targeted cell-free DNA methylation haplotype signatures in prostate cancer progression*  
Jodie Wong, Moffitt Cancer Center
- 10:30am – 10:40am      *Multiomic 6-base data from cell-free DNA enhances the performance of liquid biopsy classifiers*  
Tom Charlesworth, biomodal Ltd
- 10:45am – 10:55am      *Multi-ancestry transcriptome-wide association analyses on single-cell deconvoluted expression data to identify cell-type specific risk genes for colorectal cancer*  
Qing Li, Vanderbilt University Medical Center

**11:00am – 12:00pm: Polygenic Models of Cancer Risk**

- 11:00am – 11:10am    *Translating genomic risk models to clinical trials in a learning health system: the Prostate Cancer integrated Risk Evaluation (P-CARE) model*  
Jason Vassy, Harvard Medical School at VA Boston Healthcare System
- 11:15am - 11:25am    *Multi-Ancestry Analysis Identifies Susceptibility Variants and Improves Polygenic Risk Scores for Breast Cancer Subtypes*  
Haoyu Zhang, National Cancer Institute
- 11:30am – 11:40am    *Implementation of breast cancer polygenic risk scores in a personalized screening trial*  
Yiwey Shieh, Weill Cornell Medicine
- 11:45am – 11:55am    *Population-enriched germline variants in Finns pinpoint shared mechanisms shaping hematopoietic mosaic chromosomal alterations and diverse solid tumors*  
Aoxing Liu, Broad Institute & Massachusetts General Hospital