2025

THE EARLY DETECTION OF CANCER CONFERENCE

Portland, OR, USA

#EDxConf25

OCTOBER 21-23

OHSU KNIGHT CANCER Institute

CANCER RESEARCH UK

CANARY CENTER AT THE STANFORD SCHOOL OF MEDICINE

www.earlydetectionresearch.com

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2025

THE EARLY DETECTION OF CANCER CONFERENCE

October 21-23

This conference will use an online question submission system.

To participate go to **Slido.com** and enter the code: **Early**

PORTLAND MARRIOTT DOWNTOWN WATERFRONT

1401 SW Naito Parkway
Portland, OR 97201

WEDNESDAY October 22
CONFERENCE DINNER

The Tiffany Center
1410 SW Morrison St
Portland, OR 97205

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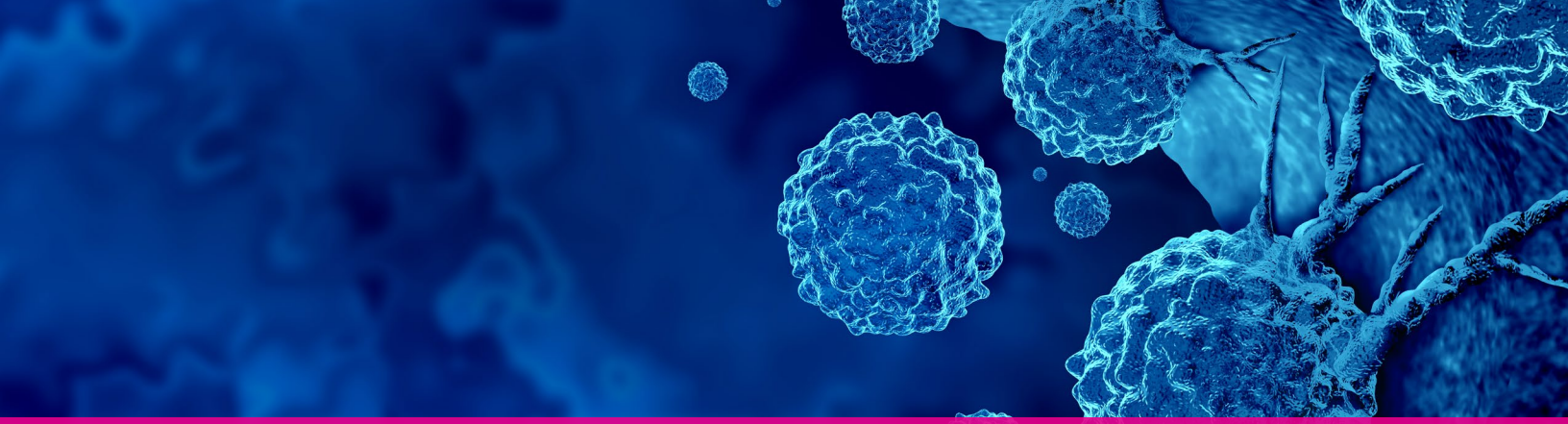

On behalf of the OHSU Knight Cancer Institute, Cancer Research UK (CRUK), and the Canary Center at Stanford, we welcome you all to Portland for the tenth Early Detection of Cancer Conference.

WELCOME

Early detection is one of the most powerful ways in which we can improve cancer survival. Improving the early detection of lethal cancers is fundamental to treating patients more effectively. However, this is a very complex field. Early detection is multi-disciplinary, requires long-term evidence to prove success and may require entirely new approaches to tackling disease. For these reasons, Cancer Research UK, the Canary Center at Stanford and the OHSU Knight Cancer Institute have joined forces to address these challenges and accelerate progress.

CRUK and OHSU's first conference brought together 120 world-leading scientists in June 2016 in Portland, Oregon. In 2017, we held another conference of 160 attendees together in Cambridge, UK. These meetings were designed to stimulate creative thinking, build relationships across the globe, and assess the state of the art in the early detection field. In 2018, the Canary Center at Stanford joined us as a third partner. Together, we are building on our meeting histories to explore the current state of the early detection field and help define key challenges through a wide range of presentations and discussions.

As leaders in your fields, you have much to contribute to this conference. We want to unite world-leading scientists from multiple disciplines, and create a global network of experts dedicated to advancing this field. Collaboration is key to making this happen, so we ask you to take advantage of the discussions and networking opportunities to develop and share ideas and identify ways of driving the field forward.

We look forward to a lively and thought-provoking conference, and to hearing from you about how we tackle this important problem. Thank you for participating to the fullest!

Laura Heiser

Associate Professor and Vice Chair
Biomedical Engineering
Oregon Health and
Science University

Fiona Gilbert

Director of Research,
Radiology Department
University of Cambridge

Parag Mallick

Associate Professor, Canary Center
for Cancer Early Detection,
Dept. of Radiology
Stanford University

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SCIENTIFIC COMMITTEE

Laura Heiser

Oregon Health and Science University

Dr. Laura Heiser is Associate Professor and Vice Chair of the Department of Biomedical Engineering at Oregon Health & Science University, Associate Director of Complex Systems Modeling at the Knight Cancer Institute Cancer Early Detection Advanced Research Center, and Co-Leader of the Knight Cancer Institute Quantitative Oncology Program. Her laboratory is focused on understanding the phenotypic and molecular responses of cancer and normal cells to diverse stimuli, with a particular interest in elucidating mechanisms of therapeutic response and resistance in cancer. Dr. Heiser has served as co-PI on an NHGRI U54 LINCS Center grant designed to interrogate the influence of microenvironmental factors on diverse epithelial cell types and as PI on an NCI U54 Cancer Systems Biology Consortium Center grant, focused on understanding the role of microenvironmental signals in modulating cell state heterogeneity and therapeutic response. She has had leadership roles in the development of international DREAM challenges and led a multi-center LINCS Common Project designed to deeply profile the dynamic molecular and phenotypic responses of mammary epithelial cells to diverse microenvironmental factors. She was inducted into the 2025 class of the American Institute for Medical and Biological Engineering (AIMBE) College of Fellows.

Fiona Gilbert

University of Cambridge

As an academic radiologist she evaluates new imaging technology and how this impacts on patients health. Her particular clinical expertise is breast cancer. She is currently working on early cancer detection, biomarkers to predict cancer and response to neoadjuvant therapy, novel imaging techniques such as sodium imaging with MRI. She is working on Artificial Intelligence and the impact on radiology services and patient care. She has worked in developing AI algorithms with academic groups and commercial companies, is currently testing new research and commercial AI tools.

She has over 300 peer reviewed publications and has over £26 million in grant applications. She is a regular speaker at international Radiology conferences including RSNA in Chicago and ECR in Vienna. She is a member of the NIHR imaging science group and past President of the European Society of Breast Imaging. She has Honorary membership of Radiological Society of North America, Honorary Fellowship of the American College of Radiologists, Gold Medal from the European Society of Radiology, Fellowship of the Royal Society of Edinburgh and Fellowship of the Academy of Medical Sciences.

She has sat on a number of committees and funding Boards and is on a number of advisory panels. She is Lead advisor for AI for Clinical Radiology for the Royal College of Radiologists. She is a director of a public financial investment company NASCIT.

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SCIENTIFIC COMMITTEE

Parag Mallick
Stanford University

Dr. Parag Mallick is an Associate Professor at Stanford University. Originally trained as an engineer and biochemist, his research spans proteomics, computational and experimental systems biology, cancer biology and nanotechnology. Dr. Mallick received his B.S. in Computer Science from Washington University in St. Louis. He then obtained his Ph.D. from UCLA in Chemistry & Biochemistry, where he worked with Dr. David Eisenberg. He completed his post-doctoral studies at The Institute for Systems Biology with Dr. Ruedi Aebersold. Dr. Mallickís group has been pioneering multi-omic and systems-biology approaches towards understanding disease mechanisms, discovering biomarkers and enabling personalized medicine. His group has also been pioneering meaningful machine learning methods that have more interpretable and accurate explanations and can be trained with smaller amounts of input data. Dr. Mallick has over 100 publications and holds patents in the fields of artificial intelligence, proteomics technology, biomarker development, and nanotechnology. Additionally, he is a co-founder of Nautilus Biotechnology and advisor to numerous biotechnology and diagnostics companies.

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CONFERENCE AGENDA

Monday, October 20

5:30pm - 8:00pm Trainee Dinner

Tuesday, October 21

8:00am - 9:00am Check-in & Breakfast

9:00am - 9:05am Welcome Remarks

9:05am - 10:05am Keynote: Innovative Technology
Peter Kuhn, University of Southern California

10:05am - 10:30am AM Break

10:30am - 12:00pm Where will AI take us with early detection?

Chairs: Parag Mallick, Stanford University
Etta Pisano, National Cancer Institute

Speakers: Animesh Acharjee, University of Birmingham
Beth Burnside, University of Wisconsin
Jiheum Park, Columbia University Medical Center
Melissa Troester, UNC Gillings School of Global Public Health

12:00pm - 12:15pm Lightning Talks: How is biology informing early detection?

Speakers: Didem Egemen
Ghulam Rasool
Paul Yousefi

12:15pm - 1:25pm Lunch

1:25pm - 2:05pm The Great Debate: The randomized control trial of cancer screening is dead

Speakers: Peter Sasieni, Queen Mary University of London
Laura Esserman, University of California, San Francisco

2:05pm - 3:35pm Mechanistic insight and early detection markers

Chairs: Shelley Hwang, Duke University
James Reading, University College London

Speakers: Rebecca Fitzgerald, University of Cambridge
Walid Khaled, University of Cambridge
James Reading, University College London
Martha Shrubsole, Vanderbilt University Medical Center

3:35pm - 3:50pm Lightning Talks

Speakers: Avathamsa Athirasala
John McClatchy
Daniel Parra-Sanchez

3:50pm - 4:15pm PM Break

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Tuesday, October 21

4:15pm - 5:15pm	Comparing healthcare systems Speakers: Robin Yabroff, American Cancer Society Paul Pharoah, Cedars-Sinai Medical Center
5:15pm - 5:35pm	Poster Pitches
5:35pm - 5:40pm	Closing Remarks Laura Heiser, Oregon Health and Science University
5:40pm - 7:10pm	Evening Poster Reception

Wednesday, October 22

8:00am - 9:00am	Check-in & Breakfast
9:00am - 9:05am	Welcome Remarks
9:05am - 10:05am	Keynote: Biology Serena Nik-Zainal, University of Cambridge
10:05am - 11:05am	Networking Activity
11:05am - 11:45am	The Great Debate: Early detection of cancer doesn't change lifespan Speakers: Mette Kalager, Oslo University Hospital Robert Smith, American Cancer Society
11:45am - 12:05pm	Poster Pitches
12:05pm - 1:05pm	Lunch
1:05pm - 2:35pm	Innovative technologies for cancer early detection Chairs: Peter Kuhn, University of Southern California Amit Roshan, Queen Mary University of London Speakers: Debiao Li, Cedars-Sinai Medical Center Amit Roshan, Queen Mary University of London Chris Sander, Harvard University and Oregon Health and Science University Christine Wang, Northwestern University
2:35pm - 2:50pm	Lightning Talks Speakers: Mark Consugar Haylie Helms Stuart Ibsen
2:50pm - 3:15pm	PM Break
3:15pm - 4:00pm	MCED Panel Discussion Speakers: Tom Callender, University of Cambridge Ruth Etzioni, Fred Hutch Cancer Center Robert Smith, American Cancer Society

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Wednesday, October 22

4:00pm - 5:00pm	Keynote: Clinical/Risk stratification Suzette Delaloge
5:00pm - 5:05pm	Closing Remarks Fiona Gilbert, University of Cambridge
5:30pm - 8:30pm	Conference Dinner/Early Detection Award and Advocate Stories Presentations **The Tiffany Center**, 1410 SW Morrison St, Portland, OR 97205

Thursday, October 23

8:00am - 9:00am	Check-in & Breakfast
9:00am - 9:05am	Welcome Remarks Parag Mallick, Stanford University
9:05am - 10:35am	Getting early detection into the community Chairs: Theodore Levin, Kaiser Permanente Brian Nicholson, University of Oxford Speakers: Chyke Doubeni, Ohio State University Lilian Lee, Freenome Christian von Wagner, University College London Renda Wiener, Boston University
10:35am - 10:50am	Lightning Talks Speakers: Charles Atwood Kiana Collins Pradeep Virdee
10:50am - 11:15am	AM Break
11:15am - 12:15pm	Discussion Panel: Evolution of early detection in the commercial landscape Speakers: Josephine Harada, Precede Biosciences Joe Horsman, Madrona Connie Lehman, Massachusetts General Hospital Puneet Souda, Leerink Partners
12:15pm - 12:20pm	Closing Remarks Parag Mallick, Stanford University

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Tuesday, October 21

SPEAKER AND SESSION INFORMATION

Keynote: Innovative Technology: Data driven innovation in early detection

Peter Kuhn
University of Southern California

Dr. Kuhn is a University Professor at USC and serves as the Director of the USC Michelson Convergent Science Institute in Cancer (CSI-Cancer). He also holds the position of Honorary Professor of Cancer Science at the University of Manchester in the United Kingdom.

Peter is a scientist, educator, and entrepreneur with a lifelong commitment to personalized medicine and individualized cancer care. Over the past three decades, he has been at the forefront of technology-enabled scientific breakthroughs. His career began as a graduate student at SUNY Albany, where he worked with Joachim Frank in electron microscopy. He then earned his PhD in crystallography by researching PNGaseF in collaboration with New England Biolabs. Following this, he joined Stanford University to develop high-throughput structural genomics approaches—contributions that directly aided in elucidating Roger Kornberg's RNA polymerase structure and Brian Kobilka's β2-adrenergic receptor structures.

For the past two decades at both Scripps Research and USC, Peter has focused on understanding how cancer evolves and disseminates through the circulatory system, leading to breakthroughs in circulating tumor cell science and its clinical applications. Although he has published over 300 papers with roughly 30,000 citations, founded companies, and advised organizations of all sizes, his mission remains steadfast: to improve the lives of those affected by cancer—viewing every scholarly achievement as a necessary step toward that goal.

Peter firmly believes that the future of cancer screening, diagnosis, and monitoring will be as simple as adding a checkbox to the standard blood testing menu, thereby enabling personalized screening pathways for every individual.

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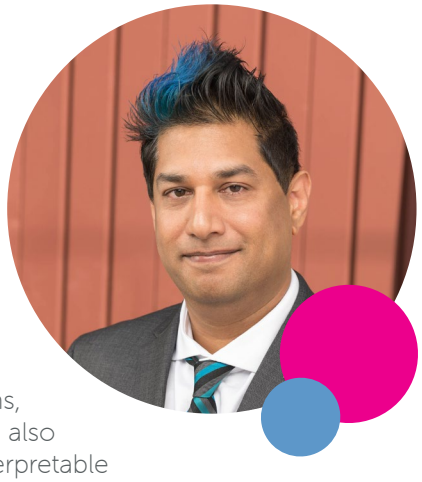
Tuesday, October 21

Where will AI take us with early detection?

AI is poised to advance cancer early detection by leveraging machine learning algorithms to analyze complex genomic, imaging, and clinical data. These models could identify subtle biomarkers and patterns that may be imperceptible using traditional methods, enabling earlier and more accurate diagnosis. Advances in AI could accelerate cancer early detection by enabling faster, more precise analysis of complex data sets, which may allow for improved image processing, mining of digital datasets and deeper insights into tumor biology. However, the potential pitfalls of AI including the tremendous challenges inherent in early detection, data sparsity, lack of training data diversity, and errors, introduce risks of unintended degradation of performance and other sources of harm. This session will explore how AI may enable us to push the boundaries of early cancer detection and to improve patient outcomes if both the promise and perils are carefully balanced.

CHAIR:

Parag Mallick
Stanford University



Dr. Parag Mallick is an Associate Professor at Stanford University. Originally trained as an engineer and biochemist, his research spans proteomics, computational and experimental systems biology, cancer biology and nanotechnology. Dr. Mallick received his B.S. in Computer Science from Washington University in St. Louis. He then obtained his Ph.D. from UCLA in Chemistry & Biochemistry, where he worked with Dr. David Eisenberg. He completed his post-doctoral studies at The Institute for Systems Biology with Dr. Ruedi Aebersold. Dr. Mallickís group has been pioneering multi-omic and systems-biology approaches towards understanding disease mechanisms, discovering biomarkers and enabling personalized medicine. His group has also been pioneering meaningful machine learning methods that have more interpretable and accurate explanations and can be trained with smaller amounts of input data. Dr. Mallick has over 100 publications and holds patents in the fields of artificial intelligence, proteomics technology, biomarker development, and nanotechnology. Additionally, he is a co-founder of Nautilus Biotechnology and advisor to numerous biotechnology and diagnostics companies.

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Tuesday, October 21

Where will AI take us with early detection?

CHAIR:

Etta Pisano

National Cancer Institute

Dr. Etta Pisano serves as the Chief Research Officer at the American College of Radiology and as the Principal Investigator for the NCI-funded ECOG-ACRIN-sponsored Tomosynthesis Mammographic Imaging Screening Trial (TMIST) which is comparing digital mammography to tomosynthesis for breast cancer screening and has recruited 108,600 women at 133 sites in the US, Canada, Argentina, Peru, Italy, Spain, Thailand, Taiwan and South Korea since it opened in July 2017. She served from March 2024 to March 2025 in the federal government at ARPA-H as the leader of an effort to help make clinical trials faster, better, cheaper and more accessible to more Americans- the Advancing Clinical Trials Readiness (ACTR) initiative and holds faculty appointments in radiology at the University of Pennsylvania and the University of North Carolina at Chapel Hill.

After completing her undergraduate degree in Philosophy at Dartmouth College, Dr. Pisano received her MD from Duke University School of Medicine. She did her radiology residency at Beth Israel Hospital at Harvard Medical School. She next served on the faculty at the University of North Carolina Medical School where she was founding Chief of Breast Imaging for 16 years before becoming Vice Dean for Academic Affairs, overseeing the research and education missions of the medical school. While at UNC, she also served as the first Principal Investigator for the CTSA grant from the National Center for Advancing Translational Sciences and the founding Director of the Biomedical Research Imaging Center. After serving as Dean of the College of Medicine and Vice President for Medical Affairs at the Medical University of South Carolina, she joined the faculty of Harvard Medical School serving as Professor in Residence at Beth Israel-Deaconess Health System from 2015-2021.

Her career has focused on breast imaging with a special focus on the development and testing of new technologies, most recently studying the application of Artificial Intelligence and Machine Learning to breast cancer screening. She has extensive experience assisting companies who are seeking authorization from the FDA for sale of their devices, including software, in the US.

Dr. Pisano is a member of the National Academy of Medicine and has received gold medals from the Radiological Society of North America, the American Roentgen Ray Society and the Association of University Radiologists. She is a Fellow of the American College of Radiology, the Society of Breast Imaging and the American Association of Women Radiologists, and is a member of the International Society of Strategic Studies in Radiology. She also has been recognized by the National Women's History Museum with the Helen Taussig Living Legacy Award and has received the Marie Curie Award from the Association of Women Radiologists.

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Tuesday, October 21

Where will AI take us with early detection?

SPEAKER:

Animesh Acharjee
University of Birmingham

Dr. Animesh Acharjee is an Associate Professor of Integrative Analytics and AI at the University of Birmingham, UK. His research team focuses on integrating multi-omics and clinical data—including genomics, proteomics, metabolomics, and single-cell sequencing—to uncover disease mechanisms and identify therapeutic targets. Leveraging AI and machine learning, they analyse both public and stakeholder-provided datasets across cancer and metabolic diseases. Key examples include microbiome-inflammation links in infant cohorts and multi-omics integration in colon cancer. The team also develops bioinformatics tools and identifies diagnostic biomarkers from cytokines, miRNAs, and metabolites using advanced AI and computational methods.

SPEAKER:

Elizabeth Burnside
University of Wisconsin

Elizabeth Burnside is a professor of radiology at the University of Wisconsin (UW) School of Medicine and Public Health. Her degrees include an MD combined degrees in Public Health as well as Medical Informatics. Her research investigates the use of computational methods to improve breast cancer detection/diagnosis and risk prediction. In recent years, Dr. Burnside has focused on leadership assuming a role as Associate Dean of Team Science and Interdisciplinary Research in the SMPH and Co-Executive Director of the Institute for Clinical and Translational Research. Dr. Burnside is the Co-Site-PI of the UW *AllofUs*–Wisconsin Consortium.

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Tuesday, October 21

Where will AI take us with early detection?

SPEAKER:

Jiheum Park

Columbia University Medical Center

Dr. Jiheum Park, Ph.D., is an Assistant Professor of Medical Sciences (in Medicine) at Columbia University Medical Center and a member of the Herbert Irving Comprehensive Cancer Center (HICCC). Her research focuses on cancer, with particular emphasis on early detection and treatment outcomes. She applies advanced computational approaches—including artificial intelligence (AI), machine learning, deep learning, and simulation modeling—to address complex challenges in healthcare and translate scientific discoveries into clinical applications.

Dr. Park specializes in leveraging longitudinal electronic health records (EHRs) and genomic data to develop robust, integrative models that improve predictive accuracy and support clinical decision-making. Her research is supported by a K25 career development award from the National Cancer Institute (NCI) and a Department of Defense Pancreatic Cancer Research Program (PCARP) grant, for which she serves as Principal Investigator. Through her contributions to predictive analytics and translational research, Dr. Park is committed to advancing precision medicine and improving patient outcomes.

SPEAKER:

Melissa Troester

UNC Gillings School of Global Public Health

Dr. Melissa Troester, Professor of Epidemiology jointly appointment in Pathology & Laboratory Medicine, leads the Carolina Breast Cancer Study for Lineberger Comprehensive Cancer Center. Dr. Troester is Associate Director for Population Sciences in Lineberger and is Director of the UNC Center for Environmental Health and Susceptibility. Her research focuses on biomarker development and validation, genomic methods, epidemiologic methods, and breast cancer. Her long-term goal is to support multi-level approaches that integrate tumor biology with individual, community, and health services data to improve breast cancer outcomes.

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Tuesday, October 21

Lightning Talks: Where will AI take us with early detection?

AI-Assisted Visual Evaluation Test for Cervical Screening: Lessons Learned

Didem Egemen
National Cancer Institute, National Institutes of Health

HybridSybil: Integrating 3D-CNN and Vision Transformer for Longitudinal Lung Cancer Risk Prediction from LDCT

Ghulam Rasool
Moffitt Cancer Center

Leveraging proteomics and deep learning for non-invasive head and neck cancer detection through passive saliva monitoring (SensOrPass)

Didem Egemen
National Cancer Institute, National Institutes of Health

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Tuesday, October 21

The Great Debate: The randomized control trial of cancer screening is dead

Randomized Controlled Trials (RCTs), are traditionally considered the gold standard in clinical research, however, RCTs aiming to show an impact on mortality from a new ED&D test tend to be complex, large (due to low incidence of cancer), long (due to years of follow-up needed between diagnosis and death) and costly. This debate will explore whether Randomised Controlled Trials (RCTs), which are traditionally considered the gold standard in clinical research, are essential for evaluating new detection methods or whether the real-world environment offers a more streamlined and relevant approach to validating early detection signatures and evaluate tests.

MODERATOR:

Fiona Gilbert

University of Cambridge

As an academic radiologist she evaluates new imaging technology and how this impacts on patients health. Her particular clinical expertise is breast cancer. She is currently working on early cancer detection, biomarkers to predict cancer and response to neoadjuvant therapy, novel imaging techniques such as sodium imaging with MRI. She is working on Artificial Intelligence and the impact on radiology services and patient care. She has worked in developing AI algorithms with academic groups and commercial companies, is currently testing new research and commercial AI tools.

She has over 300 peer reviewed publications and has over £26 million in grant applications. She is a regular speaker at international Radiology conferences including RSNA in Chicago and ECR in Vienna. She is a member of the NIHR imaging science group and past President of the European Society of Breast Imaging. She has Honorary membership of Radiological Society of North America, Honorary Fellowship of the American College of Radiologists, Gold Medal from the European Society of Radiology, Fellowship of the Royal Society of Edinburgh and Fellowship of the Academy of Medical Sciences.

She has sat on a number of committees and funding Boards and is on a number of advisory panels. She is Lead advisor for AI for Clinical Radiology for the Royal College of Radiologists. She is a director of a public financial investment company NASCIT.

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Tuesday, October 21

Mechanistic insight and early detection markers

SPEAKER "FOR":

Peter Sasieni

Queen Mary University of London

Peter Sasieni CBE FMedSci is Professor of Cancer Epidemiology at Queen Mary University of London. He is Director of the Cancer Research UK Cancer Prevention Trials Unit at QMUL and Co-Lead of the Centre for Cancer Screening, Prevention and Early Diagnosis in the Wolfson Institute of Population Health.

After graduating in biostatistics, he worked with Jack Cuzick at the Imperial Cancer Research Fund and later at Queen Mary University of London before moving to King's College London where he was Director of King's Clinical Trials Unit.

Professor Sasieni's research applies epidemiological methods to cancer screening. He designs and runs clinical trials of early detection and prevention interventions.

He has published extensively on cervical screening and HPV vaccination including on the YouScreen trial of self-sampling in cervical screening non-attenders. He is currently collaborating with Professor Rebecca Fitzgerald to evaluate her oesophageal capsule sponge technology; and is one of the lead investigators on the NHS-Galleri Trial evaluating GRAIL's multi-cancer early detection blood test in population screening.

Peter Sasieni is a member of several trial oversight committees and national advisory boards. In 2023 he received The Don Listwin Award for Outstanding Contribution to Cancer Early Detection.

In March 2025 Peter was awarded Commander of the Most Excellent Order of the British Empire (CBE) for services to cancer early detection and prevention.

SPEAKER "AGAINST":

Laura Esserman

University of California, San Francisco

Laura Esserman, MD, MBA is Professor of Surgery and Radiology at the University of California, San Francisco (UCSF) and director of the UCSF Breast Care Center. Her work in breast cancer spans the spectrum from basic science to public policy issues, and the impact of both on the delivery of clinical care. Dr. Esserman is recognized as a thought leader in cancer screening and over-diagnosis, as well as innovative clinical trial design. She led the creation of the University of California-wide Athena Breast Health Network, a learning system designed to integrate clinical care and research as it follows 150,000 women from screening through treatment and outcomes. The Athena Network launched the PCORI-funded WISDOM Study, which tests a personalized approach to breast cancer screening in 100,000 women. She is also a leader of the innovative I-SPY TRIAL model, designed to accelerate the identification and approval of effective new agents for women with high risk breast cancers. In 2020 she got FDA approval for an I-SPY COVID trial, designed to rapidly screen and confirm high impact treatments to reduce mortality and time on ventilators.

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Tuesday, October 21

Mechanistic insight and early detection markers

This session will explore the underlying biological mechanisms behind the transition from pre-cancerous lesion to metastatic tumour. It could address why do some lesions develop into consequential cancers whilst others remain indolent? This session will examine the various biological processes that are driving the transformation of normal cells into malignant ones, including genetic mutations, epigenetic alterations, immune evasion, and microenvironment changes. By developing our understanding of these early cancer processes, we can pinpoint biomarkers and molecular signatures that could serve as the foundation for early detection approaches.

CHAIR:

Shelley Hwang
Duke University

Dr. Shelley Hwang, MD, MPH is the Mary and Deryl Hart Professor of Surgical Oncology, Vice Chair of Research in the Department of Surgery, and Director of the Breast Cancer Program for the Duke University Comprehensive Cancer Center. Her research focus includes breast cancer prevention, identifying less invasive treatments for early-stage breast cancers including ductal carcinoma in situ (DCIS), and understanding the genetic and stromal determinants of cancer progression. Dr. Hwang is an experienced clinical trialist with an interest in the treatment of early-stage breast cancer including DCIS. She is lead investigator (PI) of a national cooperative group study through the ALLIANCE evaluating the role of active surveillance, de-escalating surgery for low-risk DCIS. She serves as Co-Chair of the National Cancer Institute Breast Cancer Steering Committee (BCSC) and member of the NCCN Screening Guidelines Committee. Other interests of the Hwang Lab include the evolutionary role of tumor and environmental heterogeneity in driving DCIS progression and the impact of the breast density, microenvironmental factors, and the stromal immune infiltrate in determining breast cancer phenotype and response to chemotherapy. Her team incorporates computational models of cancer progression, and has developed progression models for invasive breast cancer. In 2016 she was honored by TIME magazine for her contributions to improving quality of life for patients diagnosed with breast cancer. Her work has been supported by the NIH, NCI, DoD, PCORI, Komen, Cancer Research UK, and the Breast Cancer Research Foundation.

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Tuesday, October 21

Mechanistic insight and early detection markers

CHAIR:

James Reading
University College London

Dr James Reading is Associate Professor, UKRI Future Leaders Fellow and leader of the Pre-cancer Immunology laboratory at the UCL Cancer Institute. His group are using the immune system as a platform for the early detection and interception of lung cancer. To achieve this his laboratory study the initiation and regulation of early T cell responses in human and murine peripheral blood and pre-malignant lesions during pulmonary pre-invasive disease via antigen specific multi-omics analysis.

Dr Reading's team aim to identify characteristics of the early T cell response that can be used to track carcinogenesis and target underlying mechanisms of nascent immune regulation. It is hoped that this understanding of early immune engagement and dysfunction will help inform future clinical strategies to eliminate precancerous lesions; building a new roadmap for precision immune interception of lung cancer.

James obtained his PhD from King's College London studying CD4 T cells in HIV-1 infection before partnering with industry to develop novel Treg-cell therapies for autoimmunity and transplantation. He subsequently trained with Prof Sergio Quezada and Prof Charles Swanton within the lung TRACERx study to analyse neoantigen specific T cells and checkpoint inhibitor responses, laying the foundation for his team's work on immune responses during lung cancer development.

SPEAKER:

Rebecca Fitzgerald
University of Cambridge

Rebecca Fitzgerald OBE FRS FMedSci HonFREng FRCP EMBO is Professor of Cancer Prevention and Founding Director of the Early Cancer Institute and Head of University Dept of Oncology at the University of Cambridge and practices medicine as Hon. Consultant in Gastroenterology and Cancer Medicine at Addenbrooke's Hospital. After training in Cambridge, Stanford and London she moved to Cambridge to focus on research to understand how tissues become cancerous and whether identifying pre-cancer at scale can reduce cancer morbidity and mortality, focussing on the upper GI tract. Interdisciplinary research is key to her approach, especially with bioengineering and public health, which forms the philosophy underpinning the Early Cancer Institute. Her work to develop and implement a non-endoscopic capsule sponge and related biomarker assays for detection of Barrett's oesophagus and associated dysplasia has gone from inception to clinical implementation through her start-up Cyted Health. Rebecca has contributed to evidence reviews and policy work around screening including for the Department of Health in the UK and led a review of cancer screening for the European Commission that led to new screening policy for EU member states. She been awarded several prizes including the Westminster Medal, an NHS Innovation prize, and the Don Listwin Early Detection Prize. In 2022 Rebecca was awarded an OBE for services to cancer research.

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Tuesday, October 21

Mechanistic insight and early detection markers

SPEAKER:

Walid Khaled
University of Cambridge

Walid's team studies the earliest stages of tumour initiation at the single cell level, tracking how tissues change from health to disease. By revealing these first cellular events, they aim to enable the early detection and prevention of breast cancer. Walid earned his PhD in 2007 at the University of Cambridge under the supervision of Professor Christine Watson, focusing on mammary gland development. The following year, he was elected to a Junior Research Fellowship at King's College, Cambridge, and joined the Sanger Institute as a Postdoctoral Fellow with Dr Pentao Liu, studying BCL11A and triple negative breast cancer. In 2013, Walid returned to Cambridge as a Lecturer in the Department of Pharmacology, receiving a CRUK Career Establishment Award to pursue research on breast epithelial tumour biology. In 2021, he was awarded a Programme Foundation Award to extend his studies into epithelial tumour initiation. His team was among the first to apply single cell genomics to characterise cellular changes in normal and preneoplastic mouse and human mammary glands, culminating in the landmark publication of the Human Breast Cell Atlas in 2024. In 2025 Walid was awarded an ERC Advanced grant to develop new preventative approaches for breast cancer. Walid currently serves as Deputy Director of the Cambridge Stem Cell Institute, is faculty of the Breast Cancer Programme at the Cambridge Cancer Centre, and is a Fellow of Magdalene College, Cambridge.

SPEAKER:

Martha Shrubsole
Vanderbilt University Medical Center

Martha J. Shrubsole, PhD, is Research Professor of Medicine in the Department of Medicine at Vanderbilt University Medical Center (VUMC) where she leads a research portfolio of molecular, nutritional, and interventional epidemiology. A major focus of Dr. Shrubsole's research is to understand the etiology of gastrointestinal neoplasia. She seeks to identify and evaluate modifiable factors, biomarkers, and molecular mechanisms for the prevention, early detection, and precision-based interception of cancer and its precursor lesions with emphasis on sessile serrated polyps and conventional colorectal adenomas. Some of these areas of study include nutrients such as one-carbon metabolism, inflammatory markers, gut microbiome, molecular landscape of colorectal polyps, and predictors of metachronous adenomas including in the NCI Moonshot Human Tumor Atlas Network. She is also a PI of the Southern Community Cohort Study and the Southern Environmental Health Study, two large NCI-funded cohort studies seeking to understand and study the causes and burden of cancer and other diseases in the general population in the US South. In addition, Dr. Shrubsole has had leading roles in multiple randomized trials and other large-scale epidemiologic studies based in the US and globally. Dr. Shrubsole also leads the International Epidemiology Field Station at VUMC and the Vanderbilt Survey Research Shared Resource and co-leads the Cancer Epidemiology Research Program at the Vanderbilt-Ingram Cancer Center.

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Tuesday, October 21

Lightning Talks: Mechanistic insight and early detection markers

A Vascularized Bone-on-a-Chip Platform Reveals Bone Microenvironment Induced Nuclear Damage Primes Circulating Prostate Cancer Cells for Aggressive Reprogramming

Avathamsa Athirasala
Oregon Health and Science University

Germline Runx1 mutations in cooperation with Tet2 loss-of-function promote the fitness and self-renewal of progenitors, dysregulating hematopoiesis via cell intrinsic and extrinsic mechanisms

John McClatchy
Oregon Health and Science University

Circulating Biomarker Discovery in PSC and CCA: A Proteomic Approach to Early Detection

Daniel Parra-Sanchez
University College London

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Tuesday, October 21

Panel Discussion: Comparing healthcare systems

This session will explore the underlying biological mechanisms behind the transition from pre-cancerous lesion to metastatic tumour. It could address why do some lesions develop into consequential cancers whilst others remain indolent? This session will examine the various biological processes that are driving the transformation of normal cells into malignant ones, including genetic mutations, epigenetic alterations, immune evasion, and microenvironment changes. By developing our understanding of these early cancer processes, we can pinpoint biomarkers and molecular signatures that could serve as the foundation for early detection approaches.

PANELIST:

Paul Pharoah

Cedars-Sinai Medical Center

Paul Pharoah is a Professor of Cancer Epidemiology in the Department of Computational Biomedicine at Cedars Sinai Medical Center, Los Angeles.

He is qualified in medicine from the University of Oxford in 1986. After a series of posts in internal medicine he worked for a year in Malawi on a leprosy vaccine trial. Then completed training in public health medicine before taking up a post as research fellow in the CRC Human Cancer Genetics Group at the University of Cambridge in 1996. Having completed his doctoral studies in 1999, he won a Cancer Research UK Senior Clinical Research Fellowship. On completion of this fellowship in 2009, was appointed Reader in Cancer Epidemiology and promoted to a personal Chair in the Department of Public Health and Primary Care, University of Cambridge in 2012. Paul moved to Cedars Sinai Medical Center in November 2022.

Paul Pharoah's major research interests are; common genetic variation and breast and ovarian cancer susceptibility; polygenic risk models and early detection; and the role of germline genotype in determining the clinical and molecular pathological characteristics of breast and ovarian cancer.

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Tuesday, October 21

Panel Discussion: Comparing healthcare systems

PANELIST:

Robin Yabroff

American Cancer Society

Robin Yabroff, PhD, is an epidemiologist and Scientific Vice President, Health Services Research, at the American Cancer Society. She conducts research on the economic burden of cancer; patterns of cancer care, including high-cost prescription drugs; health insurance benefit design; and patient, provider, and health system factors associated with the quality and value of cancer care.

Dr. Yabroff has more than 25 years of health services research experience and currently has adjunct positions within the Department of Medicine, Johns Hopkins University, and the Rollins School of Public Health, Emory University. Prior to joining the American Cancer Society, she held positions within the Office of Health Policy, Assistant Secretary for Planning and Evaluation (ASPE) in the US Department of Health and Human Services, the Health Services and Economics Branch of the National Cancer Institute, and the faculty of the Lombardi Cancer Center, Georgetown University. She earned her PhD in epidemiology from the Johns Hopkins School of Public Health and received an MBA from the University of Rochester.

Dr. Yabroff has co-authored over 350 peer-reviewed journal articles and invited editorials, commentaries, and book chapters. She is an Associate Editor for the Journal of the National Cancer Institute, a founding member of the Editorial Board of the Journal of Cancer Survivorship, and a member of the Editorial Board of the JCO Oncology Practice. Dr. Yabroff has received multiple National Institutes of Health Merit Awards for her research leadership and mentorship. She was recognized as a Fellow of the American Society of Clinical Oncology (FASCO) in 2024.

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Poster Pitch Presentations

	Name	Affiliation	Title
1	Cigdem Ak	Oregon Health and Science University	Enhancing Interpretability of Single-Cell Multi-Omics Analysis
2	Susan Astley Theodossiadis	University of Manchester	The impact of age at first pregnancy on AI-assessed breast density
3	Isis Diaz Monarrez	Oregon Health and Science University	Early Markers of Barrett's Oesophagus Progression Identified Through Spatial Transcriptomics
4	Karen B. Eden	Oregon Health and Science University	Identifying women with actionable risk factors for breast cancer in primary care practice
5	Andrew Gilmore	University of Manchester	Understanding breast cancer risk associated with mammographic breast density in premenopausal women
6	Juliane Griesbach	University Medical Center Mainz	Developing and assessing of a new biomarker panel for early detection of lung cancer - in vivo
7	Sarah L. Harbach	University of Manchester	Fallopian tube lavage sampling for early detection of pre-invasive ovarian cancer
8	Kaisa Huhtinen	University of Turku	CA-125 glycovariant assays improve the detection of early-stage epithelial ovarian cancer
9	Abigail McElhinny	AOA Dx	Multi-omic profiling of ovarian cancer serum in a population of individuals experiencing vague abdominal symptoms
10	Sarah Mitchell	Oregon Health and Science University	Using Dielectrophoresis to Isolate Tumor-Derived Nanoparticles from Human Plasma for Biomarker Discovery and Cancer Detection
11	Ghulam Rasool	Moffitt Cancer Center	A Multimodal AI Biomarker for Early Detection of Cancer Cachexia Integrating Clinical, Radiologic, and Laboratory Indicators
12	Mehrzad Sasanpour	Oregon Health and Science University	Improving the Consistency of Cancer Biomarker Detection Using Dielectrophoresis-Based Nanoparticle Recovery from Plasma via an Internal Standard Approach
13	Rose Wang	University of Missouri Kansas City	FTIR Imaging and Machine Learning for Early Detection of Oral Cancer in Precancerous Lesions
14	Yujia Zhang	Oregon Health and Science University	Multiplexed super-resolution imaging of mitochondria in clinical tissue sections reveals systematic structural rearrangements during pancreatic cancer progression

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Wednesday, October 22

SPEAKER AND SESSION INFORMATION

Keynote: Deep analyses of pre-malignant breast lesions reveal inception sites and strikingly early evolution of structural variations

Serena Nik-Zainal
University of Cambridge

Serena is an NIHR Research Professor in Genomic Medicine and Bioinformatics at University of Cambridge. She is also an NHS Honorary Consultant in Clinical Genetics. Serena has pioneering expertise in cancer whole genome sequencing (WGS) and big data analytics, with a specific interest in using the totality of cancer multi-omic data to fully understand cancer biology. She was central to the development of the field of mutational signatures in cancer, uses experimental systems to validate her analytical work, and explores other age-related progressive diseases such as neurodegeneration. Serena uses machine-learning methods to develop clinical computational tools to accelerate the translation of genomic innovations towards patients. Her team have undertaken the largest WGS pan-cancer data analysis including data from NHS cancer patients recruited via the 100,000 Genomes Project integrated with mortality data from the Office of National Statistics. She is the recipient of the Royal Society Sir Francis Crick Medal, Foulkes Foundation Medal, and Dr Josef Steiner Cancer Research award in recent years.

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Wednesday, October 22

The Great Debate: Early detection of cancer doesn't change lifespan

MODERATOR:

Parag Mallick

Stanford University

Dr. Parag Mallick is an Associate Professor at Stanford University. Originally trained as an engineer and biochemist, his research spans proteomics, computational and experimental systems biology, cancer biology and nanotechnology. Dr. Mallick received his B.S. in Computer Science from Washington University in St. Louis. He then obtained his Ph.D. from UCLA in Chemistry & Biochemistry, where he worked with Dr. David Eisenberg. He completed his post-doctoral studies at The Institute for Systems Biology with Dr. Ruedi Aebersold. Dr. Mallickís group has been pioneering multi-omic and systems-biology approaches towards understanding disease mechanisms, discovering biomarkers and enabling personalized medicine. His group has also been pioneering meaningful machine learning methods that have more interpretable and accurate explanations and can be trained with smaller amounts of input data. Dr. Mallick has over 100 publications and holds patents in the fields of artificial intelligence, proteomics technology, biomarker development, and nanotechnology. Additionally, he is a co-founder of Nautilus Biotechnology and advisor to numerous biotechnology and diagnostics companies.

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Wednesday, October 22

The Great Debate: Early detection of cancer doesn't change lifespan

This lively debate will examine whether early detection truly extends life or merely shifts the point of diagnosis. The session will explore how "lifespan extension" should be defined, what constitutes meaningful benefit, and how evidence should inform future screening policies and public messaging.

SPEAKER "FOR":

Mette Kalager

Oslo University Hospital

Mette Kalager is Professor of Medicine at the University of Oslo, Researcher at Oslo University Hospital and Family practioner in a rural town in Norway. She is an Associate Editor of *Journal of the Norwegian Medical Association*. Dr. Kalager is head of the Clinical Effectiveness Research Group, Institute of health and Society at University of Oslo and Department of Transplantation Medicine at Oslo University Hospital.

Mette Kalager received her MD in 1996 from the University of Oslo, Norway, and her PhD from the University of Oslo in 2012. After her internship she worked in general practice and surgery and was the Head of the Norwegian Breast cancer Screening Program at the Cancer Registry of Norway Dr. Kalager's main research interests include clinical trials, epidemiology and public health. She is involved in several large-scale international trials in colorectal cancer screening and surveillance, and has recently written a book about Proportionality in Health Crisis. Dr. Kalager serves on the Board of the French Insitute du Cancer and is the elected leader of the Norwegian Medical Reseach Society.

SPEAKER "AGAINST":

Robert Smith

American Cancer Society

Robert A. Smith, PhD is a cancer epidemiologist and Senior-Vice President, Cancer Screening, at the American Cancer Society (ACS). He also is Director, American Cancer Society Center for Early Cancer Detection Science (CECDS); Adjunct Professor of Epidemiology at the Rollins School of Public Health, Emory University School of Medicine; and Honorary Professor, the Wolfson Institute of Preventive Medicine, Barts & The London School of Medicine & Dentistry, Queen Mary University of London. He received his PhD at the State University of New York at Stony Brook in 1984, and before coming to the ACS he held positions at the Boston University School of Public Health, and the Centers for Disease Control. His principal interests are cancer screening, quality assurance, and health services research. At the ACS he leads the development of ACS cancer screening guidelines, various research and policy initiatives focused on early cancer detection, including R&D initiatives focused on new screening technology, including the ACS Multi-Cancer Detection Initiative.

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Poster Pitch Presentations

	Name	Affiliation	Title
1	Cigdem Ak	Oregon Health and Science University	Spatial Analysis of Androgen Receptor's Role in Prostate Cancer Across Multiple Scales
2	Christopher Boniface	Oregon Health and Science University	Mutation-agnostic detection and lineage tracing of pre-cancer clones for AML risk stratification
3	Stephen Deppen	Vanderbilt University Medical Center	Vanderbilt's Thoracic Biorepository: Advancing Lung Cancer Research Through Biospecimen Collection and Distribution
4	Alice Groves	University of Cambridge	The ACED Cohort study supporting future early detection of cancer research
5	Tiffani Howard	Oregon Health and Science University	Adapting Outreach for the Black Community: Engaging Community Champions to Boost Trial Enrollment
6	Laura King	GRAIL Bio UK, Ltd.	NHS-Galleri trial: approaches to retain a diverse participant cohort across multiple trial appointments
7	Sanjay Khanna	The Royal Marsden and Institute of Cancer Research	Large language models as a decision-aid tool in lung cancer screening: An assessment of quality and feasibility
8	Sanjeev Kulgod	Dognosis	Multi-Cancer Screening Using AI-Enhanced Canine Olfactory Detection: Interim Results from a Multi-Center Breath Analysis Study in India
9	Henson Lee Yu	Early Cancer Institute	Multi-omic Profiling of Localised Prostate Cancer Reveals Early Lineage and Microenvironmental Reprogramming with Potential to Inform Risk Stratification
10	Matt Leipzig	Stanford University	Decomposing the Causal Chain of Cancer Screening
11	Megan Lonhart	Oregon Health and Science University	E.N.G.A.G.E.: A Collaborative Model for Diverse Clinical Research Empowerment, Navigation, Growth, Access, Guidance, and Equity
12	Celine Marquez	Henry Ford Health	Baseline participant characteristics from PATHFINDER 2, a prospective interventional study of a multi-cancer early detection test in a population setting
13	Cyril Osifo-Doe	Stanford University	Assessing the Usability of PSA Self-Testing to Address Prostate Cancer Disparities Among Black South African Men: A Mixed-Methods Study
14	Balram Rai	Karolinska Institutet	Understanding the paradox of prostate cancer testing and socio-economic position for equitable early detection: Evidence from a population-based multilevel study
15	Jackilen Shannon	Oregon Health and Science University	Barriers to participation in Pancreatic Cancer Early Detection in the Community

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Wednesday, October 22

Innovative technologies for cancer early detection

This session will explore the potential of innovative technologies to advance early detection of cancer this could cover how wearable technologies, implantable sensors and synthetic biomarkers are set to transform the future of cancer early detection. A key theme of this session would be exploring how these innovations can enable continuous, real-time monitoring of biomarkers. The session could unite expertise in sensor tech, data analytics, and AI. Could also address challenges related to data privacy, device accuracy, and the scalability of these technologies in clinical practice, while exploring the future of personalised healthcare. Could cover how these technologies are tackling the challenge of low biomarker availability in single blood draws, and the problem of inter-individual variability in marker baselines, through continual/repeat monitoring.

CHAIR:

Peter Kuhn
University of Southern California

Dr. Kuhn is a University Professor at USC and serves as the Director of the USC Michelson Convergent Science Institute in Cancer (CSI-Cancer). He also holds the position of Honorary Professor of Cancer Science at the University of Manchester in the United Kingdom.

Peter is a scientist, educator, and entrepreneur with a lifelong commitment to personalized medicine and individualized cancer care. Over the past three decades, he has been at the forefront of technology-enabled scientific breakthroughs. His career began as a graduate student at SUNY Albany, where he worked with Joachim Frank in electron microscopy. He then earned his PhD in crystallography by researching PNGaseF in collaboration with New England Biolabs. Following this, he joined Stanford University to develop high-throughput structural genomics approaches—contributions that directly aided in elucidating Roger Kornberg's RNA polymerase structure and Brian Kobilka's β2- adrenergic receptor structures.

For the past two decades at both Scripps Research and USC, Peter has focused on understanding how cancer evolves and disseminates through the circulatory system, leading to breakthroughs in circulating tumor cell science and its clinical applications. Although he has published over 300 papers with roughly 30,000 citations, founded companies, and advised organizations of all sizes, his mission remains steadfast: to improve the lives of those affected by cancer—viewing every scholarly achievement as a necessary step toward that goal.

Peter firmly believes that the future of cancer screening, diagnosis, and monitoring will be as simple as adding a checkbox to the standard blood testing menu, thereby enabling personalized screening pathways for every individual.

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Innovative technologies for cancer early detection

CHAIR & SPEAKER:

Amit Roshan

Queen Mary University of London

Dr. Amit Roshan is a Senior Lecturer at the Queen Mary University of London, and a board-certified surgical oncologist at the Cambridge University Hospitals, UK.

He has a focus on translating next generation sequencing-based liquid biopsies for clinical applications. His doctoral work explored cancer genomics and stem cell biology of mutated epithelia at the University of Cambridge, for which he received the Hunterian Professorship from the Royal College of Surgeons. Since 2019, Dr. Roshan has been focussing on developing NGS-based liquid biopsies in small amounts of clinical material such as Dried Blood Spots for Early Detection, and in translating ctDNA applications in minimal residual disease after curative cancer treatment.

Dr. Roshan was co-Director of Research (Biology theme) for the Alliance for Cancer Early Detection between 2022-2025. His work is currently funded by grants from Cancer Research UK, the Rosetrees Trust, and EU Horizon/ UK Research & Innovation."

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Innovative technologies for cancer early detection

SPEAKER:

Debiao Li
Cedars-Sinai Medical Center

Debiao Li received his PhD in Biomedical Engineering from the University of Virginia in 1992.

Since 2010, Dr. Li has been the inaugural Director of the Biomedical Imaging Research Institute and holds the Karl Storz Chair in honor of George Berci at Cedars-Sinai Medical Center in Los Angeles. He is also a Professor of Medicine and Bioengineering at the University of California, Los Angeles.

Prior to his current roles, Dr. Li was an Assistant Professor of Radiology at Washington University in St. Louis from 1993 to 1998, before moving to Northwestern University in Chicago, where he served as an Associate Professor (1998-2004), Professor (2004-2010) of Radiology and Biomedical Engineering, and Director of Cardiovascular Magnetic Resonance Research (2004-2010). He has published over 430 original research articles and more than 20 book chapters.

Dr. Li has held prominent positions in professional organizations, serving as President of the International Society for Magnetic Resonance in Medicine (ISMRM) from 2011 to 2012, the premier professional society dedicated to advancing the innovation and application of magnetic resonance techniques in medicine and biology. He was also President of the Society for Magnetic Resonance Angiography (2006-2007) and served on the Board of Trustees for the Society for Cardiovascular Magnetic Resonance (SCMR) from 2009 to 2012. Additionally, he is an Associate Editor for Magnetic Resonance in Medicine (MRM) and a fellow of ISMRM, SCMR, the American Institute for Medical and Biological Engineering, and the International Academy of Medical and Biological Engineering.

Dr. Li's research focuses on developing and applying quantitative MR imaging techniques to solve technical challenges in both cardiovascular and oncological imaging. His team has also developed artificial intelligence models from medical imaging to predict biological aging and disease risk, especially pancreatic cancer.

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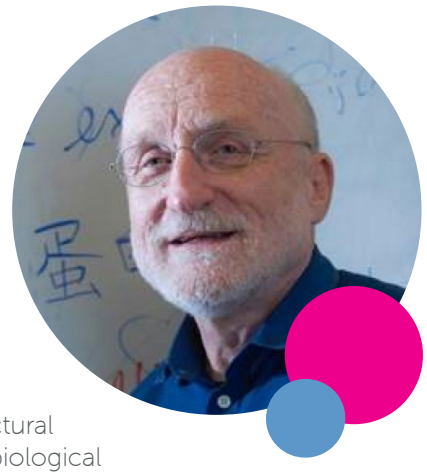
Wednesday, October 22

Innovative technologies for cancer early detection

SPEAKER:

Chris Sander

Harvard University and Oregon Health and Science University



Chris Sander is a pioneer in biological data science, with recent innovation in computational cell biology, anti-resistance cancer therapy and AI on EHRs for cancer risk prediction. He is faculty in Systems Biology at Harvard Medical School and associated with the Broad Institute, Mass General Hospital and the Cedar Center at the OHSU Knight Cancer Institute. He previously founded the Biocomputing Program at EMBL, the EMBL-EBI research program, the Computational Biology Program at MSKCC in New York and the cBio Center at Dana-Farber Cancer Institute.

Sander made significant contributions to systems biology, cancer biology, structural biology, protein folding from evolutionary sequence information, and AI for biological problems. He was a leader in The Cancer Genome Atlas (TCGA) project. His group created the cBioPortal for Cancer Genomics and the Pathway Commons knowledge base. He recently pioneered the use of AI methods on longitudinal health records for the assessment of cancer risk in real-world patient populations, with the goal of creating effective surveillance programs for aggressive cancer types, starting with pancreatic and ovarian cancer.

SPEAKER:

Christine Wang

Northwestern University

Shih-Ting (Christine) Wang completed her PhD studies in Materials Science at Imperial College London in 2017. She completed postdoc training at the Center for Functional Nanomaterials at Brookhaven Lab and at the Koch Institute of MIT. Since 2025, she became an assistant professor in the Department of Materials Science and Engineering at Northwestern University. Her interest lies in developing sequence and structure-defined biomaterials for biological and medical applications. Recently, she has worked on synthetic biomarkers for early diagnosis of lung cancer and infection.

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Wednesday, October 22

Lightning Talks: Innovative technologies for cancer early detection

The early detection of colorectal cancer from cfDNA can be improved through the detection of 6-base (5mC and 5hmC) biomarkers

Mark Consugar
Biomodal

3D Bioprinted Tumor Avatars as a Functional Platform for Early Cancer Modeling

Haylie Helms
Oregon Health and Science University

Early-Stage Pancreatic Cancer Detection Using Cancer-Derived Nanoparticles Recovered from Plasma by Three Electrode Cluster Dielectrophoresis

Stuart Ibsen
Oregon Health and Science University

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Wednesday, October 22

MCED Panel Discussion

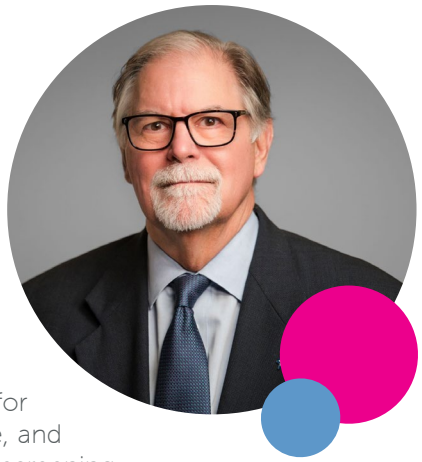
Several networks and consortia have been formed to accelerate the development of multicancer early detection (MCED) tests with the aim of improving detection of early-stage cancer. This panel discussion, featuring representatives from these initiatives, will explore key questions surrounding the future of MCEDs, including:

- At what stage of the cancer screening pathway are MCEDs most likely to be integrated? Should they be used before screening for risk stratification, used for site-specific screening—either as a standalone tool or alongside current methods—or introduced for screening of multiple cancers? Or are they better placed for triaging patients with non-specific symptoms for further investigations?
- How close are we to integrating these tests into established cancer screening pathways? Will the requirement for randomised controlled trials (RCTs) with a mortality endpoint pose a significant barrier, or might evidence requirements be evolving?
- What are the considerations around public acceptance and cost-effectiveness of MCEDs in screening programs?

MODERATOR:

Robert Smith

American Cancer Society



Robert A. Smith, PhD is a cancer epidemiologist and Senior-Vice President, Cancer Screening, at the American Cancer Society (ACS). He also is Director, American Cancer Society Center for Early Cancer Detection Science (CECDS); Adjunct Professor of Epidemiology at the Rollins School of Public Health, Emory University School of Medicine; and Honorary Professor, the Wolfson Institute of Preventive Medicine, Barts & The London School of Medicine & Dentistry, Queen Mary University of London. He received his PhD at the State University of New York at Stony Brook in 1984, and before coming to the ACS he held positions at the Boston University School of Public Health, and the Centers for Disease Control. His principal interests are cancer screening, quality assurance, and health services research. At the ACS he leads the development of ACS cancer screening guidelines, various research and policy initiatives focused on early cancer detection, including R&D initiatives focused on new screening technology, including the ACS Multi-Cancer Detection Initiative.

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Wednesday, October 22

MCED Panel Discussion

SPEAKER:

Tom Callender
University of Cambridge

Dr Tom Callender MBChB PhD MRCP FFPH is a clinical fellow at the University of Cambridge, honorary consultant in public health medicine at Cambridge University Hospitals, and faculty member of the Cambridge Centre for AI in Medicine. Tom trained in medicine in Manchester, Oxford, and London before specialising in public health. Prior to joining Cambridge, Tom was a clinical research fellow at UCL and public health registrar at the UK National Screening Committee (NSC) in the Department of Health and Social Care. He continues to contribute to the NSC Multi-Cancer Detection Task Group and the NSC Research and Methodology Group. His research interests span screening, simulation modelling, and AI in medicine.

SPEAKER:

Ruth Etzioni
Fred Hutch Cancer Center

Ruth Etzion is a Professor in the Biostatistics Program, Public Health Sciences Division, at the Fred Hutch Cancer Center, where she holds the Rosalie and Harold Rea Brown Endowed Chair. She has been involved in cancer early detection research since the early days of PSA, when she became fascinated with the many ways of screening for cancer using blood-based biomarkers. The driving motivation of her research program is to develop the evidence needed to inform decisions about how best to screen for different cancers. She has worked primarily in prostate cancer but also in breast and ovarian cancer. She is currently supported by an NCI Outstanding Investigator Award to develop models and methods for novel cancer diagnostics with a primary focus on multi-cancer early detection tests.

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Wednesday, October 22

Keynote: Building personalized prevention of cancer: A transversal crosstalk from basic research to social sciences

SPEAKER:

Suzette Delaloge

Gustave Roussy

Dr. Delaloge, MD, MSc, is a medical oncologist and researcher. She is a breast cancer and cancer prevention specialist, and an Associate Professor of Medical Oncology in the Department of Cancer Medicine of Gustave Roussy. She leads the Interception personalized prevention research programme at Gustave Roussy. Her major areas of expertise and development are precision risk-based cancer prevention, real world data, cancer precision oncology, and the organization of care in oncology. She is the chair of the large H2020 EU-funded MyPeBS project, which aims at demonstrating the value of risk-based breast cancer screening among more than 53,000 women randomized in 6 European countries, with the participation of 27 international partners. Dr. Delaloge is the author of more than 370 international peer-reviewed publications and more than 900 presentations at international conferences.

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Wednesday, October 22

Advocate Stories and Panel

MODERATOR:

Fiona Gilbert

University of Cambridge

As an academic radiologist she evaluates new imaging technology and how this impacts on patients health. Her particular clinical expertise is breast cancer. She is currently working on early cancer detection, biomarkers to predict cancer and response to neoadjuvant therapy, novel imaging techniques such as sodium imaging with MRI. She is working on Artificial Intelligence and the impact on radiology services and patient care. She has worked in developing AI algorithms with academic groups and commercial companies, is currently testing new research and commercial AI tools.

She has over 300 peer reviewed publications and has over £26 million in grant applications. She is a regular speaker at international Radiology conferences including RSNA in Chicago and ECR in Vienna. She is a member of the NIHR imaging science group and past President of the European Society of Breast Imaging. She has Honorary membership of Radiological Society of North America, Honorary Fellowship of the American College of Radiologists, Gold Medal from the European Society of Radiology, Fellowship of the Royal Society of Edinburgh and Fellowship of the Academy of Medical Sciences.

She has sat on a number of committees and funding Boards and is on a number of advisory panels. She is Lead advisor for AI for Clinical Radiology for the Royal College of Radiologists. She is a director of a public financial investment company NASCIT.

ADVOCATE REPRESENTATIVE:

Raquel Aguillon

Raquel Aguillon is committed to strengthening the connection between research and community at Oregon Health & Science University (OHSU). She serves on the OHSU OCTRI External Community Advisory Committee, the Knight Cancer Institute External Advisory Committee, and the OHSU Scientific Research Advocates Advisory Committee. With family and friends who have faced cancer challenges, Raquel brings both personal experience and professional insight to her advocacy. In her day-to-day work, she is part of the management team at a government social services agency, where she supports programs that serve the community.

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Wednesday, October 22

Advocate Stories and Panel

ADVOCATE SPEAKER:

Linda Galbraith

Linda worked as a hospital manager and a management consultant but was forced to give up work due to complications with treatment, compromising her immune system. Since starting PPIE work four years ago, she now leads ACED PPIE group particularly important to her, as she was not diagnosed for three years from first presenting to doctors. She now is PPI lead in RadNet Scotland, Co-Chair of the Scotland Cancer Centres, on Flatiron PVP. Linda also works with the MHRA and is Co-investigator in 10 studies.

ADVOCATE REPRESENTATIVE:

Misha Hawk-Wyatt

A survivor of three primary cancers: AYA cancer patient (breast cancer at 16 years old and cervical cancer at 29 years old), angiosarcoma of the head/neck, 2018, with an initial chronic leukemia (CML) diagnosis in 2003,

Patient advocate with Stanford Medical School and the Healthcare Primary Care Practice Enhancement Program (PC PEP) Quality Improvement programs.

Patient advocate, the University of Colorado, Anschutz Medical Campus, Center for Bioethics and Humanities panelist, an artificial intelligence-based prognostication panel whose purpose is to help create guidelines for the ethical use of artificial intelligence (AI)-based tools in palliative care settings.

ADVOCATE SPEAKER:

Vivian Lee

A breast cancer survivor since 2000, Vivian applies her personal experience as a patient, and professional experience as a life science industry consultant, to her cancer advocacy work. Vivian collaborates with research investigators at academic institutions across the US and abroad to provide patient perspective in shaping grant applications and research projects. She has served as a Consumer Reviewer for the US Department of Defense Breast Cancer Research Program, and as a Peer Reviewer for Komen grants on the national and local levels, as well as for American Cancer Society.

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Wednesday, October 22

Advocate Stories and Panel

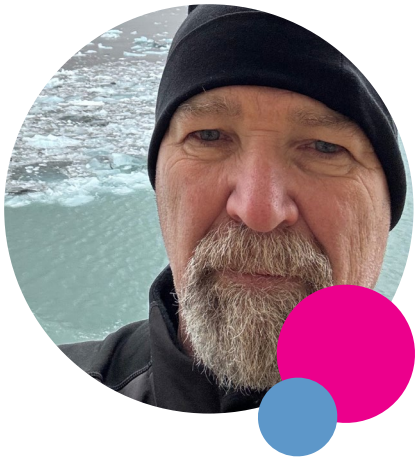
ADVOCATE SPEAKER:

Sally Jo Little

Sally Jo is a two-year colorectal cancer survivor whose cancer was first suspected through a mailed stool test, despite having no symptoms or family history. Early detection and colonoscopy led to timely diagnosis, treatment, and survival. With a background as a clinical research associate and in developing tools to improve physician–patient interaction, she now serves as a Research Advocate with the OHSU Knight Cancer Institute, promoting patient perspectives in the research process.

ADVOCATE SPEAKER:

Brian Smith



My name is Brian Smith, and I was diagnosed with AML in August of 2023. I was given a transplant in March of 2024, and I joined the OHSU advocacy group in the Spring of 2025. I want to advocate for anything blood cancer related trying to specialize in peer support for those going through a blood related cancer.

ADVOCATE REPRESENTATIVE:

Srdjan Stakic

A survivor of stage 4 plasmablastic lymphoma (diagnosed Jan 2024), Srdjan applies his lived experience as a patient and his professional background in global health and media to his advocacy work. He holds an EdD in Health Education from Columbia University and previously worked with the United Nations on using media for social development. Today, he is the founder of GuardianCare AI, a privacy-first care monitoring platform that empowers families and caregivers with real-time safety alerts and objective quality-of-care measures, while also creating opportunities for patient self-advocacy. Srdjan is a graduate of the Stanford Medicine's Patient Advocacy Training in Health Sciences and serves on the Patient & Family Advisory Council of both the Stanford Cancer Center and the Emergency Department. He is a member of the Scientific Review Committee of the Stanford Cancer Institute and collaborates with researchers and healthcare organizations to bring patient perspectives into technology design. His work is committed to advancing dignity, transparency, and accountability in care.

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Thursday, October 23

Getting early detection into the community

This session will explore innovations in early cancer detection within primary care, and could explore technologies such as wearables, mobile apps, and decision-making tools. Discussions will address strategies to improve uptake and accessibility while minimising burdens on healthcare teams, including potential community-based delivery models, such as home-based tests or pharmacy availability. Exploring how early detection can be integrated into routine patient care before symptoms arise. By educating technology/test developers on these factors, this session aims to drive innovations that support widespread patient adoption and improved outcomes.

CHAIR:

Theodore Levin
Kaiser Permanente

Dr. Levin is a Gastroenterologist and the Clinical Lead for Colorectal Cancer Screening at the Permanente Medical Group, Inc, and the Associate Director for Cancer Research at the Kaiser Permanente Division of Research in Pleasanton, California. A graduate of the Emory University School of Medicine, he completed internal medicine residency, gastroenterology fellowship and health policy fellowship at UCSF. His research focuses on health care delivery of standard of care and new technologies for colorectal cancer screening, including fecal DNA, fecal immunochemical tests, colonoscopy and blood-based screening tests.

CHAIR:

Brian Nicholson
University of Oxford

Brian is a General Practitioner working in the English NHS and an Associate Professor of Primary Care. He Co-Directs the NIHR Policy Research Unit for Cancer Awareness Screening and Early Diagnosis. His group, based at the Nuffield Department of Primary Care Health Sciences at the University of Oxford, focusses on improving the diagnosis of cancer in symptomatic patients combining risk profiling using electronic health records data, qualitative methods to understand diagnostic reasoning, implementation science to enhance diagnostic processes, and prospective studies and trials of new cancer detection technologies. As clinical lead for Early Detection for the CRUK Oxford Cancer Centre he is leading a programme of work to evaluate multi-cancer tests in the community for symptomatic people, including SYMPLIFY and the AcceleRated Multi-cAncer DIagnostic evaLuatiOn (ARMADILO) platform study to evaluate multiple multi-cancer tests in 10,000 symptomatic people.

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Thursday, October 23

Getting early detection into the community

SPEAKER:

Chyke Doubeni
Ohio State University

Dr. Chyke Doubeni professor of family medicine, the Klotz Chair in Cancer Research, and an associate director in the Comprehensive Cancer Center at the Ohio State University Wexner Medical Center. Dr. Doubeni is a clinical epidemiologist whose research and policy work focuses on improving the care continuum related to disease prevention and screening, with colorectal cancer as a model. He has led major studies demonstrating the effectiveness of colorectal cancer screening as well as harmful variations in the quality of cancer screening, the need for timely follow-up care for abnormal screening tests, and health system and societal barriers to care. He was a recipient of the Presidential Early Career Award for Scientists and Engineers. He also served on the US Preventive Services Task Force from 2017-2021. At the USPSTF, he led work to transform the recommendation development process through a framework to improve the delivery of clinical preventive services to everyone, irrespective of social or economic barriers.

SPEAKER:

Lilian Lee
Freenome

Lilian C. Lee, Ph.D. is the Sr. Director of Clinical Science at Freenome, where she leads a team that drives clinical study design, clinical study planning, medical reviews, and evidence strategy in Freenome's colorectal cancer, lung, and multicancer programs. Lilian's focus is on building strong clinical strategy and evidence supporting novel medical device development. Prior to Freenome, Lilian held leadership roles in cardiovascular research at Medtronic in global evidence strategy, clinical study execution and cross functional product development teams. Lilian has Ph.D. in Pharmaceutical Sciences from the University of Southern California and a B.A. from the University of California, Berkeley.

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Thursday, October 23

Getting early detection into the community

SPEAKER:

Christian von Wagner
University College London

Christian von Wagner is Professor of Behavioural Science at University College London. His research focuses on socioeconomic inequalities in colorectal cancer (CRC) screening uptake. This programme of work has included an emphasis on public understanding of cancer screening, engagement with information and invitation materials, attitudes and preferences towards the different testing modalities and the acceptability and patient experience of participation in colorectal cancer screening. More recently, his work into early detection and diagnosis of colorectal cancer has focused on the potential role of community pharmacy leveraging their unique position within particularly socioeconomically deprived and ethnically diverse communities. Prof von Wagner receives fundings from National Institutes of Health Research, Cancer Research UK, has published over 100 articles and is Programme Lead for the MSc in Health Psychology.

SPEAKER:

Renda Wiener
Boston University

Dr. Renda Wiener is a pulmonologist, health services researcher, and implementation scientist at the Center for Health Optimization & Implementation Research at the VA Boston Healthcare System, a Professor of Medicine at Boston University Chobanian & Avedisian School of Medicine, and the Deputy Chief Consultant of VA's National Center for Lung Cancer Screening. A main focus of her research is to develop, implement, and evaluate strategies to optimize quality, patient-centeredness, and equity of lung cancer screening, and she has participated in several guidelines and policy statements in these areas. Dr. Wiener is multi-principal investigator of a pragmatic randomized trial to implement prediction modeling at the point of care to optimize patient selection and shared decision-making about lung cancer screening.

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Wednesday, October 22

Lightning Talks: Getting early detection into the community

REFLECTION: Real-World Evidence Study of Multi-Cancer Early Detection (MCED) Among Veterans in the Veterans Affairs Healthcare System (VA)

Charles Atwood
VA Pittsburgh Healthcare System

Personalized Prostate Specific Antigen (PSA) Retesting Intervals in Primary Care

Kiana Collins
University of Oxford

Blood test trends for cancer detection in patients presenting with non-specific symptoms in primary care: a diagnostic accuracy, longitudinal cohort study

Pradeep Virdee
University of Oxford

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Thursday, October 23

Discussion Panel: Evolution of early detection in the commercial landscape

Over the past decade, the commercial funding landscape for cancer early detection and diagnosis has undergone significant transformation, driven in part by advancements in technology and evolving investor interests. Previously, this was an area treated with caution, grappling challenges with accuracy, scalability, and regulatory hurdles. However, the landscape began to shift with the rise of innovative technologies, such as liquid biopsy, AI-driven diagnostics, and next-generation sequencing, which offered the potential for earlier, less invasive detection. These innovative breakthroughs sparked renewed investor interest. However, significant challenges remain in this sector regarding regulatory approval, evidencing clinical validity and market adoption. This panel will address how perceptions of diagnostics and early detection have shifted among commercial funders over the past decade. It will consider how cancer detection technologies have evolved, what commercial funders are looking for today, and predictions for what the next five years will hold for investors, innovators, and patients.

MODERATOR:

Josephine Harada
Precede Biosciences

Josephine N. Harada is currently Vice President, Corporate and Business Development with Precede Biosciences. Previously, Josephine was Vice President of Business Development at Exact Sciences following the acquisition of Thrive Earlier Detection, a healthcare company focused on developing a blood-based multi-cancer early detection test. Prior to Thrive, she led Business Development at 10x Genomics where she oversaw all business development activities and implemented strategic partnerships to accelerate and strengthen 10x Genomics' platform and application pipeline. Josephine additionally executed numerous partnerships as part of the Biopharma business development team at Foundation Medicine. She started her scientific career at the Genomics Institute of the Novartis Research Foundation developing advanced genomic technologies. Josephine completed her PhD in Molecular Biology at UCLA and received her MBA with a focus on Health Care Management and Finance from the Wharton School.

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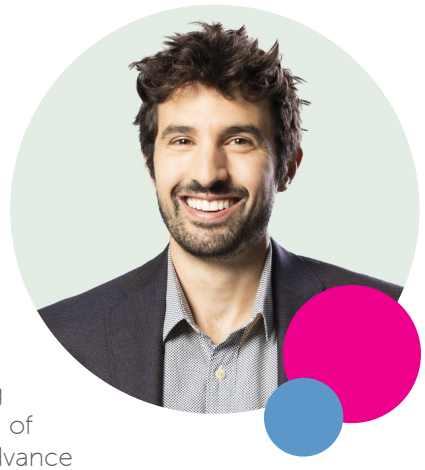
Thursday, October 23

Discussion Panel: Evolution of early detection in the commercial landscape

SPEAKER:

Joe Horsman
Madrona



Joe joined Madrona in 2022. He focuses on sourcing and evaluating new investment opportunities across Madrona's investment themes with a focus on the intersection of life and computer sciences. He also supports the growth and strategy of current portfolio companies. Joe is a scientist at heart and is particularly interested in working with founders combining AI/ML and high-plex multi-omics to uncover unique biology.

Before joining Madrona, Joe worked in business development at Roche, focusing on accelerating DNA sequencing. Joe came to Roche through the acquisition of Stratos Genomics, where he led business development, wearing many hats to advance Stratos's single molecule, nanopore sequencing technology. Earlier in his career, Joe worked at NanoString commercializing multi-omic technologies and was an associate at the W Fund, investing in early-stage startups in Washington.

Outside the office, Joe is usually exploring the great outdoors of the PNW. Climbing mountains in the summer and skiing down them in the winter. He is also an avid runner, biker, and coffee drinker. He shares this passion for getting outside by volunteering with the Washington Alpine Club teaching alpine climbing and backcountry skiing.

Joe holds a doctorate in biochemistry from the University of Washington, where he studied the molecular mechanisms underlying the response to H2S. As an undergrad, Joe attended the University of San Diego, graduating magna cum laude and Phi Beta Kappa in biochemistry. While at USD, Joe competed in track and field for four years.

SPEAKER:

Connie Lehman
Massachusetts General Hospital

Constance "Connie" Lehman, MD PHD is Professor of Radiology at Harvard Medical School, breast imaging specialist, Founder and co-Director of the Breast Imaging Research Center at the Massachusetts General Brigham, and co-Founder of Clairity, Inc. Collectively, her research leverages advanced tools of Artificial Intelligence to promote targeted screening strategies and more effective methods of risk reduction and cancer prevention at the individual level.

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Thursday, October 23

Discussion Panel: Evolution of early detection in the commercial landscape

SPEAKER:

Puneet Souda

Leerink Partners

Puneet Souda is a Senior Research Analyst at Leerink Partners covering Life Science Tools and Diagnostics. His research focuses on companies and technologies within the Life Science Tools subsector, the Diagnostics subsector, and selected areas of Pharmaceutical Services. Prior to joining the Firm in 2014, Puneet was a Senior Associate at Citigroup covering Medical Devices. Before joining Wall Street, he spent over a decade in core and basic research labs at UCLA and Purdue University. In this work, he was a customer and collaborator of many Life Science Tools and Diagnostic companies. Puneet has direct experience in the acquisition, management, and utilization of many life sciences technologies for molecular analysis and diagnostics. He has co-authored over 45 peer-reviewed scientific papers and has built an extensive network of colleagues and collaborators among academic lab researchers and Life Science Tools suppliers. He earned an M.B.A. from University of California-San Diego and undertook graduate study in biotechnology and earned a B.A. in Biology from Purdue University.

EARLY DETECTION IMPACT AWARD

For Outstanding Contributions to Cancer Early Detection

2025 RECIPIENT:

Ruth Etzioni

Fred Hutch Cancer Center

Ruth Etzion is a Professor in the Biostatistics Program, Public Health Sciences Division, at the Fred Hutch Cancer Center, where she holds the Rosalie and Harold Rea Brown Endowed Chair. She has been involved in cancer early detection research since the early days of PSA, when she became fascinated with the many ways of screening for cancer using blood-based biomarkers. The driving motivation of her research program is to develop the evidence needed to inform decisions about how best to screen for different cancers. She has worked primarily in prostate cancer but also in breast and ovarian cancer. She is currently supported by an NCI Outstanding Investigator Award to develop models and methods for novel cancer diagnostics with a primary focus on multi-cancer early detection tests.

About the award

The Early Detection Impact Award for Outstanding Contribution to Cancer Early Detection recognizes a sustained contribution to, or singular achievement in, the cancer early detection field.

AN INTERNATIONAL COLLABORATION

Cancer Research UK, the largest independent funder of cancer research globally, and the Knight Cancer Institute at Oregon Health & Science University, a leader in precision cancer medicine, formed an international collaboration in 2016 to accelerate research in the early detection of cancer. In 2018, they welcomed the Canary Center at Stanford to the partnership. The Canary Center was founded in 2009 as the first research center in the world dedicated to cancer early detection and now elevated to include precision treatment.

The goal of this unique trans-Atlantic agreement is to find lethal cancers as they're forming so they can be treated more effectively. Survival increases significantly when the disease is treated at an early stage.

The collaboration also seeks to accelerate progress by breaking down barriers for scientists, including:

- A lack of cohorts of sufficient size and a shortage of clinical samples available for research
- Development and deployment of new technologies
- Lack of understanding of the biology of early cancer and technologies to detect its features

FUNDING OPPORTUNITIES IN EARLY DETECTION RESEARCH

Cancer Research UK is happy to support international collaborations in early detection research through our Early Detection Research funding committee.

We accept applications from UK-based lead researchers for Programme, Project and Primer Awards, which can include joint lead applicants and coinvestigators from outside of the UK. We can support running expenses and named research staff based at international institutions through these awards.

Please **click here** for more information.

For more information on these awards, please contact **early.detection@cancer.org.uk**

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ORGANIZING INSTITUTIONS

ABOUT THE KNIGHT CANCER INSTITUTE

The Knight Cancer Institute at Oregon Health & Science University is a pioneer in the field of precision cancer medicine.

The institute's chief executive officer, Brian Druker, MD, helped prove it was possible to shut down just the cells that enable cancer to grow. This breakthrough has made once-fatal forms of the disease manageable and transformed how cancer is treated.

The OHSU Knight Cancer Institute is the only National Cancer Institute-designated Comprehensive Cancer Center between Sacramento and Seattle – an honor earned only by the nation's top cancer centers. In addition to offering patients the latest treatments and technologies, as well as hundreds of research studies and clinical trials, the institute is headquarters for one of the National Cancer Institute's largest research collaboratives, SWOG.

ABOUT CANCER RESEARCH UK

Cancer Research UK is the world's leading cancer charity, dedicated to saving and improving lives with research, influence and information. Their vision is for a world where everybody lives longer, better lives, free from the fear of cancer.

Over the past 120 years, they have made discoveries about cancer that have saved countless lives and benefit millions each year, from discovering the link between tobacco and cancer to contributing to the development of the HPV vaccine.

They support research into all aspects of cancer through the work of over 4,000 scientists, doctors and nurses, based in CRUK Centres and Institutes across the UK.

ABOUT THE CANARY CENTER AT STANFORD

The Canary Center at Stanford is the first research center in the world entirely dedicated to cancer early detection.

The Canary Center at the Stanford School of Medicine was founded in 2009 through a unique alliance between Canary Foundation, the Department of Radiology at the Stanford University School of Medicine, and the Stanford Cancer Institute (a National Cancer Institute-designated Comprehensive Cancer Center).

In 2024 we have expanded our mission to include other disease foci. Our mission is to meet clinical needs with both in vivo and in vitro diagnostics and delivery technologies developed by the deep biomedical and engineering expertise that we have at Stanford University.

Our vision is to develop innovative and cost-effective new approaches for early detection and coupled precision treatments that are enabled by the fusion of engineering and medicine.

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SPONSORS

NATERA

Natera™ is a global leader in cell-free DNA (cfDNA) testing, dedicated to oncology, women's health, and organ health. We aim to make personalized genetic testing and diagnostics part of the standard of care to protect health and inform earlier, more targeted interventions that help lead to longer, healthier lives.

AbbVie In Oncology

At AbbVie, we are committed to transforming standards of care for patients living with difficult-to-treat cancers. We are advancing a dynamic pipeline of investigational therapies across a range of cancer types in both blood cancers and solid tumors. We are focusing on creating targeted medicines that either impede the reproduction of cancer cells or enable their elimination. We achieve this through various, targeted treatment modalities including Antibody Drug Conjugates (ADCs), Immuno-Oncology, bi-specific/multi-specific antibody and CAR-T platforms. Our dedicated and experienced team joins forces with innovative partners to accelerate the delivery of potential breakthrough medicines.

biomodal

Biomodal is focused on building technologies and analytics as research tools for life scientists & clinical developers. We enable you to capture the 6-base genome and provide insight into the complexity and dynamism of cellular interactions. Our solution works with your existing infrastructure, integrating a pre-sequencing workflow with post-sequencing informatics to generate highly accurate genetic and epigenetic data from a single sample in a single run.

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SPONSORS

EXACT SCIENCES

We help bring clarity to cancer. Cancer creates so many uncertainties. We're committed to answering questions, solving problems, and making a lasting, positive impact on people's lives. Our tests explore hereditary risks, screen for cancer's presence, and examine the unique genomic alterations of an individual's cancer after a diagnosis to help guide their treatment.

GRAIL

Our mission is to detect cancer early, when it can be cured. GRAIL is focused on alleviating the global burden of cancer by using the power of next-generation sequencing, population-scale clinical studies, and state-of-the-art machine learning, software, and automation to screen for many of the deadliest cancer types before symptoms appear.

Incyte

Incyte is a biopharmaceutical company on a mission to *Solve On*. *Solve On.* speaks to our relentless pursuit to find answers for patients by following the science. It inspires us to bring advances for those with unmet medical needs, regardless of the disease or size of the patient population. And, it reminds us that patients are waiting. That spirit, energy and excitement is felt across the company each day. How do we *Solve On*? By following the science...to find new ways to manage rare and often hard-to-treat diseases. By deciphering new pathways...to discover first-of-their-kind treatments.

SPONSORS

Menarini Group / Stemline

Stemline is part of the Menarini Group, a leading international pharmaceutical and diagnostics company, with a turnover of over $4 billion and over 18,000 employees. Menarini is focused on therapeutic areas with high unmet needs with products for cardiology, oncology, pneumology, gastroenterology, infectious diseases, diabetology, inflammation, and analgesia.

Merck

At Merck, known as MSD outside of the United States and Canada, we are unified around our purpose: We use the power of leading-edge science to save and improve lives around the world. For more than 130 years, we have brought hope to humanity through the development of important medicines and vaccines. We aspire to be the premier research-intensive biopharmaceutical company in the world — and today, we are at the forefront of research to deliver innovative health solutions that advance the prevention and treatment of diseases in people and animals. We foster a diverse and inclusive global workforce and operate responsibly every day to enable a safe, sustainable and healthy future for all people and communities.

Pfizer

At Pfizer, we apply science and our global resources to bring therapies to people that extend and significantly improve their lives. We strive to set the standard for quality, safety, and value in the discovery, development, and manufacture of health care products. Our global portfolio includes medicines and vaccines as well as many of the world's best-known consumer health care products. Every day, Pfizer colleagues work across developed and emerging markets to advance wellness, prevention, treatments, and cures that challenge the most feared diseases of our time. Consistent with our responsibility as one of the world's premier innovative biopharmaceutical companies, we collaborate with health care providers, governments, and local communities to support and expand access to reliable, affordable health care around the world. For more than 170 years, Pfizer has worked to make a difference for all who rely on us.

SPONSORS

SpringWorks Therapeutics

People with cancer can't wait. Let's go. The full potential of targeted oncology is waiting to be unlocked. That's why we relentlessly pursue every possibility to create new cancer breakthroughs and power our approach with people who think hard, care hard and act with urgency. At SpringWorks, we bring tenacity to work every day because patients need answers now.

Takeda

Creating better health for people and a brighter future for the world is our purpose. The science and technology we advance are constantly evolving. But through our enduring values, our ambition remains steadfast. We strive to deliver truly transformative treatments, contributing significant value to society while creating an exceptional experience for our people.

TerSera Therapeutics

We follow the science to uncover and expand new possibilities for patients. Our team is tenacious in our pursuit of unique therapeutic opportunities. We combine a science-led approach with a holistic view of how patients experience treatment to uncover therapeutics with untapped potential in disease areas where there are limited or no known treatment options. We amplify each product's ability to address unmet need and make a meaningful difference in patients' lives.

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SPONSORS

Twist Bioscience

At Twist Bioscience, we work in the service of customers who are changing the world for the better. In fields such as medicine, agriculture, and industrial chemicals, by using our synthetic DNA tools, our customers are developing ways to better lives and improve the sustainability of the planet.

10x Genomics

We deliver powerful, reliable tools that fuel scientific discoveries and drive exponential progress to master biology to advance human health. Cited in more than 10,000 research papers, our innovative single cell, spatial, and in situ technologies enable discoveries across oncology, immunology, neuroscience, and more. Our talented, dedicated science professionals have a distinguished record of creating innovative instruments, reagents, and software that analyze biological systems at a resolution that matches the complexity of biology.

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CONFERENCE STAFF ORGANIZERS

While many individuals came together to make this conference possible, listed below are the main staff organizers of the 2025 conference:

Cigdem Ak	OHSU, Abstract Review Committee
Colin Bergstrom	Stanford University, Abstract Review Committee
Lina Cheuy	Stanford University
Rebecca Clifford	Cancer Research UK
Jackie Dingman	OHSU
Hoda Hashemi	Stanford University, Abstract Review Committee
Jake Howden	Cancer Research UK
Joanna Janus	Cancer Research UK
Ellen Langer	OHSU, Abstract Review Committee
Jillian Martin	OHSU
Katie Pontius	Stanford University
Talisia Quallo	Cancer Research UK
Lucy Stuart	Cancer Research UK
Farbod Tabesh	Stanford University, Abstract Review Committee
Stephanie Torres	OHSU
Ashley Williams	Stanford University
Christian von Wagner	University College London, Abstract Review Committee

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POSTER MENU

	First Name	Last Name	Abstract Title
1	Ishfaq	Ahmad	Evaluation of multicancer early detection testing vs recommended colorectal cancer screening: a modeling approach
2	Cigdem	Ak	Enhancing Interpretability of Single-Cell Multi-Omics Analysis
3	Cigdem	Ak	Capturing Cross-Modality Epigenomic and Transcriptomic Interactions in Single-Cell Cancer Data
4	Cigdem	Ak	Spatial Analysis of Androgen Receptor's Role in Prostate Cancer Across Multiple Scales
5	Isaac	Allen	Lethal progression risk following low-risk and favourable-intermediate-risk prostate cancer in a prospective cohort of US health professionals
6	Arslan	Amer	Development of 3D bioprinted tissue models to study the role of proximity-based cancer-stromal crosstalk that regulates progression from premalignancy to lethal disease in PDAC.
7	Susan	Astley Theodossiadis	The impact of age at first pregnancy on AI-assessed breast density
8	Avathamsa	Athirasala	A Vascularized Bone-on-a-Chip Platform Reveals Bone Microenvironment Induced Nuclear Damage Primes Circulating Prostate Cancer Cells for Aggressive Reprogramming
9	Charles	Atwood	REFLECTION: Real-World Evidence Study of Multi-Cancer Early Detection (MCED) Among Veterans in the Veterans Affairs Healthcare System (VA)
10	Greg	Baker	CD45R+ CD8+ T Cells as a Biomarker of Brain Tumor-Associated Neuroinflammation
11	Jenna	Beckwith	A Longitudinal Comprehensive Biospecimen and Clinical Data Repository for Individuals at Increased Risk of Cancer: The InAdvance Study
12	Tomasz	Beer	Influence of initial imaging type on time-to-diagnosis among cancers without routine screening programs: a SEER-Medicare study
13	Tomasz	Beer	The Potential of Multi-Cancer Early Detection Tests for Reducing Cancer Mortality in the Context of Improving Cancer Survival
14	Tomasz	Beer	The Potential of Multi-Cancer Early Detection Screening in Reducing Cancer Incidence and Mortality in High-Risk Groups: A Modeling Study
15	Tomasz	Beer	Training and Testing of a Modified Multi-Cancer Early Detection (MCED) Blood Test Algorithm for Detection of Pancreatic Ductal Adenocarcinoma with Intended Use in High-Risk Individuals

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16	Brian	Befano	A Novel Cervical Screening Strategy with Extended HPV Genotype Testing and AI-Based Visual Evaluation
17	Michelle	Beidelschies	Lung cancer screening adherence among participants in DETECT-A, the first prospective interventional trial of a multi-cancer early detection (MCED) blood test
18	Michelle	Beidelschies	Evidence of Improvement in Relative Survival Among Many Cancer Types
19	Michelle	Beidelschies	Performance of multi-biomarker class reflex testing in a prospectively-collected cohort
20	Michelle	Beidelschies	Performance of a multi-cancer early detection (MCED) blood test for breast and gynecologic cancers in a prospectively-collected cohort
21	Doreth	Bhairosing	Detecting what matters: Innovation in Early Cancer Detection at NKI-AVL
22	Andrew	Blake	A novel bioreactor platform for immune biomarker discovery in early lung cancer
23	Kate	Bloch	Enhancing Early Lung Cancer Detection Through Explainable Multi-Modal Deep Learning for Indeterminate Pulmonary Nodule Classification
24	Berit	Blume	Phosphatidylinositol lipids as potential early detection markers for PDAC
25	Oleg	Blyuss	PROGRESS Prostate: A Dynamic Predictive Model for Baseline and Follow-up Risk Assessment of Prostate Cancer Progression on Active Surveillance
26	Chris	Boniface	Mutation-agnostic detection and lineage tracing of pre-cancer clones for AML risk stratification
27	Rob	Bristow	Multiomics and Models of Lynch Syndrome-Associated Prostate Cancer to Inform Early Detection and Interception
28	Frederik	Brøndsted	A new drug-dye conjugate, Adagrasib-OF650, allows for selective labeling of G12C PDAC tumors for fluorescence guided surgery.
29	Megan	Burger	Identification of tumor-intrinsic factors mediating the early immune suppression program in lung cancer
30	Hongui	Cha	Preinvasive Exhausted $CD8^+$ T Cells and Regulatory T Cells Co-define Targetable Immune Regulation for Multi-Cancer Interception
31	Tirtha	Chanda	Interaction-Centred AI, Teledermoscopy, and Pathology: A Unified Route to Early Melanoma Detection
32	Kiana	Collins	Personalised Prostate Specific Antigen (PSA) Retesting Intervals in Primary Care
33	Kiana	Collins	Prostate Specific Antigen (PSA) retesting intervals between 2000 - 2018 in England: A study of 10 million patients
34	Mark	Consugar	The early detection of colorectal cancer from cfDNA can be improved through the detection of 6-base (5mC and 5hmC) biomarkers

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35	Carmen	Curry	Pancreatic Cancer Screening: Early Detection
36	Jessica	Dalton-O'Reilly	Generating a tissue resource within the Novel Early Markers for Ovarian cancer (NEMO) study: A multicentre study for the early detection of high grade serous ovarian cancer through fallopian tube sampling
37	Stephen	Deppen	Vanderbilt's Thoracic Biorepository: Advancing Lung Cancer Research Through Biospecimen Collection and Distribution
38	Isis	Diaz Monarrez	Early Markers of Barrett's Oesophagus Progression Identified Through Spatial Transcriptomics
39	Henry Mark	Dunnenberger	Falcon – Exact Sciences' Multicancer Early Detection (MCED) Real World Evidence (RWE) Registry
40	Karen	Eden	Identifying women with actionable risk factors for breast cancer in primary care practice
41	Didem	Egemen	AI-Assisted Visual Evaluation Test for Cervical Screening: Lessons Learned
42	Kyle	Ellrott	Calypr: A platform to enable consortium cancer analysis
43	Andrei	Enica	Spatially informed immune interception of squamous lung cancer
44	Joshua	Fieggen	Dysregulated Immune Proteins in Plasma in the UK Biobank Predict Multiple Myeloma 12 years Before Clinical Diagnosis
45	Cristina	Garcia Toche	Advancing Diverse Enrollment in Multi-Cancer Early Detection Clinical Research Trials: Partnerships to recruit and enroll non-white patients with the Oregon Rural Practice-based Research Network
46	Tana	Gazdik	Analyzing Pancreatic Intraepithelial Neoplasia Progression in High-Risk Human Donor Pancreata to Understand Hereditary Pancreatic Ductal Adenocarcinoma
47	Andrew	Gilmore	Understanding breast cancer risk associated with mammographic breast density in premenopausal women.
48	Alec	Gosiak	3D Printing of Tissue Models using Dissolvable Photo-poly(N-isopropylacrylamide) as Sacrificial Templates
49	Joseph	Grieco	Stress-induced transdifferentiation in prostate cancer is mediated by mitochondrial trafficking of NRXN1 to adhesion sites
50	Juliane	Griesbach	Developing and assessing of a new biomarker panel for early detection of lung cancer - in vivo
51	Aaron	Grossberg	Biological Determinants of the Plasma Proteome in Pancreatic Ductal Adenocarcinoma
52	Alice	Groves	The ACED Cohort study supporting future early detection of cancer research
53	Dmytro	Grygoryev	Identification of Transcriptionally High-Risk PanIN Lesions and Their Early Biomarkers Using Spatial Transcriptomics in Human PDAC Samples

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54	Toumy	Guettouche	Transforming Cancer Detection: Scalable and Sensitive Liquid Biopsy Powered by Extracellular Vesicle Protein Colocalization
55	Nina	Haindl	LEGACY - DeLinEatinG the tumorAl and Clinical evolution of hereditarY pancreatic cancer
56	Sarah	Harbach	Fallopian tube lavage sampling for early detection of pre-invasive ovarian cancer
57	Haylie	Helms	3D Bioprinted Tumor Avatars as a Functional Platform for Early Cancer Modeling
58	Samuel	Hervas Gomez	Does Ethnicity Impact AI performance in Breast Density Prediction?
59	Ryan James	Hodgetts	Using immune biomarkers to improve early lung cancer detection during community lung health checks.
60	Christian	Hoerner	Utilizing the B Cell Response for Early Detection of Renal Cell Carcinoma
61	Yiyang	Hou	Detecting Early Cancer Using cfDNA Methylation and Fragmentation Signatures
62	Tiffani	Howard	Adapting Outreach for the Black Community: Engaging Community Champions to Boost Trial Enrollment
63	Hsiao-Yun (Ivy)	Huang	Developing and Evaluating a Blood-Based Early Cancer Detection (ECD) Test for Colorectal Cancer (CRC): Insights from the PROCEED-CRC Study
64	Kaisa	Huhtinen	CA-125 glycovariant assays improve the detection of early-stage epithelial ovarian cancer
65	Jihyun (Luna)	Hwang	Minimally Invasive Collection of Dermal Interstitial Fluid via 3D-Printed Microneedles for Early Cancer Detection
66	Stuart	Ibsen	Early-Stage Pancreatic Cancer Detection Using Cancer-Derived Nanoparticles Recovered from Plasma by Three Electrode Cluster Dielectrophoresis
67	Maria Agustina	Ipina	Risk-based breast cancer screening: an expert Delphi consensus assessment of evidence under the EUCanScreen initiative
68	Maria Agustina	Ipina	Risk-Based Breast Cancer Screening: mapping three decades of evidence under the EUCanScreen Initiative
69	Joseph	Kawuki	Barriers to Breast and Cervical Cancer Screening Among Adolescent Girls and Young Women in Kenya: A Nationwide Cross-sectional Survey
70	Asif	Khan	Pancreatic cancer risk prediction using deep sequential modeling of longitudinal diagnostic and medication records
71	Sanjay	Khanna	Large language models as a decision-aid tool in lung cancer screening: An assessment of quality and feasibility.
72	Patrick	Kierkegaard	The Political Economy of Externalised Risk: A New Framework for Understanding Diagnostic Delays for Pancreatic Cancer in Primary Care

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73	Laura	King	NHS-Galleri trial: approaches to retain a diverse participant cohort across multiple trial appointments
74	Eric	Klein	Molecular Cancer Signal Localization in Multi-Cancer Early Detection (MCED) Testing Minimizes Radiation and Imaging Burden Compared to Whole Body Imaging Approaches
75	Aditi	Kothari	A novel mouse model for early detection of high-risk HPV-associated head and neck squamous cell carcinoma (HNSCC)
76	Madeline	Kuhn	Investigating the Impact of Heterozygous BRCA2 Mutations in the Tumor Microenvironment on PDAC Progression
77	Akash	Kulgod	Multi-Cancer Screening Using AI-Enhanced Canine Olfactory Detection: Interim Results from a Multi-Center Breath Analysis Study in India
78	Karolina	Kutnik	Integrated Recruitment Strategies to Enhance Representation in a Large Colorectal Cancer Screening Study
79	Emily F.	Lane	Assessing the utility of predicted mortality as a surrogate endpoint in six lung cancer screening trials.
80	Jane	Lange	MCEDsim: a simulation platform for projecting the population impact of multicancer early detection testing
81	Natalie	Lau	Key Risk Factors for 5- and 10-Year Relative and Absolute Multi-Cancer Risk
82	Henson	Lee Yu	Multi-omic Profiling of Localised Prostate Cancer Reveals Early Lineage and Microenvironmental Reprogramming with Potential to Inform Risk Stratification
83	Matt	Leipzig	Decomposing the Causal Chain of Cancer Screening
84	Thomas	Li	RECAST: A Novel Platform Trial Combining Active Surveillance and Endocrine Therapy to Investigate Alternative Strategies for DCIS Management and Breast Cancer Prevention
85	Megan	Lonhart	E.N.G.A.G.E.: A Collaborative Model for Diverse Clinical Research Empowerment, Navigation, Growth, Access, Guidance, and Equity
86	Zhengchun	Lu	Effectiveness of HPV Self-Collection for Cervical Cancer Screening in Community Outreach Programs
87	Theresa	Lusardi	Scaling Up: A flexible framework to guide early development of biomarker-based classifiers
88	Steve	Lyons	Patient-derived Models of BRCA2 Hereditary Prostate Cancer to Inform Early Detection and Interception Strategies
89	Mao	Mao	A blood-based low-cost MCED test to assist cancer diagnosis in patients with tissue masses
90	Mao	Mao	OncoSeek 2.0, an upgraded blood-based test for better sensitivity of multi-cancer early detection

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92	Mao	Mao	Reducing false positives in protein tumor marker-based cancer detection: AI-integrated and sequential testing strategies
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ABSTRACTS

Poster #1

Evaluation of multicancer early detection testing vs recommended colorectal cancer screening: a modeling approach

PRESENTING AUTHOR:

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COMPANY/INSTITUTION:

Oregon Health and Science University

Currently recommended colorectal cancer (CRC) screening—which includes colonoscopy and fecal immunochemical testing (FIT)—is effective at reducing CRC mortality by up to 67%. Colonoscopy, in particular, reduces incidence by detecting precancerous adenomas (~20%). Previously, de Lima (2024) showed that novel single-cancer blood/stool CRC tests meeting the minimal standard set forth by the Centers for Medicare & Medicaid Services will save fewer lives than recommended strategies due to low adenoma sensitivity. Multicancer early detection (MCED) tests offer a promising new approach to cancer screening by detecting multiple cancer types through a single blood draw. The question arises: would replacing recommended CRC screening with MCED screening result in more lives saved?

MCED tests have unknown sensitivity for adenomas but have the potential to offer additional benefits by detecting other cancers. There is currently no data on how MCED testing will change population cancer outcomes in the presence of existing screening. To address this evidence gap, this study uses a simulation modeling approach to evaluate the population-level impact of MCED testing relative to recommended CRC screening strategies. We developed a simulation framework (MCEDsim) that incorporates natural history models for 13 solid cancer sites and projects screen and clinical diagnoses, as well as stage-specific and other-cause mortality. We harnessed an existing framework, CRC-SPIN, to simulate adenoma development, CRC diagnosis, and CRC death.

Based on a simulated cohort of 10 million individuals, we assessed various screening strategies: no screening, recommended CRC screening, CRC blood tests, and MCED testing at different intervals (1-year, 2-year, and 3-year intervals). We evaluated the difference in mean life-years across the strategies, as well as the burden of false-positive tests. As a base case, we used the GRAIL Galleri test as our exemplar MCED and assumed an overall preclinical detectable period of 2 years and sensitivity equal to that of clinically diagnosed individuals. As sensitivity analyses, we varied the early-stage preclinical detectable window for MCED tests, as well as the early-stage sensitivity, to determine the MCED screening characteristics needed to surpass recommended CRC screening in terms of mean life-years.

These analyses will inform how MCED screening strategies stack up against recommended screening programs.

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Poster #2

Poster Pitch

Enhancing Interpretability of Single-Cell Multi-Omics Analysis

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Sam D. Kupp, Ian A. VanGordon Jr, Sebnem E. Eksi, Sadik Esener, Cigdem Ak

COMPANY/INSTITUTION:

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The rapid advancement of single-cell technologies has led to the development of various analysis methods, each with trade-offs between predictive power and interpretability particularly for multimodal data integration. Complex machine learning models achieve high accuracy, but they often lack transparency, while simpler models are more interpretable but less effective for prediction. We introduce an innovative method for single-cell analysis using Multiple Kernel Learning (scMKL), that merges the predictive capabilities of complex models with the interpretability of linear approaches, aimed at providing actionable insights from single-cell multiomics data. scMKL excels at classifying healthy and cancerous cell populations across multiple cancer types, utilizing data from single-cell RNA sequencing, ATAC sequencing, and 10x Multiome. It outperforms existing methods while delivering interpretable results that identify key transcriptomic and epigenetic features, as well as multimodal pathways– that existing methods have failed to achieve, in breast, lymphatic, prostate, and lung cancers. Leveraging insights from one dataset to inform analysis in a new dataset, scMKL uncovers biological pathways that distinguish treatment responses in breast cancer, low-grade from high-grade prostate tumors, and subtypes in lung cancer, thereby enhancing our understanding of cancer biology and tumor progression.

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Poster #3

Capturing Cross-Modality Epigenomic and Transcriptomic Interactions in Single-Cell Cancer Data

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COMPANY/INSTITUTION:

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Single-cell (sc) multiomics assays simultaneously measure transcriptomic, epigenomic, and proteomic modalities in single cells. These multimodal assays enable deeper characterization of cells compared to single-omic assays by offering a more comprehensive measurement of the cell state. Additionally, they can identify cross modality associations, such as promoter-enhancer linkages. Recently, numerous computational methods for sc-multiomics data have been released; however, there is a dearth of interpretable methods While matrix factorization and deep learning approaches, such as MOFA+ and scVI, are effective at cell type clustering; however, these methods are difficult to interpret, masking the underlying biology that defines cell states. Our solution, EpiConfig, is a multimodal topic model that can accurately cluster cells based on cell types and yields biological insights by jointly modeling transcriptomic and epigenetic states combinations. Unlike other sc-multiomics topic models, EpiConfig explicitly models cross modality associations. Furthermore, we describe important cell filtering and subsetting approaches to speed up and improve the convergence of topic model. Benchmarking EpiConfig on publicly available scRNA+ATAC datasets to healthy and cancerous cell populations, we show that EpiConfig outperforms competing methods, such as Cobolt and MOFA. Furthermore, EpiConfig cross modality associations cell type capture 3D genome interactions. Modeling sc-multiomics data from lymphoma, EpiConfig identifies topics for cancerous cells. Coupled with our model interpretation R Shiny app, EpiConfig allows for the interpretation and identification of associations between transcriptomic and epigenomic features that define cell types and states.

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Poster #4

Poster Pitch

Spatial Analysis of Androgen Receptor's Role in Prostate Cancer Across Multiple Scales

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COMPANY/INSTITUTION:

Oregon Health and Science University

Mapping the spatial interactions of cancer, immune and stromal cells presents novel opportunities for patient stratification and for advancing immunotherapy. While single-cell studies have revealed significant molecular heterogeneity in prostate tumors, there is currently no understanding of how immune cell heterogeneity impacts spatial coordination between tumor and stromal cells in localized tumors. To address this gap, we used cyclic immunofluorescent imaging on whole-tissue sections to uncover novel spatial associations between cancer and stromal cells in low- and high-grade prostate tumors and tumor-adjacent normal tissues. We conducted a series of rigorous statistical analyses to validate the robustness and consistency of our findings. These included: (i) generating in silico tissue to augment sample size and to address sample variability, (ii) performing leave-one-patient-out analysis to assess the impact of patient-to-patient variability on the results, (iii) conducting subsampling analysis to estimate the variability in our results and demonstrate the stability of our findings, (iv) employing permutation test to provide additional validation and reinforce the robustness of our results. Our results provide a spatial map of single-cells and recurrent cellular neighborhoods in the prostate tumor microenvironment of treatment-naïve patients. We report unique populations of mast cells that show distinct spatial associations with M2 macrophages and regulatory T cells. Our results show disease-specific neighborhoods that are primarily driven by androgen receptor-positive (AR+) stromal cells and identify inflammatory gene networks active in AR+ prostate stroma.

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Poster #5

Lethal progression risk following low-risk and favourable-intermediate-risk prostate cancer in a prospective cohort of US health professionals

PRESENTING AUTHOR:

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Hari Iyer, Kevin Kensler, Edward Giovannucci, Meir Stampfer, Hannah Guard, Bailey Vaselkiv, Sinead Flanagan, Andreas Pettersson, Keyan Salari, Mark Preston, Jaime Hart, Lorelei Mucci, Timothy R. Rebbeck

COMPANY/INSTITUTION:

Dana Farber Cancer Institute

Background: Many prostate cancers are detected early. Resultant low-risk (grade group 1, stage≤cT2a, PSA<10) or favourable-intermediate risk (grade group 1, stage cT2b–cT2c or PSA 10–20, or grade group 2, stage≤cT2a and PSA<10) prostate cancer can be treated with active surveillance/watchful waiting. Studies of progression post-active surveillance/watchful waiting are few, mostly with follow-up of under 5 years. We estimated 15-year lethal progression risks in a prospective health professionals cohort with low/favourable-intermediate-risk prostate cancer.

Methods: We followed 2784 men from diagnosis (1986-2019) to lethal progression (prostate cancer death/metastasis), censoring at other death, 15 years, or December 2022. We estimated Kaplan-Meier cumulative incidences by active treatment (radical prostatectomy/radiotherapy) vs. active surveillance/watchful waiting (time accrued for the latter switched to the former at treatment switch). We assessed risk by treatment, sociodemographics, prostate cancer pathology, and lifestyle with Cox models.

Results: We saw 99 events over a median follow-up of 15 years (IQR:3.7 years). 2345 (84%) of patients had active primary treatment (1105 radical prostatectomy, 1240 radiotherapy), with 80 events. 439 had active surveillance/watchful waiting (153 switched to active treatment) with 19 events, 8 after switching. Those older at diagnosis had higher lethal progression risks (+1 year–Hazard Ratio (HR):1.07, 95%CI:1.03-1.10). We saw lower risks in those with healthy post-diagnosis lifestyle scores (based on smoking, BMI, physical activity) (HR:0.71, 95%CI:0.52-0.97) and perhaps low vs. favourable-intermediate-risk prostate cancer (HR:0.72, 95%CI:0.51-1.01). We saw no association with prostate cancer family history (HR:1.11, 95%CI:0.74-1.65), race (Non-White v White:HR:0.82, 95%CI:0.30-2.24), or neighbourhood deprivation (+1 standard deviation–HR:0.94, 95%CI:0.79-1.10). 15-year risks were 4.0% (95%CI:3.2-4.9%) post-active treatment and 6.5% (95%CI:2.0-10.8%) post-active surveillance/watchful waiting, with no variation after adjusting for the factors above (active surveillance/watchful waiting HR:0.99, 95%CI:0.51-1.90).

Conclusion: In one of the longest ongoing prospective cohort studies, we saw no clear lethal progression risk difference post-active treatment vs active surveillance/watchful waiting and lower risk with healthier post-diagnosis lifestyles. This may inform clinical management of prostate cancer detected early.

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Poster #6

Development of 3D bioprinted tissue models to study the role of proximity-based cancer-stromal crosstalk that regulates progression from premalignancy to lethal disease in PDAC.

PRESENTING AUTHOR:

Author

AUTHORS:

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COMPANY/INSTITUTION:

Oregon Health and Science University

Pancreatic ductal adenocarcinoma (PDAC) is projected to be the second leading cause of cancer related mortality by 2030. Understanding tumor biology of PDAC progression is important for disease treatment and intervention. PDAC progression is widely accepted to occur by sequential genetic mutations. PDAC is also characterized by dense, fibrotic stroma which occupies the bulk of the tumor mass. During pancreatic cancer development, stromal cells co-evolve with changing pre-neoplastic and neoplastic cells and are modulated by genetic changes occurring in these cells. Intriguingly, stromal cells have been shown to exert both tumor-promoting and tumor-restrictive functions, suggesting a dynamic and context-dependent role in PDAC pathogenesis. Despite this, how stromal cell phenotypes are shaped in response to specific oncogenic events during early tumor evolution remains poorly understood.

To address this gap, we have begun developing a 3D bioprinted human tissue model that recapitulates the cellular complexity of early pancreatic neoplasia. In this model, we are incorporating primary human pancreatic ductal epithelial cells engineered with inducible driver mutations along with stromal cells in a spatially organized manner to enable stepwise modeling of pancreatic intraepithelial neoplasia (PanIN) progression. We have modified these cells with TurboID proximity labeling system and are in the process of verifying its downstream processes. This enables us to profile dynamic changes in the epithelial cell secretome in response to sequential activation of key oncogenic drivers. This will identify unique molecular signals at distinct stages of progression that are likely to influence stromal reprogramming. In parallel experiments, we have transduced the epithelial cells with a niche-labeling system which enables us to isolate and characterize stromal cells in direct proximity to transformed epithelial cells, providing insight into how stromal phenotypes are modulated by evolving epithelial signals.

By integrating secretome data with stromal transcriptional profiles, this project will generate a comprehensive map of epithelial-stromal interactions during early PDAC progression. These findings are expected to uncover novel mechanisms of stromal regulation and identify potential therapeutic targets aimed at reprogramming the stroma to support tumor suppression rather than tumor promotion.

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Poster #7

Poster Pitch

The impact of age at first pregnancy on AI-assessed breast density

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COMPANY/INSTITUTION:

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Background

Mammographic density, usually measured as the proportion of dense fibroglandular tissue in the breast, is a known risk factor for breast cancer, with a 4-6-fold increase in risk for women with the highest densities, and is associated with the sensitivity of mammography. Women who have never been pregnant and those with a late first pregnancy are also at increased risk. In this work we investigate the relationship between parity and breast density, using a novel approach to density estimation that uses AI to learn expert reader assessments.

Methods

Data from 14234 women aged 47-73 in the UK Predicting Risk Of Cancer At Screening (PROCAS) study were analysed. Breast density was estimated from GE mammographic images using MAI-VAS, an AI method trained using an independent cohort from the study. MAI-VAS takes as input mammographic images, and is trained to predict the average expert assessment of percentage breast density recorded on Visual Analogue Scales (VAS). Expert VAS assessment has been shown to be more predictive of breast cancer risk than other methods. PROCAS participants provided information including age, parity, height, weight, menopausal status and ethnic origin via a questionnaire completed at time of entry to the study. Multivariate analysis using ANCOVA took into account age at consent to PROCAS, Body Mass Index, menopausal status and ethnic origin.

Results

1977 (13.9%) of women in the study group had never been pregnant. 6541 (46.0%) had their first pregnancy aged under 25, 3507 (24.6%) between 25 and 29, 1521 between 30 and 34 and 688 over 35 years of age. Women who had never been pregnant and those over 35 at the age of first pregnancy had the highest mean breast densities of 34.1% and 35.6% respectively. The mean breast density in women under 25 at first pregnancy was significantly lower (26.4%) than that in all other age groups and in nulliparous women.

Discussion

Our results show the that nulliparous women and those who had their first pregnancy over the age of 35 had higher breast density. This is associated both with increased risk of developing breast cancer and reduced sensitivity of mammographic screening. Strengths of the work presented here are the large sample size, homogeneity of the imaging, and use of the AI-based density method to eliminate subjectivity, however further work is needed to understand the association between breast density changes due to age at first pregnancy and breast cancer risk.

ABSTRACTS

Poster #8

Lightning Talk

A Vascularized Bone-on-a-Chip Platform Reveals Bone Microenvironment Induced Nuclear Damage Primes Circulating Prostate Cancer Cells for Aggressive Reprogramming

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COMPANY/INSTITUTION:

Oregon Health and Science University

The bone microenvironment presents a unique combination of structural rigidity, nanoscale mineralization, and diverse resident cell populations that can profoundly influence the behavior of circulating tumor cells (CTCs). Yet, these features are largely absent from current in vitro models. We developed a biomimetic bone-on-a-chip platform that integrates nanoscale mineralized collagen, embedded osteoblasts, osteocytes, mesenchymal stem cells, and a perfusable, pericyte-supported microvasculature. This system supports real-time tracking of CTC dynamics, including intravascular migration and extravasation, within a physiologically relevant bone-like matrix. In an application of this platform to study prostate cancer progression in bone, tumor cells showed a marked preference for transiting through the engineered microvasculature and infiltrating the mineralized bone-like matrix, compared to non-mineralized controls. This migration through the dense, calcified environment induced pronounced nuclear deformation, rupture and elevated γH2AX foci, consistent with DNA damage, suggesting that physical features of the bone microenvironment may drive genomic instability and early molecular changes associated with tumor aggressiveness. Spatial transcriptomic analyses of CTCs near vasculature within the engineered bone microenvironment showed differential expression of genes associated with tumor proliferation and migration as well as chromatin regulators when compared to non-mineralized controls, indicating early stress adaptation and plasticity. These findings demonstrate that the physical properties of the bone microenvironment can rapidly induce nuclear stress and transcriptomic reprogramming in circulating tumor cells, highlighting the role of early microenvironmental cues in driving cellular plasticity and promoting the emergence of aggressive phenotypes.

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Poster #9

Lightning Talk

Real-World Evidence Study of Multi-Cancer Early Detection (MCED) Among Veterans in the Veterans Affairs Healthcare System (VA)

PRESENTING AUTHOR:

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AUTHORS:

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COMPANY/INSTITUTION:

VA Pittsburgh Healthcare System

Background: REFLECTION is a multicenter, prospective, observational, cohort study of the real-world experience of MCED via the Galleri® test in clinical settings, focusing on the veteran population.

Methods: Since Oct 2022, veterans aged ≥22 yrs in the VA who opted to be screened with the MCED test were recruited across 7 sites. Individuals who received a cancer signal detected (CSD) result were worked up at each respective institution and cancer status ascertained. We report cancer outcomes data available to date.

Results: Among 6,419 veterans (median age 60 yrs [interquartile 48-70]), the overall cancer signal detection rate (SDR) was 1.09% (95% confidence interval [CI]: 0.86%, 1.38%). SDR increased with age: individuals ≥65 yrs old had an SDR (95% CI) of 2.03% (1.53%, 2.67%) vs 0.54% (0.36%, 0.82%) for those <65 yrs old. Men had a higher SDR (1.22% [0.96%, 1.56%]) vs women (0.50% [0.23%, 1.10%]). SDR was 2.50% in those with cancer history in the last 5 yrs vs 1.03% without. Current and former smokers had a higher SDR (1.20% and 1.29%, respectively) vs non-smokers (0.90%). SDR was 1.13% in those reporting toxic exposure vs 0.97% in those reporting no toxic exposure. Among the 70 individuals with a CSD result, 19 had a confirmed diagnosis of cancer within 12 months of follow-up. An additional 23 individuals have completed at least 12 months of follow-up without a confirmed cancer diagnosis to date. The remaining 28 cases have had less than 12 months of follow-up and are still undergoing diagnostic evaluation. In this prevalent screening round, the 18 cancers for which stage information was available included: 1 stage I; 5 stage II; 4 stage III; and 8 stage IV. Follow-up is ongoing for all participants. Median time from test result to cancer diagnosis was 54 days (interquartile 35-71). Studied Veterans were 81% male; among non-missing: 17% Black or African American [Non-Hispanic], 66% White [Non-Hispanic], 15% Hispanic/Latino; 54% have ever smoked, of them 13% are current smokers; 13% reported personal cancer history (4% within last 5 yrs). Males were older: 40% males vs 21% females were ≥65 yrs old at screening.

Conclusion: In this diverse veteran cohort, initial observations suggest that the Galleri test performs consistently with previously reported metrics in other clinical settings, supporting timely investigation and cancer detection. Ongoing follow-up of this cohort will further clarify the value of MCED testing in veteran health care.

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Poster #10

CD45R+ CD8+ T Cells as a Biomarker of Brain Tumor-Associated Neuroinflammation

PRESENTING AUTHOR:

Greg Baker

AUTHORS:

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COMPANY/INSTITUTION:

Oregon Health and Science University

Glioblastoma (GBM) is an aggressive brain cancer with a median survival of just 15 months—an outcome with little improvement in two decades. Diagnosis typically occurs after neurological symptoms appear, when tumors are already advanced and treatment-resistant. Thus, there is an urgent need for earlier-stage biomarkers of this disease.

Using our lab's systemic immune profiling platform (SYLARAS, Baker et al., Cell Systems 2020), we have identified a distinct population of circulating CD8+ T cells expressing CD45R/B220 (B220T cells) in healthy and glioma-bearing mice. These cells respond to glioma by trafficking to the tumor microenvironment, where they occupy spatial niches distinct from other CD8+ T cells. Importantly, we also observe B220T cells in a subset of human gliomas across tumor grades and independent of IDH-1 status, supporting their clinical relevance.

Others have shown that B220T cells can suppress immune responses to self-antigens, similar to tumor-derived neoantigens. Our own data demonstrate that B220T cells increase in gliomas resistant to anti-PD-1 therapy and decline following successful treatment, suggesting a role in immune suppression. RNA-seq reveals enrichment of non-polymorphic MHC class Ib molecules, including Qa-1 (analogous to human HLA-E), further implicating these cells in immune evasion.

We hypothesize that a drop in circulating B220T cells may signal early brain tumor development, and that their targeted depletion could be therapeutically beneficial. To further define the role of B220T cells in glioma, we are now conducting: (i) multiplex immunofluorescence imaging of human glioma biopsies, including antibodies to detect B220T cells, (ii) deep single-cell profiling of B220T cells from patient blood, and (iii) functional studies in engineered and orthotopic mouse models.

This work aims to improve early brain tumor detection and demonstrates the utility of systemic immune profiling tools (like SYLARAS) in identifying novel immuno-oncology biomarkers. Future efforts will explore strategies to selectively ablate B220T cells using bispecific antibodies targeting B220 and CD8 antigens, or CAR T cells engineered to recognize and deplete CD8+ B220+ T cells in tumor-bearing hosts.

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Poster #11

A Longitudinal Comprehensive Biospecimen and Clinical Data Repository for Individuals at Increased Risk of Cancer: The InAdvance Study

PRESENTING AUTHOR:

Jenna Beckwith

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Kauffman TL, Babic A, Marinac CR, O'Donnell E, Parmigiani G, Adams K, Brantley KD, Chowdhury D, Crompton B, Diller L, Garber JE, Hanna GJ, Kamihara J, King T, Mittendorf E, Partridge AH, Sands J, Weeks LD, Yurgelun M, Ghobrial I, Rebbeck T, Syngal S

COMPANY/INSTITUTION:

Dana-Farber Cancer Institute

Clinical and sample biobanking efforts have focused on cancer-affected and average-risk populations, but there is a paucity of comprehensive and longitudinal data repositories in individuals at increased risk of cancer. The InAdvance Study through the Centers for Early Detection and Interception (CEDI) at Dana-Farber Cancer aims to fill this gap by creating a robust infrastructure supporting a longitudinal biospecimen and data repository for collaborative early detection research.

Recruitment for the InAdvance Study (NCT:05463796) focuses on four broad categories: 1) presence of inherited cancer risk; 2) presence of cancer precursor conditions; 3) individuals with a positive signal on multi-cancer early detection tests; and 4)) exposure that increases cancer risk (e.g. prior cancer treatment). Participants consent on a web-based platform, allowing for enrollment outside of a clinical encounter, and complete annual surveys assessing demographics, lifestyle exposures, and medical history using validated instruments. Annual biospecimen collection, completed during medical encounters or remote phlebotomy, includes urine and ~50cc of blood banked as plasma for cfDNA, serum, and peripheral blood mononuclear cells, with optional stool and oral swab collection. Data integration links longitudinal participant information from medical records, survey responses, and biospecimens into a centralized dataset.

Since enrollment launch in April 2023, over 1,100 participants aged 21-100 years have joined, representing conditions including inherited cancer risk (70%), oral potentially malignant disorders (OPMDs) (8%), gastrointestinal cancer precursors (9%), clonal hematopoiesis (CH) (1%) individuals with a cancer signal detected on a multi-cancer early detection test (6%), and other high risk groups (5%). Participants are 73% female, 89% White, and 88% non-Hispanic.

The InAdvance Study's strengths lie in its longitudinal comprehensive data collection including linked biospecimens, validated survey measures, and integration of diverse data types. It will be a valuable resource that enables studies aimed at shifting cancer care towards prevention and earlier detection. Examples include identifying risk factors that impact progression from precursor lesion to malignant disease, evaluating interception strategies that prevent such progression, and discovery of early cancer biomarkers and multi-cancer early detection tests.

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Poster #12

Influence of initial imaging type on time-to-diagnosis among cancers without routine screening programs: a SEER-Medicare study

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Tomasz M. Beer

AUTHORS:

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COMPANY/INSTITUTION:

Exact Sciences Corporation

Background: Timely diagnosis is an important but understudied component of the cancer care continuum, particularly for cancers without screening programs. Existing diagnostic experience can provide insights to the design of diagnostic strategies accompanying novel screening tests. Guidelines recommend computed tomography (CT) scan as the initial imaging procedure for many abdominal cancers. We examined the association between the initial use of CT scan, time-to-diagnosis, and peri-diagnostic imaging use among Medicare beneficiaries diagnosed with pancreatic, bladder, liver, and ovarian cancers.

Methods: Patients aged ≥65 years diagnosed between 2010 and 2019 were identified from SEER-Medicare data. We examined the relationship between CT scan as the first imaging procedure and: (1) number of imaging tests from first imaging through treatment initiation; (2) days from first imaging test to diagnosis. We used negative binomial models to analyze count data, adjusting for sociodemographic and clinical characteristics.

Results: A total of 169,781 patients (mean [SD] age: 76.6 [7.5]; 41.4% female) met inclusion criteria: 80,000 bladder, 48,751 pancreatic, 24,493 liver, and 16,537 ovarian patients. Overall, patients averaged 3.0 imaging tests (SD: 1.5) over 81 days (SD: 102). CT scan was the initial imaging test for 57% pancreatic, 54% liver, 62% ovarian, and 44% bladder patients. CT scan vs. other initial tests was associated with shorter time to diagnosis (days,95%CI): (pancreatic: -29, (-31, -27); bladder: -29,(-31, -28); liver: -42,(-46, -38); ovarian: -38,(-42, -35), and fewer imaging procedures (pancreatic: -0.7,(95%CI: -0.8, -0.6); bladder: -0.2,(-0.3, -0.2); liver: -0.32,(-0.4, -0.2); and ovarian: -0.6,(-0.6, -0.5).

Conclusions: Patients aged ≥65 years with CT scan as their first imaging test experienced shorter time to diagnosis and fewer peri-diagnostic imaging procedures. CT scanning first offers an efficient imaging-based diagnostic resolution when an abdominal cancer is suspected clinically. This approach is worthy of evaluation in the setting of novel screening technologies like MCED.

ABSTRACTS

Poster #13

The Potential of Multi-Cancer Early Detection Tests for Reducing Cancer Mortality in the Context of Improving Cancer Survival

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COMPANY/INSTITUTION:

Exact Sciences Corporation

Purpose: Cancer screening models typically use survival curves based on historic data. This neglects future improvements in cancer care and leads to underestimation of the impact of the cancer screening tests. Here we propose a method to model hypothetical improvements in cancer survival and its effect on mortality reduction yielded by supplemental screening with a multi-cancer early detection (MCED) test.

Methods: We developed Simulation Model for MCED (SiMCED), a continuous-time, discrete-event microsimulation model of 14 solid tumor cancers. Cancer type- and stage-specific MCED test sensitivities were derived from a large, prospectively collected, retrospective case-control study (ASCEND 2). The MCED test was administered at the beginning of each year to individuals aged 50-84 years over 10 years. After a cancer diagnosis, individuals followed SEER survival curves to determine the time and cause of death (cancer- or non-cancer). Scenario analysis was performed using hypothetical survival curves that emulate improving survival over time. First, we estimated hazard ratios (HRs) of SEER 10-year survival at the cancer type-stage level between individuals diagnosed in 2010 versus an earlier calendar year. We then applied the HRs to the present-day survival curves in two different ways: constant over all time points, and linearly decreasing from 1.0 at time zero to the SEER-estimated value after the same interval as between 2010 and the reference year. Finally, the adjusted survival curves were mathematically derived from the transformed hazard functions. We used 1993 as the reference year.

Results: Compared to usual care, supplemental screening with an MCED test reduced stage IV cancer incidence by 42% (2,117 vs 1,229 per 100,000) and cancer mortality by 18% (2,612 vs 2,149 per 100,000). Among the cancer types for which there is no routine screening, the mortality reduction was 16% (1,198 vs 1,010 per 100,000). Applying linearly decreasing HRs to survival curves, MCED screening resulted in an 18% (2,567 vs 2,099/100,000) 10-year mortality reduction, same as the base case. Applying a constant HR to survival curves, MCED screening resulted in a 21% (2,275 vs 1,808/100,000) 10-year mortality reduction.

Conclusion: Our study suggests that MCED screening could be effective for reducing both stage IV cancer incidence and mortality, especially in the context of improving cancer survival. This abstract was previously presented at SMDM 2025.

ABSTRACTS

Poster #14

The Potential of Multi-Cancer Early Detection Screening in Reducing Cancer Incidence and Mortality in High-Risk Groups: A Modeling Study

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COMPANY/INSTITUTION:

Exact Sciences Corporation

Background: Emerging liquid biopsy multi-cancer early detection (MCED) tests have the potential to revolutionize early cancer detection. Using a simulation model, we estimated their impact on cancer incidence and mortality in high-risk groups.

Methods: We developed Simulation Model for MCED (SiMCED), a microsimulation model of 14 solid tumor cancer types. MCED test sensitivities were derived from the ASCEND-2 case-control study. Using a 10-year horizon, we simulated the life course of 100,000 adults aged 50-84 years, representing the US general population. In addition, we simulated screening in three high-risk groups: smokers (former and current), heavy alcohol users, and individuals with a family history of cancer in 1 or more first-degree relatives (FDRs). Cancer diagnosis could arise from usual care or annual MCED screening. After a cancer diagnosis, individuals followed SEER survival curves to determine the time and cause of death (cancer- or non-cancer-related).

Results: Among smokers, MCED screening had the greatest impact (in absolute reduction) on lung cancer, accounting for more than 50% of late-stage incidence over the 10-year period; compared to usual care only, MCED screening reduced stage IV lung cancer incidence and cancer mortality by, respectively, 43% (2,028 vs 1,146) and 16% (2,589 vs 2,247). Among heavy alcohol users, MCED screening had the greatest impact on lung, colorectal, and head and neck cancer. The stage IV incidence reduction in these three cancer types were, respectively, 44% (805 vs 454), 57% (286 vs 122), and 33% (398 vs 265). The cancer mortality reduction in these three cancer types were, respectively, 14% (1,014 vs 876), 33% (371 vs 248), and 16% (265 vs 223). In the familial cancer cohort, MCED screening had the greatest impact on lung, colorectal, and pancreatic cancer. The stage IV incidence reduction in these three cancer types were, respectively, 44% (821 vs 461), 57% (257 vs 111), and 58% (233 vs 98). The cancer mortality reduction in these three cancer types were, respectively, 14% (1,030 vs 888), 33% (328 vs 220), and 14% (326 vs 279). We will also present overall reductions in stage IV cancer incidence and all cancer mortality in the general population.

Conclusions: Our study suggests that MCED screening could be effective for reducing cancer incidence and mortality in the general population as well as in high-risk groups.

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ABSTRACTS

Poster #15

Training and Testing of a Modified Multi-Cancer Early Detection (MCED) Blood Test Algorithm for Detection of Pancreatic Ductal Adenocarcinoma with Intended Use in High-Risk Individuals

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COMPANY/INSTITUTION:

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Background: MCED tests are trained at very high specificity for use in average risk populations; performance in high-risk individuals (HRIs) has not been optimized. Pancreatic ductal adenocarcinoma (PDAC) is a lethal cancer and early-stage detection by screening improves survival in HRIs. Lower specificity thresholds may be tolerated to optimize sensitivity of early-stage detection for PDAC screening in HRIs. Here, we retrained the algorithm of an existing MCED assay for detection of early-stage PDAC and measured the false positive rate in disease controls.

Methods: In a data set of methylated DNA and protein markers (MP) across 21 cancer types, we filtered for candidates with lowest cross-reactivity to cancer-free controls and highest signal strength in early-stage PDAC. From these, a linear model with 2 parameters (MP), was fit and cross-validated in silico before testing in a hold-out data set. We estimated the locked model performance in an independent set of cancer-free controls, disease controls with chronic pancreatitis (CP), pancreatic cystic lesions (PCL) and HRIs with familial or germline risk of PDAC (Fam/Gen), and age- and sex-matched positive control advanced-stage PDAC cases.

Results: The training set included 37 PDAC cases (stage I (11), II (11), III (5) and IV (10) and 2373 cancer-free controls. At 91% specificity, the cross-validated model (MDM plus P) detected 97% of PDAC cases. The hold-out test set included 2516 cancer-free controls and 39 PDAC cases (stages I (7), II (8), III (9) and IV (14)). The model correctly classified 33/39 (85%) PDAC cases (95% CI:70-93%) which was greater than CA19.9 alone, which detected 24/39 (62%) PDAC cases (95% CI:46-75%), ($p<0.05$). 11/15 (73%) of stage I+II PDAC were detected by this model at overall specificity of 91%. The independent test set included 20 cancer-free controls, 60 disease controls (20 CP, 20 PCL, 20 Fam/Gen), and 20 PDAC cases (Stage III (1) and IV (19)). All PDAC cases were detected (20/20) and true negative results were seen in 76/80 controls [19/20 normal controls and 57/60 disease controls at 95% specificity].

Conclusion: MP can be trained to enhance single-organ sensitivity while preserving acceptable test specificity. This lays the foundation for an innovative approach of tailoring MCED assay platforms to patient-level cancer risk and develop a paradigm of risk-based individualized PDAC screening. This abstract was previously presented at DDW 2025.

ABSTRACTS

Poster #16

A Novel Cervical Screening Strategy with Extended HPV Genotype Testing and AI-Based Visual Evaluation

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Background: Each year, more than 300,000 women lose their lives to cervical cancer, with over 90% of these deaths occurring in resource-limited settings due to lack of screening. We developed a novel screening and triage approach based on a low-cost extended HPV genotyping test and an on-device deep-learning-based visual test to triage the risk of HPV-positive individuals. The study design emphasized portability, point-of-care turnaround, and rigorous verification in diverse settings.

Methods: This study includes clinics in Brazil, Cambodia, the Dominican Republic, El Salvador, Eswatini, Honduras, Malawi, Nigeria, and Tanzania, and enrolled over 50,000 women aged 25–49. The HPV-AI-Assisted Visual Evaluation (PAVE) protocol[1] includes self-collection with FLOQSwabs, same-visit ScreenFireTM HPV extended genotype testing (HPV16; HPV18/45; HPV31/33/35/52/58; HPV39/51/56/59/68, in decreasing precancer or cancer risk order), and image capture with the IRIS mobile colposcope (Liger). The AI-assisted visual evaluation (AVE) model uses Densenet121 architecture with Monte Carlo dropout to classify cervical images into three classes of severity (normal-indeterminate-severe). All ScreenFire-positive women were invited for imaging and biopsy, with histologically confirmed and expert-reviewed precancers and cancers (cervical intraepithelial neoplasia grade 3 or worse finding, CIN3+).

Results: Within the PAVE consortium cohort, 16.5% of the participants were women living with HIV (WLHIV). HPV prevalence was 40% and 28% among WLHIV and HIV-negative participants, respectively. Among both cohorts, the combined strategy with HPV genotyping and AVE, discriminates risk better than either test on its own ($p < 0.001$). Prior to any screening test, precancer or worse finding (CIN3+) risk was 12% and 5.1% among WLHIV and HIV-negative participants, respectively. After implementing the PAVE strategy, CIN3+ risk ranged from ~0% (HPV39/51/56/59/68+ and Normal AVE) to 42% (HPV16+ and Severe AVE) among WLHIV, and 0.8% (HPV39/51/56/59/68+ and Normal AVE) to 25% (HPV16+ and Severe AVE) among HIV-negative individuals.

Conclusion: A low-cost HPV extended genotyping test and AI-Assisted Visual Evaluation test can sort HPV-positive women into sharply separated risk bands, paving the way for risk-based management guidelines that match treatment thresholds to local capacity. The PAVE blueprint shows how precision screening can be delivered almost anywhere.

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ABSTRACTS

Poster #17

Lung cancer screening adherence among participants in DETECT-A, the first prospective interventional trial of a multi-cancer early detection (MCED) blood test

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COMPANY/INSTITUTION:

Exact Sciences Corporation

Background Lung cancer is a leading cause of cancer death. Adherence to guideline-recommended low-dose CT screening is poor and late-stage diagnosis is common. MCED tests may improve early cancer detection if adherence to guideline-recommended screening is maintained. The DETECT-A study evaluated an MCED test in 9,911 women in Geisinger Health System (GHS), age 65-75, without personal cancer history. This study evaluates lung cancer screening adherence among DETECT-A participants to determine if adherence changed significantly following MCED testing.

Methods We used monthly screening eligibility and adherence data from 09/2016 – 05/2020 for DETECT-A participants and a randomly selected control group of screening-eligible women in GHS who met DETECT-A eligibility criteria but did not participate in DETECT-A. Analyzed participants had ≥24 consecutive months of adherence data centered around the consent month. The proportion adherent at consent month and the end of active study participation at 12 months were calculated. Changes in adherence over time and group comparisons were assessed using mixed effects logistic regression.

Results DETECT-A participants (n=364) and controls (n=2,548) had similar demographic distributions. The odds of adherence (12 months) were significantly higher than at consent for both DETECT-A participants (OR: 3.20, p=0.042) and controls (OR: 2.02, p=0.006). The odds of adherence increase between consent and 12 months was not significantly different between the groups (OR: 1.58, p=0.461). DETECT-A participant adherence was 28.0% in the consent month and increased to 38.5% at 12 months. 68.6% of DETECT-A participants adherent in the consent month were also adherent at 12 months. Control adherence was 16.0% in the consent month and increased to 20.2% at 12 months; 63% of controls adherent in the consent month were also adherent at 12 months.

Conclusions DETECT-A participation did not negatively affect lung cancer screening adherence in this subset of participants. Screening adherence increased over time in both DETECT-A participants and controls; most DETECT-A participants adherent in the study consent month were also adherent 12 months later. Effectiveness of GHS screening programs, DETECT-A participant self-selection and educational efforts promoting screening may have contributed to these results. This abstract was previously presented at the AACR Special Conference in Cancer Research: Liquid Biopsy 2024.

ABSTRACTS

Poster #18

Evidence of Improvement in Relative Survival Among Many Cancer Types

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COMPANY/INSTITUTION:

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BACKGROUND: Cancer survival has improved over the last 20 years. Quantifying these improvements can help in assessing the progress made so far and inform the value of early cancer detection. We computed increases in 5-year age-standardized relative survival (a measure of cancer related survival that accounts for differences in population age distribution and differences in other-cause mortality rates) for 21 different cancer types.

METHODS: Using NCI's SEER incidence registry database, which covers approximately 50% of the US population (SEER-22), we collected age-standardized relative survival probabilities by cancer type and stage for the population aged 15+ years. We computed the difference of the 5-year relative survival between patients diagnosed in 2004-2006 versus 2014-2016.

RESULTS: The 5-year relative survival for patients diagnosed in 2004-2006 across all cancer types and stages was 63.6%, which increased to 66.4% for patients diagnosed in 2014-2016. Increases over all stages were statistically significant for 16 of 21 cancer types examined. Stage-wise relative survival rates were 89.7%, 59.4%, and 22.2% for the localized, regional, and distant stages for patients diagnosed in the earlier time frame, and increased to 90.1%, 63.8%, and 29.0%, respectively. The cancer types with the greatest relative survival increases over all stages were myeloma (15.6%), leukemia (8.7%), and lung (8.1%). The cancers with the greatest relative survival increases for localized, regional, and distant stages were pancreatic (18.6%), skin (11.6%) and myeloma (15.9%), respectively. Among the cancers with recommended screening, lung and breast exhibited the greatest relative survival improvement, with overall increases of 8.1% and 2.4% respectively.

CONCLUSIONS: We estimated 5-year age-standardized relative survival improvements for many cancer types, including cancers for which screening programs have not been implemented. The relative survival improvements among cases diagnosed in localized and regional stages were greater than those diagnosed at a distant stage for esophageal, gastric, liver, lung, and pancreatic cancers indicating more treatment improvements in earlier stages for these cancers. Treatment improvements in earlier stages of cancer amplify the opportunity for effective early detection programs to contribute to future survival improvements. This abstract was presented at ASCO 2025.

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ABSTRACTS

Poster #19

Performance of multi-biomarker class reflex testing in a prospectively-collected cohort

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COMPANY/INSTITUTION:

Exact Sciences Corporation

Background: We previously trained and independently assessed the performance of two biomarker classes (methylation and protein; MP) for multi-cancer early detection (MCED) in a prospectively collected study. Here, we assessed the addition of a somatic mutation reflex approach to samples with initially negative MP-results (MP-reflex; MP-r).

Methods: This study included 3,160 samples (739 cancer and 2421 non-cancer) representing 20 organ types and stages. Samples with negative MP results at a specificity threshold of ≥ 98.5% and detectable MP signals above pre-specified lower thresholds were analyzed for mutations using next generation sequencing. Classifier models and thresholds were developed using an independent training set. Sensitivity of the MP biomarker classifier was determined at a combined specificity of ≥98.5%. We also compared the performance of MP and MP-r configurations with prostate (n=52) and breast (n=88) organ types excluded.

Results: At 98.5% specificity, MP overall sensitivity was 52.9%, with sensitivities of 15.3%, 39.8%, 71.2%, 87.2%, 26.7% and 37.5% for stages I, II, III, IV, I/II and unknown, respectively. At a specificity of 98.5%, when an MP-r configuration was utilized, overall sensitivity was 55.8%, with sensitivities of 19.1%, 42.2%, 72.3%, 89.9%, 29.9% and 46.9% for stages I, II, III, IV, I/II and unknown, respectively. MP-r showed absolute sensitivity increases of 3.8%, 2.5%, 1.1 %, 2.8%, 3.2%, 9.4%, and 2.8%, for stages I, II, III, IV, I/II, unknown, and overall, respectively.

Excluding breast and prostate cancers, MP overall sensitivity was 59.3%, with sensitivities of 17.2%, 51.9%, 76.4%, 88.3%, 31.9% and 41.4% for stages I, II, III, IV, I/II and unknown, respectively. With MP-r, overall sensitivity was 62.3% %, with sensitivities of 22.1%, 54.7%, 76.4%, 91.4%, 35.9% and 51.7% for stages I, II, III, IV, I/II and unknown, respectively. MP-r demonstrated absolute sensitivity increases of 4.8 %, 2.8%, 0.0%, 3.1%, 4.0%, 10.3%, and 3.0% for stages I, II, III, IV, I/II, unknown, and overall, respectively.

Conclusions: Compared to MP (breast and prostate cancers excluded), MP-r resulted in a relative sensitivity increase of 28% in Stage I cancers and 12.5% for Stage I/II cancers. MP-r is an efficient strategy to add a third biomarker class and enhance sensitivity of MP for early-stage cancer detection. This abstract was previously presented at AACR Special Conference in Cancer Research: Liquid Biopsy 2024.

ABSTRACTS

Poster #20

Performance of a multi-cancer early detection (MCED) blood test for breast and gynecologic cancers in a prospectively-collected cohort

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Objective: An estimated 427,000+ women in the U.S. will be diagnosed with, and almost 75,000 will die from, breast, ovarian, uterine, cervical, and vulvar cancers in 2025. American College of Obstetricians and Gynecologists (ACOG) recommended screening for breast and cervical cancers has reduced disease mortality; however, approximately 25% of screening-eligible women are not up to date with screening. In addition, screening programs are not available for ovarian, uterine, and vulvar cancers. MCED tests, which are intended to be used in conjunction with recommended screening, have the potential to detect a broad range of cancer types and stages. Using a subset of female participant samples from a large, multi-center, prospectively collected study, we assessed the performance of two biomarker classes (cfDNA plus select proteins), focusing on breast, ovarian, uterine, cervical, and vulvar cancers.

Design: The ASCEND 2 study enrolled participants from 157 sites within the U.S. and Europe. The study population included subjects ≥50 years old with known cancer, suspicion of cancer, and controls without suspicion of cancer. All subjects provided informed consent and were assessed for study participation eligibility. The ASCEND-2 subset we describe herein included 3,478 (742 cancer and 2,736 non-cancer) female participant samples with breast, ovarian, uterine, cervical, and vulvar cancers of all stages, divided approximately equally between a training/validation set (n=1,698) and a test set (n=1,780). Sensitivity of a combined DNA methylation and protein biomarker classifier was determined at a combined specificity of ≥98.5%. For detailed methods see Cancer Res,2024;84(7Supp):LB100.

Results: The test set participant mean age was 65.3 years old. Test set participants were broadly representative of the U.S. population. Non-cancer and cancer participants were similar for age, sex, and race/ethnicity distributions. At 98.5% specificity, overall sensitivities were 33.3%, 34.1%, 38.5% (95% CI: 17.7-64.5), 71.4% (95% CI: 45.4-88.3), and 76.9% (95% CI: 49.7-91.8) for uterine (n=39), breast (n=88), vulvar (n=13), ovarian (n=14), and cervical cancers (n=13), respectively.

Conclusion: MCED testing has the potential to extend cancer screening to women's cancers that are not screened for currently and complement standard of care cancer screening as part of a comprehensive cancer risk management strategy.

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ABSTRACTS

Poster #21

Detecting what matters: Innovation in Early Cancer Detection at NKI-AVL

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COMPANY/INSTITUTION:

NKI Center Early Cancer Detection

The NKI-AVL Center for Early Cancer Diagnostics, founded three years ago, is an initiative housed within the Netherlands Cancer Institute – Antoni van Leeuwenhoek (NKI-AVL), the largest cancer hospital and research institute in the Netherlands. At our center, individuals at increased risk of breast, prostate, colorectal, or skin cancer are welcomed in a calm, non-clinical setting designed to facilitate the early detection of malignant lesions. Timely intervention at this stage can significantly improve survival, enhance quality of life, and reduce healthcare costs. Central to our approach is the continuous pursuit of the right balance between overdiagnosis and underdiagnosis.

Our center benefits from close collaboration with the world-renowned Antoni van Leeuwenhoek Hospital and the Netherlands Cancer Institute - both located next to our Center. Together, they provide synergistic expertise in oncology and cutting-edge translational research, ensuring continuous innovation in early cancer detection. To support this mission, we maintain and expand a comprehensive biobank that collects biospecimens (blood, urine) and clinical data from high-risk individuals. This resource is designed to facilitate academic and commercial research across Europe and beyond, enabling real-world studies into early cancer biology, risk stratification, and the development of novel diagnostics.

Our referrals originate from general practitioners, medical specialists, and national screening programs. Most assessments are completed within a single half-day, enabling rapid turnaround, efficient multidisciplinary input, and minimal uncertainty for clients. Annually, we assess approximately 8,000 individuals, not including those participating in research studies.

Ongoing studies include the development of non-invasive alternatives to digital rectal examination for prostate evaluation, AI-driven smartphone tools for skin cancer detection, and clinical decision aids for risk-based referral in primary care. We aim to generate practical, scalable tools that support earlier cancer recognition in the population at large.

With its integrated structure, translational focus, and individual-centered design, the NKI-AVL Center aims to redefine the landscape of early cancer detection.

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ABSTRACTS

Poster #22

A novel bioreactor platform for immune biomarker discovery in early lung cancer

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COMPANY/INSTITUTION:

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Objectives: As a result of inadequate early detection, lung cancer is the largest cause of cancer-related death worldwide. It is well established that the immune system influences cancer development, however the first contacts between immune cells and early lung cancer are poorly understood. We aim to discover early detection biomarkers at the interface between lung cancer and the systemic immune system. We have therefore developed a novel bioreactor which is more versatile and physiologically relevant than existing co-culture systems and in vivo cancer models, for immune biomarker discovery in early lung cancer.

Methods: Bioreactors were designed using SolidWorks® and manufactured from liquid photopolymer resins by stereolithography. To validate immune crosstalk and test biocompatibility, jurkat T cells were stimulated by ionomycin and co-cultured for 48h with THP-1 monocytes, before measuring phenotype changes by flow cytometry and metabolic viability by AlamarBlue assay in our bioreactor compared to gold-standard Transwell® plates. To explore changes in immune phenotypes upon interaction with lung cancer, human cancer-naïve peripheral blood mononuclear cells (PBMCs) from whole blood were cultured alone or with A549 or 16hbe cells for 48h, before staining extracellular markers for high-dimensionality immune profiling by CyTOF.

Results: Stimulated Jurkat T cells induced the differentiation of THP-1 monocytes into a macrophage phenotype, which was confirmed by changes in morphology and extracellular marker expression. This illustrates that our bioreactor successfully enables immune crosstalk between compartments. Compared to gold-standard transwell plates, there was no loss in metabolic activity and viability of A549 and 16hbe cell. We also showed by immune profiling within heterogenous PBMCs by mass cytometry (CyTOF) that myeloid cells frequency was significantly reduced when in co-culture with 16hbe bronchial epithelial cells but not with A549 lung adenocarcinoma cells or PBMCs cultured alone.

Conclusions: We have developed and validated a reusable bioreactor which enables multi-directional immune crosstalk in a 24-compartment customisable grid design. By showing that changes occur in myeloid cells in co-culture with bronchial epithelial cells compared to lung adenocarcinoma cells, we have a potential biomarker of early lung cancer to explore further our novel bioreactor platform.

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ABSTRACTS

Poster #24

Phosphatidylinositol lipids as potential early detection markers for PDAC

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Lipids play a crucial role in pancreatic ductal adenocarcinoma (PDAC) tumor progression, influencing cell signaling, tumor metabolism, and therapeutic resistance (Yin et al., 2022). To improve the overall survival of patients with PDAC, the establishment of reliable biomarkers for early-stage PDAC diagnosis is urgently needed. Currently, PDAC is mostly looked for at the protein level while lipids are rarely considered. A single FDA-approved serological marker (CA19-9) is used as a surrogate marker for early detection of PDAC (Reese et al., 2024). However, 6% of Caucasians and 22% of non-Caucasians lack the Lewis antigen A and cannot produce CA19-9 (Chan et al., 2014). Therefore, a small-molecule-based diagnostic marker might improve (early) detection and survival of those patients. We are aiming for establishing changes in small molecules, namely defined lipid species, as early biomarkers.

Our preliminary high-resolution lipidomic data on two pancreatic cancer cell lines (PANC1 and MiaPaCa2) showed strikingly up- and down-regulated phosphatidylinositol lipids compared to immortalized healthy cells (HPNE). One particular set of elevated species showed the unique fatty acid composition of 38:2. This finding opens the door to explore one specific lipid type for (early) detection of PDAC and precancerous lesions in biopsies and potentially blood. From a mechanistic point of view, it is possible that this group of metabolically connected lipids is crucial for tumor progression and its biosynthesis could serve as a potential target for cancer treatment.

Our preliminary deep proteomic analysis, generated on the same cell samples in parallel, revealed PIK3CB downregulation in both MiaPaCa2 and PANC1 cell lines, suggesting disruption of PI3K signaling in PDAC. Conversely, several lipid-handling enzymes were significantly elevated including CERS2, CPTP, ELOVL5, and ORMDL3, while other differential proteins have prognostic significance in PDAC (Human Protein Atlas), including ANXA6, PIK3CB, JAG1, INPP5K, SERPINE1, LDAH, and OSBPL10. Notably, DGKE is of particular interest due to its role in diacylglycerol metabolism within the phosphatidylinositol turnover cycle, which directly impacts lipid signaling pathways relevant to PDAC progression.

We are currently applying the same lipidomic/proteomic workflow in human pancreatic tissue samples to confirm the identified potential (early) detection biomarkers.

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ABSTRACTS

Poster #25

PROGRESS Prostate: A Dynamic Predictive Model for Baseline and Follow-up Risk Assessment of Prostate Cancer Progression on Active Surveillance

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Purpose

To develop a dynamic predictive model for baseline detection and follow-up re-evaluation of the risk of prostate cancer (PCa) progression on active surveillance (AS).

Methods

422 AS patients were included in this study, of whom 82 (19.4%) experienced either histological PCa progression or radiological stage progression (PRECISE 5) over a median follow-up of 4.5 years. The baseline model included initial serum prostate-specific antigen (PSA) and PSA density (PSAD), MRI-derived Likert score, tumour diameter, and tumour grade group. The follow-up model included baseline Likert score along with longitudinal PRECISE scores, PSAD measurements, and repeat biopsy results. Model training and testing were performed in the 50/50 data split using several neural networks, with three-year progression as the outcome.

Results

The best-performing baseline model was a generalised additive model (GAM) including baseline PSAD and Likert score. With an overall test AUC of 0.65, the model achieved a 21% specificity at 95% sensitivity in the test set, which may be used to avoid repeat biopsies in a substantial proportion of patients with minimal risk of missing disease progression. The follow-up model, comprised of a long short-term memory recurrent neural network, included baseline Likert score together with longitudinal PRECISE and PSAD measurements, with its test AUC of 0.75 being significantly higher compared to that of PRECISE alone (AUC=0.61, P<0.01).

Conclusions

As the development of MRI-driven risk-adapted AS predictive models is a high research priority in the field; this study shows the promise of the proposed approach to objectively stratify patients at baseline and significantly improve the performance of current standard-of-care PRECISE assessment for detecting disease progression in the follow-up.

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ABSTRACTS

Poster #26

Poster Pitch

Mutation-agnostic detection and lineage tracing of pre-cancer clones for AML risk stratification

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COMPANY/INSTITUTION:

OHSU and University of Cambridge

Clonal expansion of a single stem-cell lineage is a hallmark of pre-cancer in both solid tissue tumors and hematological malignancies. In traditional models of tumorigenesis, stems cells acquire random somatic mutations that drive clonal expansion by conferring a selective advantage. However, precancer expansions are not always accompanied by known driver mutations. For example, clonal expansions in blood stem cells, known as clonal hematopoiesis (CH), often occur as a normal part of human aging. However, ~1% of CH cases can transform into serious blood cancers like acute myeloid leukemia (AML). While driver mutations in cancer-associated genes are associated with increased risk of CH-to-AML transformation, these mutations can persist in healthy tissue without ever developing into cancer; conversely, malignant transformation can also occur in their absence with no known underlying driver mechanism. This gap in our understanding of precancer evolution greatly hinders the detection and risk assessment of precancerous states. To address this gap, our lab has developed a novel method of using fluctuating CpGs (called "fCpGs") to detect clonal expansions and track their evolution in leu of somatic mutations. We have identified novel regions of phasable fCpGs that can function as in situ cell lineage barcodes for detecting and quantifying clonal expansions in bulk methylation sequencing. Using hundreds of serial blood samples collected in 50 donors over a decade prior to AML diagnosis, we have found that short fCpG barcode patterns quantitatively reflected the dynamics of precancer clonal stem cells. Furthermore, we found pre-AML donors that lacked detectable driver mutations often had pre-existing clonal expansions and growth dynamics that were detectable by our method. Finally, we leveraged long-read methylation sequencing to generate epiallele barcodes with hundreds of fCpGs to reconstruct previously published, mutation-based clonal phylogenies for three individuals with blood cancer. We confirmed the clonal origin of each epiallele barcode by phasing them to somatic mutations and found high concordance between our phylogenies and those previously published. This suggests that epiallele barcodes can serve has in situ heritable markers for accurate reconstruction of stem cell lineages. Our approach is an inexpensive and powerful tool to detect and quantify precancer clonal expansions and study cancer evolution in bulk tissues.

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ABSTRACTS

Poster #27

Multiomics and Models of Lynch Syndrome-Associated Prostate Cancer to Inform Early Detection and Interception

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COMPANY/INSTITUTION:

Manchester Cancer Research Centre

Inherited defects in DNA mismatch repair (MMRd) are associated with increased microsatellite instability (MSI) and predispose to colorectal, endometrial and prostate cancer, within the context of Lynch Syndrome. Germline MSH2 and MSH6 (gMSH2/gMSH6) mutations confer a 2-4-fold increased risk of developing high-risk localised prostate cancer (HR-PCa) and lead to more aggressive local and systemic disease. These clinical characteristics underpin targeted prostate-specific antigen (PSA) screening from age 40 to identify Lynch Syndrome carriers that may have clinically significant prostate cancer. Arguably, this group of patients would benefit from early detection and interception with immune checkpoint inhibition (ICI).

A better understanding of gMSH2 tumour evolution and relative risk between at risk Lynch Syndrome patients would discriminate additional genomic or tumour microenvironmental factors (TME) that predict aggression. Using whole exome sequencing, we initially characterised samples of HR-PCa from 20 patients with MMRd, 23 patients with germline defects in homologous recombination (HRd; such as BRCA1/2-defective cancers) and 20 patients with sporadic PCa. MSI was heterogenous and statistically increased only in the MMRd cohort which also had the lowest number of copy number alterations. Predicted T-cell fraction was increased in MMRd patients relative to HRd patients. These data were validated using Visium 10x spatial transcriptomics and multiplex IHC in which we observed increased PD-L1, M1/M2 TAM and CTLA4+ T-helper and T-cytotoxic cells consistent with T-cell exhaustion. We developed an immortalized prostate epithelial cell (PrEC) model following biallelic CRISPR KO of MSH2 and show these cells are immediately resistant to the MMR-specific agent, MNNG; yet they only develop MSI after 30 subsequent passages in culture. These genotypes/phenotypes were partially reversed with MSH2 reconstitution.

Overall, our HR-PCa studies suggest that high-MSI may be secondary to loss of primary MSH2 with subsequent loss of MSH6 expression and T cell exhaustion. To our knowledge, these are some of the first spatial data and models of MMR-deficiency in primary prostate cancers allowing an understanding of MMR-dependent tumour progression. Our work suggests that high MSI may be a late feature of MMRd in localised disease and that IHC may predict early lesions for interception approaches using ICIs.

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Poster #28

A new drug-dye conjugate, Adagrasib-OF650, allows for selective labeling of G12C PDAC tumors for fluorescence guided surgery.

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COMPANY/INSTITUTION:

Oregon Health and Science University

Pancreatic ductal adenocarcinoma (PDAC) is the third leading cause of cancer mortality and continues to increase in both incidence and fatality, where improved therapy is urgently needed. Mutation rates of the KRAS oncogene are >90% in PDAC, where small molecule inhibitors such as sotorasib and adagrasib have been as developed potential treatments for KRAS G12C mutant cancers. The gain of a nucleophile through the glycine to cysteine mutation at codon 12 allowed the development of covalent KRAS targeted therapeutics that previously were thought to be undruggable. Herein, we describe a drug-dye conjugate utilizing adagrasib as a molecular target, allowing for specific labeling of KRAS G12C. This novel probe could act as a companion imaging probe with applications for fluorescence guided surgery (FGS). Computational modeling was used to investigate the effects of appending our zwitterionic, environmentally inert fluorophore, OregonFluor650 (OF650) to adagrasib. Adagrasib-OF650 (Ada-OF650) demonstrated similar docking scores to the parent drug adagrasib. The selectivity of adagrasib was retained as Ada-OF650, which was able to distinguish between wildtype (WT), G12C and G12D KRAS mutants both in vitro in purified proteins and in cell culture. The selectivity of Ada-OF650 was also demonstrated in vivo using orthotopic PDAC murine models. Specific uptake and labeling was seen in KRAS G12C mutation positive tumors compared both KRAS G12D mutation positive tumors and healthy pancreas tissue. The specificity of KRAS G12C mutation positive tumor cell uptake and labeling were confirmed through fluorescence microscopy and histopathology of the resected tumor tissues. The development of Ada-OF650 highlights how creative linker chemistry can be used to take advantage of the tumor-specific targeting of approved drugs to create companion imaging tools for FGS approaches.

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Poster #29

Identification of tumor-intrinsic factors mediating the early immune suppression program in lung cancer

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COMPANY/INSTITUTION:

Oregon Health and Science University

During early tumor development, cancer cells reshape the tumor microenvironment to escape immune surveillance. Understanding the tumor-intrinsic drivers of this early immune suppression could uncover predictive biomarkers of immunotherapy response and reveal new therapeutic targets to halt or reverse immune dysfunction in cancer. To identify these drivers, we leveraged a Kras/Trp53-driven genetically engineered mouse model (GEMM) of lung adenocarcinoma, which allows longitudinal monitoring of tumor-immune interactions beginning from nascent, autochthonous lesions—stages that are often inaccessible in clinical samples or transplantable tumor models that use fully mature cancer cells. We profiled tumors expressing immunogenic neoantigens ("immune hot") versus those lacking such expression ("immune cold") using an integrative approach combining subcellular proteomics and single-cell RNA sequencing across time points spanning the transition from immune-permissive to immune-suppressed states. For proteomics, we employed tumor-specific expression of the ER-localized biotinylating enzyme TurboID-KDEL, enabling selective enrichment of secreted and membrane-associated proteins likely to engage local immune cells. Topic modeling uncovered striking temporal dynamics: while early "immune hot" tumors exhibited a distinct expression profile enriched in T cell recruitment signals, antigen presentation machinery, and interferon response pathways, this profile converged with that of "immune cold" tumors as immune suppression deepened. Notably, early "immune hot" tumors also upregulated stress response factors and signals attracting immunosuppressive cell populations, particularly neutrophils—suggesting a dual program of immune activation and suppression. Ongoing studies aim to define the mechanistic roles of candidate factors in driving immune dysfunction in both mouse and human lung cancer. These efforts may yield novel drug targets and biomarkers to enhance early intervention and improve immunotherapy efficacy in lung cancer patients.

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ABSTRACTS

Poster #30

Preinvasive Exhausted CD8+ T Cells and Regulatory T Cells Co-define Targetable Immune Regulation for Multi-Cancer Interception

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Background: Pre-cancerous lesions can progress into invasive tumors, but the increasing detection of these lesions through new screening programs presents a valuable opportunity to intercept cancer before malignant transformation occurs. Immune checkpoint blockade (CPI) is a promising interception strategy, potentially effective across cancer types by targeting shared antitumor immune mechanisms. However, our understanding of the immune environment in pre-cancerous lesions remains limited, particularly regarding its suitability for CPI-based interception. Here, we present a pre-cancer atlas that focuses on T cell subset composition across healthy, pre-malignant, and malignant tissues from multiple cancer types as a roadmap for immune interception protocol development.

Methods: We aggregated publicly available single-cell RNA-seq data from 331 donors across 10 tissues and 21 separate studies. To provide consistent cell type labels and robust analysis, we developed a novel tool called treelabel that stores cell type annotations for each cell at various resolutions and can integrate annotations from multiple sources. We tested for differences separately for each tissue and aggregated the results with a random-effects model.

Results: We show that the pre-cancer T cell landscape deviates from that in normal tissue to such an extent that T cell subtype composition reliably distinguishes normal from pre-malignant samples (AUC=0.83). We find that a distinct immune-suppressive microenvironment is already established in the pre-malignant stage, which is defined by an increase of regulatory T cells and exhausted CD8 T cells in pre-malignant compared to normal samples. Importantly, we also identify a larger reservoir of progenitor-exhausted CD8 T cells in pre-malignant vs tumor samples, which partly accounts for a more favorable predicted immunotherapy response score. Based on these changes and the differential gene expression across stages and between cell types, we suggest that GITR, a known immune checkpoint inhibitor target, could be a promising interception target.

Conclusions: Our study is the first systematic characterization of the changes of the tissue micro-environment in pre-malignant lesions. Our dataset is a rich resource for the community, which can be used to identify targetable changes for pre-cancer interception.

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Poster #31

Interaction-Centred AI, Teledermoscopy, and Pathology: A Unified Route to Early Melanoma Detection

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COMPANY/INSTITUTION:

German Cancer Research Center

We present a comprehensive investigation of human-AI interaction in melanoma diagnosis, demonstrating how explainable AI transforms diagnostic workflows by enhancing clinician trust, reducing cognitive burden, and improving accuracy through optimized collaboration patterns.

Our core contribution centers on the development and evaluation of a dermatologist-aligned explainable AI (XAI) system for melanoma vs. nevus classification. Through reader studies with 116 international dermatologists, we demonstrated that XAI significantly enhances clinician confidence (+12.25%) and trust (+17.5%) compared to non-explainable AI, with trust correlating with human-AI explanation overlap. Error analysis across eight human-AI collaboration scenarios revealed critical failure modes including false conflict and true confirmation errors, with XAI particularly effective at reducing "true conflict errors" where physicians initially disagreed with correct AI predictions. Our eye-tracking study with 76 dermatologists provides objective evidence that XAI support increased diagnostic accuracy by 2.8 percentage points. Eye-tracking data revealed that diagnostic disagreements substantially elevated cognitive burden (increased fixations), with experienced dermatologists demonstrating more efficient decision-making patterns.

These human-AI interaction insights address fundamental challenges revealed through our broader research program. Expert pathologist disagreement studies underscore inherent diagnostic uncertainty in early-stage melanomas, while teledermoscopy investigations demonstrate significant accuracy gaps compared to in-person diagnosis, highlighting the critical importance of contextual information that XAI systems can effectively interpret and communicate.

Our findings establish explainable AI as a paradigm shift from accuracy-focused to interaction-centered diagnostic support, where cognitive load assessment and trust calibration are equally important as performance metrics. We are expanding this framework to broader dermatological conditions and developing interactive XAI systems for medical device implementation, and exploring large language models for medical guideline-enriched, context-aware, cognitively-optimized skin cancer detection and treatment.

ABSTRACTS

Poster #32

Lightning Talk

Personalised Prostate Specific Antigen (PSA) Retesting Intervals in Primary Care

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COMPANY/INSTITUTION:

University of Oxford

Background:

The prostate specific antigen (PSA) test is a diagnostic test for prostate cancer. Optimal PSA retesting intervals are unknown [1]. We aimed to develop evidence for risk-stratified PSA retesting intervals by age and PSA to be used in primary care, that maximise the benefit of early prostate cancer diagnosis while balancing the harms of over-testing.

Methods:

We analysed English primary care electronic health record data using the Clinical Practice Research Datalink Aurum between 2000 and 2018. Eligible patients were male, did not have a prostate cancer diagnosis prior to entering the study, and aged ≥40years at their first PSA test. We compared two different methods for deriving retesting intervals: (1) Kaplan-Meier curves [2] estimated prostate cancer-free survival by PSA range and age. The retesting interval was set to the year when less than 99% of patients remained cancer-free; (2) an adapted Kirch and Klein model [3] set retesting intervals to be proportional to the square root of age and PSA-specific cancer incidence probability. For both methods, retesting intervals were calculated for five-year age bands and PSA ranges (<1, 1–1.9,2-2.9, 3–3.9, 4–4.9 ng/ml).

Results:

1,349,250 male patients were included from 1441 general practices in England. Median follow-up time in years was 5.4 (IQR 2.1 to 6.4). During follow-up, 92,919 (6.9%) patients were diagnosed with prostate cancer. An example of a recommended PSA retesting interval for patients aged between 50-54, was found to be eight-to-ten years for patients with a PSA <1ng/ml, four-to-six years for patients with a PSA 1-1.9ng/ml, and one-to-two years for patients with a PSA 2-2.9ng/ml.

Conclusion:

PSA retesting intervals could be derived based on prostate cancer incidence and survival rates, conditional on PSA value and age. Further research with joint modelling is needed to externally validate our results and develop models incorporating multiple PSA tests over time.

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Poster #33

Prostate Specific Antigen (PSA) retesting intervals between 2000 - 2018 in England: A study of 10 million patients

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Background: It is unclear whether the benefits of prostate specific antigen (PSA) testing outweigh the harms of overdiagnosis and overtreatment. In England there is no guidance that specifies PSA retesting intervals for symptomatic or asymptomatic patients in primary care. Patterns of PSA retesting intervals in patients without a prostate cancer diagnosis are unknown.

Aim: Characterise how PSA tests are utilised in primary care before a patient is diagnosed with prostate cancer.

Methods: Temporal trends and annual percentage changes were analysed using age-adjusted PSA testing rates. Negative binomial mixed effects regression models investigated rate ratios of PSA testing. Linear mixed-effects models examined the length of PSA retesting intervals. All results were analysed by region, deprivation, age, ethnicity, family history, symptom presentation and PSA value.

Results: A total of 1,521,116 patients had at least one PSA test and together had a total of 3,835,440 tests. Half of patients had at least two PSA tests. Twenty-seven percent of PSA tests were paired with a symptom. The median PSA retesting interval was 1.1 years (IQR 0.5 – 2.3 years).

PSA testing increased overtime and peaked in 2018. Rates increased more for patients without a record of a symptom and for those with low PSA values. Seventy-three percent of patients who had multiple PSA tests never presented with a PSA value above the NICE NG12 threshold. Region, ethnicity, family history, age and deprivation were significantly associated with the likelihood of PSA testing and the length of the PSA retesting interval. The South of England and areas of lower deprivation had higher rates of PSA testing but similar intervals between PSA tests. Symptoms were associated with the likelihood of PSA testing and retesting intervals but had a smaller effect on the length of the retesting intervals compared to patient ethnic and demographic characteristics.

Conclusion: We observed that PSA testing and retesting is happening in primary care for patients without a record of a symptom and for those with low PSA values. Controversial guidance on PSA retesting, combined with limited consensus on optimal retesting intervals may be leading to some patients being tested too often while others are not being tested enough. To maximise patient benefit while reducing the risk of over testing there is an urgent need for research to determine appropriate evidence-based PSA retesting intervals.

ABSTRACTS

Poster #34

The early detection of colorectal cancer from cfDNA can be improved through the detection of 6-base (5mC and 5hmC) biomarkers

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COMPANY/INSTITUTION:

biomodal

Early detection of colorectal cancer (CRC) has the potential to improve treatment outcomes and survival rates. Liquid biopsy for profiling of cell free DNA (cfDNA) in blood holds huge promise for early CRC detection in otherwise asymptomatic patients.

Epigenetic biomarkers have already been shown to significantly contribute to cancer detection in liquid biopsies, but traditional DNA methylation sequencing conflates two cytosine modifications, 5-methylcytosine (5mC) or 5-hydroxymethylcytosine (5hmC), with different and opposing biological functions. Discrimination of these two states could therefore be crucial for increasing the amount of functional information for CRC detection.

We therefore employed duet evoC, a biomodal technology that provides the 6-base genome (the complete genetic sequence whilst simultaneously distinguishing 5mC and 5hmC), to cfDNA obtained from a cohort of 32 healthy volunteers and 37 patients with colorectal cancer (CRC) at stages I and IV. Through machine learning approaches, we built classifiers to differentiate between cfDNA from patients with stage I CRC and individuals without cancer using features based 5mC alone, 5hmC alone, both 5mC and 5hmC, or the conflated 5mC/5hmC (modC, as it would be generated by traditional epigenetic technologies).

This study investigates the roles of 5-methylcytosine (5mC) and 5-hydroxymethylcytosine (5hmC) as biomarkers for early-stage colorectal cancer (CRC) detection in cell-free DNA (cfDNA). We used duet evoC, a biomodal technology that provides the 6-base genome (the complete genetic sequence whilst simultaneously distinguishing 5mC and 5hmC), to analyze cfDNA from 37 treatment-naive CRC patients and 32 healthy controls.

Our findings indicate that combining measurements of 5mC and 5hmC significantly enhances diagnostic accuracy (AUC = 0.95) compared to traditional approaches that conflate these markers. Notably, 71.7% of differentially methylated regions (DMRs) exhibiting an increase in 5hmC in stage I cfDNA also showed a corresponding decrease in 5mC in stage IV, suggesting that 5hmC can effectively track regions of demethylation during tumour development.

These results support the hypothesis that distinguishing between 5mC and 5hmC can improve the sensitivity of liquid biopsy tests for early cancer detection.

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ABSTRACTS

Poster #35

Pancreatic Cancer Screening: Early Detection

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COMPANY/INSTITUTION:

Oregon Health and Science University

Pancreatic cancer is the third leading cause of cancer related death in the United States. Early detection clinics have increased the number of patients who are diagnosed with pancreatic ductal adenocarcinoma (PDAC) at an early stage, when disease is treatable. Despite efforts to expand pancreatic cancer screening and develop more inclusive criteria for screening; the United States Preventative Services Task Force (USPSTF) recommends against screening the general population, Grade D. Educating providers and identifying patient populations who meet criteria for high-risk pancreas screening, including patients with an extensive family history of pancreatic cancer, high risk genetic mutations, and pancreatic cystic lesions, is paramount. OHSU is currently coordinating a screening and surveillance program in an effort to decrease PDAC mortality, advance research, and improve detection.

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Poster #36

Generating a tissue resource within the Novel Early Markers for Ovarian cancer (NEMO) study: A multicentre study for the early detection of high grade serous ovarian cancer through fallopian tube sampling

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COMPANY/INSTITUTION:

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Introduction: High-grade serous ovarian cancer (HGSOC), the most lethal subtype of ovarian cancer, is thought to originate from precursor lesions in the fallopian tubes (FT) known as serous tubal intraepithelial carcinoma (STIC). The NEMO (Novel Early Markers in Ovarian Cancer) study aims to identify early biomarkers including by sampling FT lavage fluid and building a biobank focused on the earliest stages of HGSOC. NEMO is a collaborative effort between five ACED institutions, University College London, University of Manchester, University of Cambridge, Stanford University, and Oregon Health & Science University, dedicated to enabling earlier ovarian cancer detection.

Methodology: Women undergoing salpingo-oophorectomy are recruited into three groups: low-risk (benign conditions), high-risk (genetic predisposition such as BRCA1/2), and cancer (receiving surgery as treatment). After consent, samples collected during surgery include urine, blood, fimbrial biopsies, and FT lavage fluid. Lavage involves flushing saline through the fimbrial end and collecting the effluent at the isthmus. Demographic and gynaecological history are documented, and pathology is reviewed for STIC. The consortium will conduct analyses across partner sites, including proteomics, transcriptomics, glycosylation profiling, and extracellular vesicle characterisation, with a primary aim to identify differences in FT lavage between cases with and without STICs. Here we report the Manchester experience of sample collection and quality assurance.

Results: In the first 9 months, 94 patients were approached at St Mary's Hospital in Manchester, and 93 consented. Of these, 19 were low-risk, 32 high-risk (BRCA1=10, BRCA2=15, PALB2=2, Lynch=4, RAD51=1), and 42 had cancer (HGSOC=21, low-grade serous=2, borderline=2, mucinous=2, endometrioid=3, other subtypes=12). The cohort reflects Manchester's ethnic diversity, with 83% identifying as white and 17% from global majority backgrounds. Urine, blood, and FT biopsies were collected from all participants. Lavage was successful in 73% of left tubes and 95% of right tubes. Average protein concentration of lavage samples was 654 µg/mL (n=87).

Discussion: Early findings show FT lavage is a feasible and acceptable method for sampling precursor lesions. The collection of high-quality samples and clinical data supports the development of a robust biobank, laying the groundwork for biomarker discovery to enable earlier detection of HGSOC.

ABSTRACTS

Poster #37

Poster Pitch

Vanderbilt's Thoracic Biorepository: Advancing Lung Cancer Research Through Biospecimen Collection and Distribution

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COMPANY/INSTITUTION:

Vanderbilt University Medical Center

Background: Vanderbilt's Thoracic Biorepository and its dedicated team of clinicians, biostatisticians, epidemiologists and researchers act as the national clinical validation center for the Early Detection Research Network's lung cancer early detection. In 2024 over 600 individuals were consented and their specimens stored in the biorepository.

Methods: The institutions contributing participants include Vanderbilt University Medical Center, Tennessee Valley Medical Center – Veterans Affairs and Washington University at St. Louis. Patients are consented under three primary studies, THO-0136 (surgery), -0398 (bronchoscopy), -1496(screening) or dual-enrolled with dedicated studies or clinical trials. Over 90% of collections occur prior to treatment. Non-necrotic tumor samples, normal lung tissue (if clinically indicated) and bronchoscopic biospies are collected under pathologist supervision.

Bronchial brushings, bronchoalveolar lavage, and biopsies are collected per study protocols. Sample processing occurs within two hours of collection, while tissue samples are obtained within three hours of resection. Investigators may request specimens via the online REDCap form (https://redcap.vumc.org/surveys/?s=MY8KTDWLT9).

Results: The biorepository houses over 150,000 biospecimens, including EDTA and Streck plasma, serum, bronchial brushings, bronchial biopsies, genomic PBMC DNA, urine, sputum, and pleural fluid. Epidemiological and clinical data including imaging and pathology, along with annual follow-up for 5 years are collected and linked to participant samples. Specimens are de-identified and logged in a HIPAA-compliant manner, utilizing a dedicated barcoding and REDCap database system for tracking. An imaging repository with over 2000 annotated CT scans have been deidentified and stored. In 2024 over 3000 specimen aliquots along with clinical or imaging data were distributed to academic, governmental and industry collaborators developing and validating biomarkers. Specimens have been used in validating the three lung cancer risk biomarkers on the market.

Summary: The Biorepository plays a crucial role in advancing lung cancer early detection research through high-quality specimen collection and distribution. Future plans include expanding Post-treatment specimen collection, enhancing database integration for improved tracking, and fostering new collaborations to support biomarker discovery and early lung cancer detection.

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ABSTRACTS

Poster #38

Early Markers of Barrett's Oesophagus Progression Identified Through Spatial Transcriptomics

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COMPANY/INSTITUTION:

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Barret's Oesophagus (BO) affects ~5% of the adult population in the United States and is characterized by the replacement of normal squamous epithelium with intestinal-like columnar cells. While BO increases the risk of Oesophageal Adenocarcinoma (OAC), the progression mechanism remains unclear. While the genomic landscape of BO and OAC has been well studied, the spatial organization of the tissue microenvironment and its role in progression remain poorly understood.

Building on our prior work using image mass cytometry (IMC) to identify risk biomarkers, we applied spatial transcriptomics (Xenium, 430-gene custom panel) to biopsy samples from 21 individuals with non-dysplastic BO —12 who progressed to dysplasia or OAC (Progressors) and 9 who remain indolent (Non-Progressors). Unsupervised clustering and odds ratio analysis linked specific cell-type densities to progression status.

We profiled ~1 million cells, and identified 18 cell phenotypes, including gastric and intestinal epithelial lineages, stromal and immune cell subsets. Notably, two intestinal lineages exhibiting clear gastric features (REG4/MUC6/OLFM4 and REG4/MUC5AC/CEACAM6), were more frequently associated with the Progressor group. Additionally, a distinct cell subset displaying a squamous-columnar transitional phenotype (KRT5/KRT7/S100A9) also showed increased association with Progressors. In contrast, Non-Progressors were more associated with intestinal lineages lacking gastric feature (REG4/ANPEP) and several immune and stromal cell subsets, including plasma cells (JCHAIN/IGKC), mast cells (CPA3/TPSAB1), and fibroblasts (POSTN/COL1A1/COL6A1 and ACTA2/RGS5). Interestingly, the only cell subsets significantly enriched in Non-Progressors is antigen-presenting cells (CD74/HLA-DRA), suggesting indolence in BO might be due to a protective immune surveillance and microenvironmental niche. A supervised classifier further demonstrated that gastric-featured intestinal phenotypes were strong discriminators of progression risk.

This study, leveraging spatial profiling of a well-characterized cohort, reveals cellular and molecular features in BO associated with progression to OAC. These discoveries offer insights into BO biology and form a basis for future strategies in early detection, risk stratification for high-risk BO patients.

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ABSTRACTS

Poster #39

Falcon – Exact Sciences' Multicancer Early Detection (MCED) Real World Evidence (RWE) Registry

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COMPANY/INSTITUTION:

Exact Sciences Corporation

Background: Earlier detection may reduce cancer morbidity and mortality by reducing the number of cancers diagnosed at advanced stages. Exact Sciences is developing an MCED test to simultaneously screen for multiple cancer types, with test-positive patients undergoing diagnostic evaluation with radiological imaging. The Falcon registry is a large prospective study of Exact Sciences' MCED test in clinically cancer-free individuals who seek cancer screening. It will examine the uptake, diagnostic journey, guideline-recommended cancer screening adherence, outcomes, and psychological impacts of MCED testing in a real-world setting.

Methods: Falcon is a multi-site registry that is enrolling ≥25,000 participants who receive the MCED test annually for three years (MCED cohort). A comparison cohort of ≥50,000 patients receiving standard-of-care clinical management only (SOC cohort) will be retrospectively constructed via a deidentified data pull. Both cohorts will include individuals 50-80 years of age presenting for primary care services who have no history of malignancy within the prior 3 years or current suspicion of cancer. SOC cancer screening will continue in the course of standard care and will not be proscribed or interrupted by study participation.

The MCED cohort will include a 10,000-participant pilot cohort and ≥15,000-participant expansion. This cohort will include individuals who provide informed consent for MCED testing and follow-up IV-contrast computed tomography (CT) and, if necessary, positron emission tomography-CT (18F FDG PET-CT) imaging following a positive MCED test. Clinical contraindications for radiological imaging (e.g. pregnancy, IV contrast allergy, renal failure) will be taken into consideration when making the decision to participate. The SOC cohort will be selected after enrollment of each MCED cohort phase and will be matched based on demographic and clinical characteristics. Self-reported measures of anxiety, cancer worry, and trauma will be routinely collected from all MCED cohort participants. Data will be collected for up to 5 years following the baseline test or, for the SOC cohort, following an index date. Periodic automated extraction of pre-specified data elements from existing electronic data sources, primarily medical records and tumor registries, will be collected from all participants. Clinical Trial Identifier: NCT06589310.

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ABSTRACTS

Poster #40

Identifying women with actionable risk factors for breast cancer in primary care practice

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COMPANY/INSTITUTION:

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Background: Primary care clinicians follow breast cancer screening and prevention guidelines that rely on understanding patients' major breast cancer risk factors. Both patient-reported family and personal history and electronic health record (EHR) data provide essential risk information.

Objective: To determine whether patient use of an electronic breast cancer risk assessment and decision tool (MammoScreen) identifies more women at risk for breast cancer compared with existing EHR data.

Design: Cross-sectional implementation study.

Participants: 2709 women aged 40-74 years with no prior diagnosis of breast or ovarian cancer; established patients at the OHSU General Internal Medicine Clinic and active users of the Epic MyChart patient portal.

Interventions: Eligible patients were invited to use MammoScreen via Epic MyChart between February 1, 2023 and April 30, 2025. Upon consent, MammoScreen securely pulled breast and ovarian cancer family history risk information from the patient's Epic chart for the patient to review. Following prompts, patients added new or missing risk information to MammoScreen. Upon completion, patients received summary reports of their known risk factors, uncertain risk information (e.g., didn't know age of diagnosis of relative with breast cancer), and recommended next steps (e.g., contact your clinician about discussing a genetic counseling referral). Clinicians received a concise summary of patient-reported risk factors, uncertain risk information, and clinical decision support based on clinical guidelines via an Epic encounter note.

Main Measures: MammoScreen patient uptake and completion rates; identification of patients with major risk factors for breast cancer.

Key Results: 82% of eligible patients read a MyChart invitation message; of these, 43% completed (965/2224) and 16% of completers (158/965) reported major risk factors for breast cancer. An additional 9% (89/965) were unsure of their personal or family history. 33% (318/965) reported new risk information that was not already documented in the chart. Assessment of the percentage of patients with risk factors prompting new screening and prevention services identified through MammoScreen is ongoing.

Conclusions: Patient uptake of MammoScreen was high and resulted in new risk information that was not recorded in the patients' EHR. A standardized and periodic approach to collecting and validating risk information could improve breast cancer screening and prevention.

ABSTRACTS

Poster #41

Lightning Talk

AI-Assisted Visual Evaluation Test for Cervical Screening: Lessons Learned

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Artificial intelligence (AI) based image recognition algorithms offer promise in improving cancer screening. However, transitioning these models into reliable clinical tools requires rigorous validation beyond internal performance metrics. In this study, we summarize key lessons learned from the development and validation of our AI-Assisted Visual Evaluation (AVE) test for cervical precancer screening.

First, to minimize the most clinically important errors (i.e., misclassification between normal cervices and precancers), we moved from case-control dichotomy into a 3-class classification framework. This approach captures equivocal images that cannot be labeled as either normal or a case, and model uncertainty within a middle category, "indeterminate". With this approach, we can better isolate precancers from normal cervices and accumulate all the model uncertainty in the middle class.

Second, clinical reliability demands test–retest repeatability on replicate images obtained from the same individuals during the same visit. Implementing Monte-Carlo dropout during inference substantially improved repeatability.

Third, distinguishing external validation from internal validation is crucial. Our AVE algorithm, originally trained on five different study datasets from North and South America and Europe, was externally validated in our recent study across nine countries (Brazil, Cambodia, the Dominican Republic, El Salvador, Eswatini, Honduras, Malawi, Nigeria, and Tanzania) with over 50,000 participants. A change in image capture device emerged as the primary factor reducing model performance. Retraining with a small sample (40 individuals' data per class) from the new device restored performance, demonstrating a practical domain adaptation strategy. In contrast, changes in geographic location or population (e.g., we tested on women living with HIV) had no adverse effect on performance.

Finally, obtaining risk stratification is essential for translating a test into clinical use. Absolute risk estimates enable the development of risk-based guidelines tailored to local resources and priorities.

In summary, reliable AI-based screening requires minimizing clinically important errors between case-control, ensuring test-retest repeatability, conducting external validation, and providing risk-stratified outputs. These elements are critical for the equitable and safe implementation of AI-based cancer screening tools in real-world settings.

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Poster #42

Calypr: A platform to enable consortium cancer analysis

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Sharing data is a major bottleneck in cancer research, especially when collaborating across institutions internationally. Simple file sharing systems don't provide the necessary security, organization, or tracking needed for complex inter-institutional research projects. These problems are accentuated in the context of international collaboration for early cancer research. To overcome these challenges, we developed Calypr, a platform built on a robust and established foundation called Gen3 (developed at the University of Chicago's Center for Translational Data Science). Gen3's architecture has been proven in other high-impact data initiatives, including The Blood Profiling Atlas in Cancer (BloodPAC) and Australian BioCommons, ensuring Calypr benefits from a mature and scalable system. Calypr provides several key functionalities to streamline cancer data collaboration. Firstly, it offers secure and controlled data sharing, enabling researchers to manage access permissions and protect sensitive patient information. Secondly, it incorporates structured metadata, creating a searchable catalog that allows researchers to easily find and utilize relevant datasets. This includes standardized descriptions and tags, promoting data discovery and reusability. Thirdly, Calypr provides integrated tools for computational analysis, allowing researchers to perform complex calculations and generate insights directly within the platform. A critical design consideration for Calypr was minimizing the costs associated with accessing data. We addressed this by supporting hybrid cloud architectures, allowing institutions to leverage their preferred storage solutions – whether on-premise servers or cloud object storage services like AWS S3. This approach significantly reduces the burden of cloud egress fees, a common obstacle to data sharing. To facilitate interoperability and accelerate progress in cancer research, Calypr utilizes a standard data format based on Fast Healthcare Interoperability Resources (FHIR). This standardized approach ensures that data from different institutions and sources can be easily combined and analyzed, fostering a more unified and collaborative research environment. Future development will focus on expanding computational tools and incorporating machine learning capabilities to further enhance data analysis workflows. Calypr aims to be a cornerstone for collaborative cancer research, accelerating discovery and improving patient outcomes.

ABSTRACTS

Poster #43

Spatially informed immune interception of squamous lung cancer

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COMPANY/INSTITUTION:

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Lung cancer remains the leading cause of cancer-related death worldwide. While checkpoint inhibitors show promise in invasive disease, we currently lack strategies for immune-prevention. Understanding how immune responses are regulated early during squamous carcinogenesis could reveal actionable targets for intercepting lung squamous cell carcinoma (LUSC) at its pre-invasive stage. We previously profiled bronchial biopsies from high-risk smokers enrolled in a surveillance programme at University College London Hospital using single-cell RNA sequencing. This revealed a suppressive subset of OX40hi GITRhi Helios+ BATF+ regulatory T cells (Tregs) enriched in carcinoma-in-situ (CIS) relative to normal epithelium. However, the spatial context and mechanisms underpinning their emergence remained unknown. To address this, we generated the first single-cell spatial atlas of the immune ecosystem in nascent LUSC using the Nanostring CosMx platform. Twelve high-grade lesions—progressive (that evolved into invasive disease) or regressive (that returned to normal)—were studied with matched normal epithelium as control. As previously described, progressive lesions displayed reduced immune infiltration and basal cell expansion.

Focusing on the remodelling of MHC-II signalling during LUSC development, we explored the spatial relationship between BATF+ Tregs and antigen-presenting cells. In progressive CIS, Tregs and dendritic cells (DCs) colocalised and showed enriched MHC-II signalling relative to regressive lesions. A proximity-dependent acquisition of an immunosuppressive Treg phenotype was observed within 100 µm of MHC-II-high DCs, but only in progressive CIS. We further identified spatially defined immune escape hubs in progressive lesions, marked by enhanced fibroblast–basal cell crosstalk and increased antigen presentation cues promoting Treg lineage commitment. In contrast, regressive CIS harboured immune elimination hubs, with enhanced interactions between basal cells and CD8 T cells and stronger cytotoxic responses, potentially driving lesion regression.

Multiplex immunofluorescence validated key regulatory interactions. Functional validation is ongoing in chemically induced mouse models and patient-derived explants. These findings reveal spatially restricted immunosuppressive niches and highlight BATF+ Tregs as candidates for immune interception in early-stage LUSC.

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Poster #44

Dysregulated Immune Proteins in Plasma in the UK Biobank Predict Multiple Myeloma 12 years Before Clinical Diagnosis

PRESENTING AUTHOR:

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COMPANY/INSTITUTION:

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Multiple Myeloma (MM) is a haematological malignancy often diagnosed at an advanced stages following clinical complications. High-throughput proteomics has emerged as a potentially rich data source to improve capacity to forecast and understand complex disease such as MM. This study explores the utility of plasma proteomics for identifying novel predictors of MM, combining machine learning with statistical approaches.

Utilising data from the UK Biobank, including proteomic profiles of over 50000 participants, we applied an "extreme gradient boosting" (XGBoost) algorithm with SHapley Additive exPlanation (SHAP) feature-importance measures to identify key proteomic biomarkers to predict onset of MM.

At least seven of the top 10 proteins identified by the pipeline are known to be related to immune function and activation of lymphoid cells, while two are validated MM targets with approved therapies. The top 10 proteins along with key clinical predictors – age, sex, haematological parameters, and typical symptoms – were further analysed using Cox proportional hazards models to assess their contribution to incident MM risk. Notably, the 10 proteomic biomarkers identified using SHAP values significantly outperformed the clinical predictors, achieving a concordance index of 0.90 and a time-dependent area under the receiver operating characteristic curve of 0.85 in the held-out test dataset, compared to 0.67 and 0.69 for clinical predictors, respectively. This superior performance was maintained over at least 12-years of follow-up. Sensitivity analyses excluding cases diagnosed within five years of baseline and participants who had or develop known monoclonal gammopathy of uncertain significance, further highlighted the robustness of identified proteomic associations.

Our findings suggest that dysregulated immune protein expression in the plasma of otherwise healthy individuals may serve as an early indicator of MM risk. This data-driven, hypothesis-free approach both presents new avenues for researching the underlying biology of MM and lays the groundwork for developing a proteomics-based screening tool for early detection. If validated in independent cohorts and prospective studies, such a strategy could lead to novel approaches to screening for MM and risk-stratifying its various precursor conditions. This is especially important in a climate of increasing discussion around population-level MGUS screening and future work should tackle this issue directly.

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ABSTRACTS

Poster #45

Advancing Diverse Enrollment in Multi-Cancer Early Detection Clinical Research Trials: Partnerships to recruit and enroll non-white patients with the Oregon Rural Practice-based Research Network

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COMPANY/INSTITUTION:

Oregon Health and Science University

Background: The Oregon Rural Practice-Based Research Network's (ORPRN) mission is to improve health and equity for all Oregonians through community partnered research, education, and policy. Both based out of Oregon Health & Science University (OHSU), ORPRN and the Knight Cancer Institute (KCI) partnered to implement Pathfinder 2, an MCED clinical trial. Together, we aimed to reach a wide network of primary care clinics in Oregon to increase engagement of non-white rural populations in the study of early cancer detection tests.

Objective: ORPRN engaged non-white participants from rural communities in Oregon's Columbia River Gorge in the Pathfinder 2 study.

Subsites that supported recruitment efforts and provided infrastructure included a rural Cancer Care Center and a Federally Qualified Health Center (FQHC) with physical locations in The Dalles and Hood River, Oregon and a mobile clinic that traveled to underserved pocket communities. ORPRN engaged these clinics based on the diverse patient populations they served, their willingness and capacity for clinical trials research, and the proximity to research staff rooted in the community.

Methods: ORPRN's strategies for participant recruitment included: 1) Connecting with community champions who are passionate about cancer screening, 2) Meaningful subsite engagement in study material development, 3) Hiring multi-cultural bilingual staff who live in the subsite communities, and 4) Continuous outreach via radio announcements, tabling at community events, direct connections with healthcare leaders and local charitable organizations. These outreach activities set off snowball recruitment amongst social networks.

Results: A two-year study enrollment led to ORPRN's enrollment of 753 participants in the Columbia River Gorge: 99% rural and 28% non-white. Snowball recruitment within family, friends, and social networks made referrals one of the largest contributors to our enrollment outreach. Other successful engagement and communication strategies for recruiting and obtaining informed consent will be shared.

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Poster #46

Analyzing Pancreatic Intraepithelial Neoplasia Progression in High-Risk Human Donor Pancreata to Understand Hereditary Pancreatic Ductal Adenocarcinoma

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COMPANY/INSTITUTION:

Oregon Health and Science University

Pancreatic Ductal Adenocarcinoma (PDAC) is a lethal disease with a 5-year survival rate of only 13.3%. This is in part due to insufficient knowledge surrounding pre-cancerous lesion progression and the lack of early detection methods, leading to late-stage diagnoses and inadequate treatment options. Low-grade pancreatic intraepithelial neoplasias (PanINs) are prevalent in the general population; however, the majority of these lesions never progress to high-grade lesions or cancer. While some well-characterized mutations such as those in KRAS have been identified to contribute to low grade PanIN formation, the cell-intrinsic and -extrinsic factors that drive progression to high-grade status in human tissues have not been identified. One of the main difficulties in understanding these factors is the lack of access to human tissues that model normal and early-stage disease without the presence of adenocarcinoma. PanINs are microscopic and impossible to visualize using clinical imaging techniques, requiring donor organ tissue samples to identify them.

Studying PanIN progression in the context of hereditary genetic mutations that increase risk of progression provides a unique opportunity to understand the genomic and microenvironmental contribution to cancer development. We are focused initially on collecting samples with identified germline mutations in hereditary homologous recombination repair deficiency (hHRD) genes, including BRCA2, which is associated with PDAC progression. Through DONATION, an ACED funded project, we have begun a rapid autopsy program to collect donor tissue from patients with hHRD to characterize and model the progression of low-grade to high-grade PanINs. This will enable understanding of how these pre-cancerous lesions and the microenvironment induce the changes necessary for PDAC development. In parallel, we have begun processing human organ donor pancreata from the general population. Both sets of tissues will serve to establish organoid and fibroblast cultures for biorepository use as well as provide tissues to study PanINs through spatial transcriptomics and whole exome/genome sequencing. In summary, using human donor pancreata from high-risk hHRD populations will help to elucidate the mechanisms that drive low-grade to high-grade PanIN progression that lead to cancer development. Understanding these mechanisms will allow the identification of future diagnostic early detection markers as well as early interception targets.

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Poster #47

Poster Pitch

Understanding breast cancer risk associated with mammographic breast density in premenopausal women.

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COMPANY/INSTITUTION:

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A better understanding of cancer initiation is needed to improve early detection and to identify at risk groups that would benefit from enhanced screening. Breast cancer incidence and mortality increase exponentially from the early 30s to the start of population screening (age 50 in the UK). Thus, current population screening does not detecting cancers in premenopausal women. Young women identified as being at increased risk can be offered early breast screening and preventive tamoxifen therapy, which reduces BC risk in premenopausal women by ~35%. However, we need to better identify young women at increased risk to detect and intercept early tumours.

Mammographic breast density (MBD), the proportion of radiologically opaque breast tissue on a mammogram, is a significant risk factor for BC. Understanding the biological basis of MBD in young women and how it influences BC risk may lead to novel targets for both early diagnostic and prevention. To characterise the features of high-risk breast tissue we examined biopsies from premenopausal women classified as high-risk and categorised into low and high MBD groups. We compared breast tissue composition between these groups using Laser Capture Microdissection-Mass Spectrometry (LCM-MS) and multiplexed Imaging Mass Cytometry (IMC). These spatial proteomic analyses revealed notable alterations in ECM protein composition within epithelial regions, with specific differences observed in high-density breast tissue compared to low-density. High-risk breast tissue also exhibited increased immune cell subtypes and increased proliferation in SOX9-expressing epithelial cells.

We examined how these features associated with high MBD might be altered by targeting hormone signalling within breast tissue. In BC prevention trials run in Manchester we have a standardised protocol to obtain serial Vacuum Assisted Biopsies (VABs) from premenopausal healthy women with increased risk, before and after 3 months of treatment. After preventative treatment, proteomic analysis suggested modifications in ECM organisation, including reduced collagen stability, and immune-related interactions, indicating potential microenvironmental normalisation.

This study highlights the value of spatial proteomics approaches in identifying microenvironmental alterations linked to breast cancer risk. Together, these data suggest that understanding changes in breast tissue associated with risk can lead to better screening and prevention strategies.

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ABSTRACTS

Poster #48

3D Printing of Tissue Models using Dissolvable Photo-poly (N-isopropylacrylamide) as Sacrificial Templates

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COMPANY/INSTITUTION:

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Spatial organization of cells within three-dimensional tissue environments plays a critical role in regulating cellular behavior, signaling, and tissue function. However, recreating this spatial complexity in vitro—particularly for large, heterogeneous tissue models—remains a major challenge in tissue engineering and disease modeling. To address this, we developed a 3D printing platform that employs dissolvable photo-poly(N-isopropylacrylamide) (photo-PNIPAM) as a sacrificial scaffold material to enable high-resolution cell patterning and the fabrication of complex tissue architectures.

Photo-PNIPAM is a temperature-responsive polymer that is hydrophobic and stable above its lower critical solution temperature (~32°C), and hydrophilic and unstable below it. It was synthesized via free-radical polymerization of N-isopropylacrylamide with the photoinitiator LAP and printed using digital light projection (DLP) on a Bionova X printer. UV exposure power was optimized to maximize print fidelity and modulate scaffold stability. Polymerization kinetics were confirmed by FTIR spectroscopy and rheological gel point analysis, and stiffness was characterized via mechanical compression testing. Scaffolds rapidly dissolved in aqueous media at 4°C.

Multiple cell types were deposited into the printed scaffolds using a Biopixlar microfluidic bioprinter, enabling precise spatial control of cellular architecture. Following scaffold dissolution, cells retained their patterned arrangement, supporting the formation of 3D constructs with tunable geometry. This approach enables both the creation of height- and shape-controlled spheroids and the generation of voids that can be populated with additional cell types to build larger, multicellular tissues with spatial heterogeneity. We demonstrated this capability in a breast cancer model using triple-negative breast cancer (TNBC) cells, MCF10A epithelial cells, and fibroblasts to form an organized ductal structure with high viability and proliferation.

Future applications will incorporate immune and stromal cells to model early tumor–immune interactions and lymphoid aggregate formation. This platform enables mechanistic studies relevant to early detection, spatial biomarker discovery, and development of immune-targeted therapies.

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ABSTRACTS

Poster #49

Stress-induced transdifferentiation in prostate cancer is mediated by mitochondrial trafficking of NRXN1 to adhesion sites

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COMPANY/INSTITUTION:

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Prostate cancer, when detected in indolent stages, has a 5-year survival rate of nearly 100%. However, once it has progressed, metastasized or transitions to neuroendocrine disease, that survival rate decreases to below 32%. Prostate cancer cells adapt to stress by elevating intracellular cAMP levels, initiating phenotypic changes that can signal disease progression. In this study, we identify the neuronal adhesion molecule NRXN1 as an early and critical mediator of this cAMP-driven reprogramming. NRXN1 is significantly upregulated in response to increased intracellular cAMP and promotes neuronal-like transdifferentiation of prostate cancer cells, leading to elongation of cellular membranes, mimicking axonal features. This phenotypic change also enhances calcium-dependent intercellular communication and cell motility. We found that NRXN1 localizes to mitochondria at adhesion sites, facilitating intercellular networking, which contributes to enhanced migration. Pharmacologic inhibition of NRXN1 disrupts these early adaptive changes, including reduced transdifferentiation and migration. These findings suggest that NRXN1 is involved in stress-induced neuronal differentiation and offers insight into how neuronal adhesion molecules are involved in the initial phases of prostate cancer progression towards a neuroendocrine-like state. Future experiments will be aimed to directly target NRXN1's functional activity in an effort to limit transdifferentiation of prostate cancer cells.

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ABSTRACTS

Poster #50

Poster Pitch

Developing and assessing of a new biomarker panel for early detection of lung cancer - in vivo

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COMPANY/INSTITUTION:

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Lung cancer remains the most lethal cancer type, accounting for 13% of all cancer cases and 22% of cancer-related deaths in Germany. As early symptoms of lung cancer often go unnoticed, the disease is typically diagnosed at an advanced stage when therapeutic options are limited. At this point, the prognosis is poor, with a five-year survival rate of approximately 9%, highlighting the urgent need for earlier detection strategies. To address this challenge, our project focuses on identifying changes in plasma protein patterns of peripheral blood that could serve as early predictive markers of lung cancer in otherwise asymptomatic patients.

To achieve this, we employed a genetically engineered mouse model that precisely mimics human lung cancer development and progression. This model allows us to investigate tumor-induced systemic changes over time and assess their correlation with disease advancement. As tumour development is influenced by chronic inflammation, our study includes normal-weight and obese cohorts. This comparison helps to distinguish diet-induced from cancer-related inflammation. Over the time of five months, serial blood samples undergo the highly sensitive PEA assay (Olink) and flow cytometry analysis. In collaboration with the working group of Prof. Dr. Phillip Wild, the identified signatures will be compared to those from lung cancer patients at various stages to determine shared pathomechanisms. Additionally, protein signatures will be analyzed in the context of cancer-related cardiovascular pathophysiology. Lastly, the tumour microenvironment will also be examined through histological analyses of mouse lung tissue to gain deeper insights.

Flow cytometry analysis of a 23-colour lymphoid panel has provided initial results, clearly visualizing lineage markers and accurately separating immune cell populations. Early findings suggest changes in T cell differentiation and activation, including an increase in effector T cells and altered PD-1 expression in tumour-bearing mice. Additionally, there are indications of differential immune responses between normal and obese mice. By October, the mouse experiments will be completed, and we anticipate obtaining the first results from the PEA assay as well as the histology, which will provide further insights into plasma protein signatures linked to tumor progression.

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ABSTRACTS

Poster #51

Biological Determinants of the Plasma Proteome in Pancreatic Ductal Adenocarcinoma

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COMPANY/INSTITUTION:

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Introduction: The biological factors that drive changes in the plasma proteome and their relationships with plasma protein abundance remain poorly characterized. Major obstacles limiting the study of this dynamic include technical challenges to proteomic blood profiling with mass spectrometry (MS) and the heterogeneity in human cancer. To address these challenges, we employed a nanoparticle-based deep plasma proteomic profiling of blood samples from genetically engineered mouse models of Kras-driven cancer to investigate the effects of genetic driver, tumor location, and disease stage on the plasma proteome.

Methods: To address the effect of cancer stage, we compared plasma from mice with Kras-driven pancreatic cancer (PDAC) collected across cancer development. The impact of genetic driver and tumor location were assessed by comparing the effect of oncogenes (Kras, Tp53, and c-Myc) or sites of cre-expression (PDAC v lung) on plasma proteome. Plasma collected from tumor-bearing mice and controls was processed using the Seer Proteograph RISE workflow. Matched pancreata were prepared using standard cryomill methods for a subset of PDAC and control mice. Peptides were analyzed by dia-PASEF on a timsTOF Pro MS Raw data were processed on Seer Proteograph Analysis Suite.

Results: Differential protein abundance was observed for all experimental comparisons. Invasive cancers were associated with increased abundance of proteins involved in inflammation and extracellular matrix composition. The addition of a second oncogenic mutation in Tp53- or c-Myc more significantly impacted the number of differentially abundant proteins than progression from PanIN to PDAC. Isogenic tumors arising in lung exhibited a plasma proteome unique from PDAC. Paired tumor-plasma tissue analysis revealed substantial overlap in the identities of upregulated proteins in each tissue. Many of those co-increased proteins are secreted, indicating their presence could reflect local or systemic release, and implicate neutrophils as the source of PDAC-specific plasma proteins.

Conclusions: These results support the power of the Proteograph platform and murine models to interrogate cancer biology. That cancer site and the identity of oncogenic drivers exhibited a larger impact on plasma proteome than progression from premalignant to invasive disease has important implications for the design and utility of protein-based liquid biopsy approaches to cancer early detection.

ABSTRACTS

Poster #52

The ACED Cohort study supporting future early detection of cancer research

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COMPANY/INSTITUTION:

University of Cambridge

This work was supported by the International Alliance for Cancer Early Detection, a partnership between Cancer Research UK (C14478/A27855), Canary Center at Stanford University, the University of Cambridge, OHSU Knight Cancer Institute, University College London, the University of Manchester, the German Cancer Research Centre (Deutsches Krebsforschungszentrum, DKFZ) and the Dana Farber Cancer Institute (DFCI), including associated researchers at Harvard University.

The ACED cohort study is a prospective, longitudinal resource of pre-symptomatic individuals over 40 years to support cancer biomarker discovery and validation across the ACED Alliance and beyond. We liaise closely with the cancer genetics service to enrich the cohort for individuals with a family history of cancer and our outreach programme seeks to ensure a diversity of ethnic, educational backgrounds.

Every year participants complete questionnaires to record: demographics, medical history and medications, familial history, health and lifestyle, environmental and toxic exposure, quality of life and anxiety scores (GAD-7, PHQ-9, EORTC QLQ-C30 Version 3), and Cancer Risk Perception. Utilising this information and the ClinRisk QCancer 10year(1) tool we generate participants' individualised risk score of developing 10 common cancers. All collected information is stored in securely under pseudonyms in an online data repository (OpenClinica).

Biological samples are collected annually and stored for future use. The standard set includes: plasma for DNA (including double spun for cfDNA) and methylation, platelet pellets, serum, buffy coat, residual red cells, fresh-frozen urine and EDTA preserved urine. In accordance with specific requests, we also save saliva, dry blood spots in patient subsets.

Since 11/2021 we have recruited 404 participants with >950 appointments with samples and data collections. The average number of samples in storage per participant is 92, with >35,000 aliquots. The average age at recruitment is 60 (range 40-80), with 68% being female. QCancer risk scores up to 22.5% (risk of developing specific cancers in the next 10 years) and 18 participants have developed cancer.

The cohort includes a wide range of educational backgrounds and socio-economic status. We continue to drive diversity by outreaching to minority ethnic groups, focusing on increasing equality, diversity and inclusion.

(1)Hippisley-Cox et al. BMJ Open 2015;5(3) doi: 10.1136/bmjopen-2015-007825

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ABSTRACTS

Poster #53

Identification of Transcriptionally High-Risk PanIN Lesions and Their Early Biomarkers Using Spatial Transcriptomics in Human PDAC Samples

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Pancreatic ductal adenocarcinoma (PDAC) is a highly lethal cancer with frequent recurrence. Its Most common precursor lesion, pancreatic intraepithelial neoplasia (PanIN), is graded as low- or high-grade based on cytological atypia While low-grade PanINs often harbor key driver mutations, not all progress to malignancy, suggesting that additional non-genetic factors may contribute to malignant transformation. We hypothesize that transcriptional heterogeneity exists within early PanIN lesions and may underlie their variable progression potential.

To investigate this, we performed spatial transcriptomic profiling using 10x Visium on isogenic pairs of PDAC and PanIN tissues located both adjacent and distal to tumors from four patient samples. We inferred clonal architecture based on copy number variations (CNVs) and stratified PanIN clones as "low-risk" or "high-risk" depending on their transcriptional and genomic similarity to PDAC clones.

Our analysis revealed a subset of PanINs with strong transcriptional and genetic similarity to PDAC, which we classified as "high-risk" PanINs. In contrast, other PanINs with distinct CNV and gene expression patterns were classified as "low-risk." Comparative analysis across these groups and PDAC identified a progression-associated gene signature, with downregulated genes enriched in transmembrane transport and metabolic pathways, and upregulated genes associated with extracellular matrix (ECM) organization—suggesting morphological transformation during progression.

We further identified seven genes significantly upregulated in high-risk PanIN clones relative to both low-risk PanIN and PDAC clones. These genes displayed spatial localization specific to high-risk regions, offering potential early biomarkers for identifying PanIN lesions with a higher risk of malignant progression.

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ABSTRACTS

Poster #54

Transforming Cancer Detection: Scalable and Sensitive Liquid Biopsy Powered by Extracellular Vesicle Protein Colocalization

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Early detection of cancer remains one of oncology's greatest challenges and opportunities. Extracellular vesicles and particles (EVPs) are nanoscale, cell-derived structures abundant in biofluids and enriched with DNA, RNA, metabolites, and proteins reflective of their cellular origin. Leveraging this distinctive biology, we have developed a liquid biopsy platform that detects cancer-specific surface protein colocalization on circulating EVPs using oligonucleotide-labeled antibodies and proximity ligation-dependent quantitative PCR (qPCR) for signal amplification.

To accelerate biomarker discovery and assay optimization, we integrated a digital twin framework, a computational model replicating the assay system and biological variability, that simulates EVP dynamics and assay performance across diverse patient populations. This approach allows for efficient in silico evaluation of biomarker combinations, thereby improving candidate selection and reducing the extent of empirical testing required in assay development.

The platform has demonstrated highly sensitive and specific detection of early-stage (Stage I/II) ovarian cancer and lung adenocarcinomas across independent clinical cohorts, highlighting its potential to identify tumor-derived EVPs at the earliest disease stages accurately. Importantly, this assay requires significantly less patient sample volume compared to traditional ctDNA-based methods. Moreover, signal intensity from the assay correlates strongly with tumor burden, reinforcing the biological relevance of biomarker-colocalized EVPs.

This approach offers scalability, multiplexing capabilities, and compatibility with high-throughput workflows, making it readily adaptable to various tumor indications and potentially applicable beyond oncology. By combining EVP surface biomarkers with proximity ligation and qPCR, the platform represents a next-generation liquid biopsy technology with broad clinical utility. Its deployment in population-level cancer screening provides a promising new strategy for early detection and improved patient outcomes.

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ABSTRACTS

Poster #55

LEGACY - DeLinEatinG the tumorAl and Clinical evolution of hereditarY pancreatic cancer

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Pancreatic ductal adenocarcinoma (PDAC) is among the deadliest cancers, largely due to its asymptomatic progression and late-stage diagnosis. While most PDAC cases are sporadic, arising without a known inherited cause, approximately 10% are non-sporadic (hereditary) and occur in high-risk individuals (HRIs) with a genetic predisposition due to germline mutations or a strong family history. Despite their significantly elevated risk, HRIs remain underrepresented in early detection strategies. The LEGACY project addresses this gap through a comprehensive framework that combines prospective risk profiling, retrospective tumor analysis, and functional modeling to identify early molecular events and improve precision surveillance for hereditary PDAC.

LEGACYrisk is the project's prospective arm, focused on identifying and longitudinally monitoring HRIs across six academic cancer centers in Bavaria. In collaboration with clinical geneticists, individuals will be enrolled based on FaPaCa/CAPS-5 criteria, germline mutation status, and polygenic risk scores. Participants will complete a structured digital questionnaire, and blood samples will be collected for biobanking of PBMCs and circulating cell-free DNA (ccDNA). All data will be integrated into a centralized data integration system (DIS), forming the basis for future biomarker and screening strategies.

LEGACYtumor retrospectively investigates the tumor microenvironment of non-sporadic PDAC by analyzing tissue samples from individuals with known germline mutations. These will be matched with sporadic cases and analyzed using tissue microarrays and spatial transcriptomics to identify gene expression and microenvironmental differences that may reflect distinct tumor evolution pathways.

LEGACYmodel will use retrospective samples to develop experimental systems that explore the biological drivers of hereditary PDAC. Planned work includes generating gene-specific knockout models (e.g., BRCA2 gene) in murine cells and establishing co-culture systems with HRI-derived PBMCs and PDOs (patient-derived organoids) to mimic tumor-stroma-immune interactions in early disease states.

Although still in an early stage with no results yet, LEGACY is a well-designed and promising project with high relevance to early cancer detection. By integrating clinical risk assessment with retrospective biological analysis, it aims to enhance risk prediction and uncover new pathways for early diagnosis in hereditary PDAC.

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Poster #56

Fallopian tube lavage sampling for early detection of pre-invasive ovarian cancer

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Ovarian cancer (OC) is the most lethal gynaecological malignancy, primarily due to its diagnosis at advanced, often incurable stages. The majority of high-grade serous OC cases originate from pre-invasive lesions in the fallopian tube (FT), specifically serous tubal intraepithelial carcinomas (STICs). However, no clinical test currently enables in vivo detection of these lesions at an early, treatable stage. To address this critical gap, we introduce FT lavage as a novel sampling approach that avoids the fimbrial ends, enabling analysis of early tumour-associated molecular changes in FT-derived biofluids, while remaining compatible with emerging in vivo sampling tools such as falloposcopy.

In this study, we performed proteomic profiling of 27 FT lavage samples from individuals with benign gynaecological conditions (9/27), BRCA1/2 mutation carriers (12/27) and OC patients (6/27). Our analysis identified an 82-protein signature featuring key factors implicated in OC progression and dysregulated in the earliest stages of disease. Notably, using this signature, we retrospectively identified a previously undetected STIC lesion in a high-risk individual. Detection of this signature in lavage samples obtained away from the fimbrial region suggests that tumour-associated molecular changes are not confined to the distal FT but occur throughout the lumen, including areas accessible only via minimally invasive techniques. To validate these findings, a subset of proteins was examined via immunofluorescent staining in five STIC lesions from an independent cohort, confirming consistent dysregulation of signature components.

Collectively, our findings support FT lavage as a promising minimally invasive method for detecting pre-malignant lesions in high-risk individuals, with potential for fertility-preserving early detection. This approach could inform screening, risk stratification, and chemoprevention strategies. However, larger studies are needed to validate its diagnostic performance and clinical utility for asymptomatic screening.

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Poster #57

Lightning Talk

3D Bioprinted Tumor Avatars as a Functional Platform for Early Cancer Modeling

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A major challenge in early detection is limited access to longitudinal data from tissues undergoing cancer initiation, especially for cancers lacking early screening programs or in hard to access sites. In vitro models such as patient derived organoids can help address this challenge, but lack precise control over cellular spatial arrangement, geometry, and heterogeneity. Here we report the development of a 3D bioprinting platform to fabricate tumor avatars that mimic the observed histology of native tumor microenvironments (TME), with 60 µm spatial resolution. A H&E stained ductal carcinoma in situ biopsy with matching spatial transcriptomics data served as our blueprint for reconstructing the TME. We identified a 1.5 x 1 mm region of interest (ROI) that contained cancer filled mammary ducts with surrounding stromal compartment of fibroblasts, immune infiltrates, and vasculature. A microfluidic dispenser (Biopixlar, Fluicell) was then used to deposit the cells in their respective neighborhoods to create 3D tumor avatars. Avatars were fabricated using cells isolated from a single human donor, or commercially available primary cells and cell lines, and cultured up to 28 days. To demonstrate the high spatial precision of our method, we first recreated the ROI using primary luminal epithelial, myoepithelial, fibroblast, macrophage, endothelial, mesenchymal stromal, and either MCF7 or MDA-MB-231. Live cell imaging confirmed cells can be patterned with high precision, density, and heterogeneity while maintaining viability, proliferation, and migrational capacity. Within 24 hours, cells spread to establish their expected morphology and cell-cell junctions, features not observed in the spheroid controls. As proof of spatiotemporal control, we printed an avatar of healthy cells, allowed it to stabilize for 24 hours, and then deposited cancer cells into the duct lumen. Finally, to assess functional responsiveness, tumor avatars were treated with 10 ng/mL TGFβ1 for 7 days. MCF7s proliferated and migrated out of the duct in the TGFβ1 treatment group whereas MCF7s stayed confined to the duct in the control. We also observed greater fibroblast density, matrix remodeling, and epithelial morphology disruption in treatment relative to control. These results highlight the potential of bioprinted tumor avatars as a controllable, high-resolution platform for advancing our understanding of early cancer biology, biomarkers, and interception targets.

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Poster #58

Does Ethnicity Impact AI performance in Breast Density Prediction?

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High breast density reduces mammography sensitivity and increases breast cancer risk. Its use in cancer risk prediction models alongside other factors has led to improvements in accuracy. We have previously developed AI-based breast density prediction models, but our training data was acquired in a clinical trial and does not reflect the ethnic diversity of the wider population. In this study, we examine the generalisability of breast density prediction models through a cross-ethnic evaluation using datasets drawn from Asian, White and Black populations.

Our models are trained on breast density assessed by experts who recorded percent density on Visual Analogue Scales (VAS), averaged across radiographic projections and readers. Data were obtained from the Predicting Risk Of Cancer At Screening (PROCAS) study of 53,596 women. We constructed 4 datasets of 969 mammograms each, evenly distributed across VAS density intervals of 5%. These were three ethnicity-specific datasets and one combined set with equal representation from all groups. Resnet101 models pretrained on ImageNet21k were trained using 10-fold cross-validation on each dataset, resulting in 40 models which were then cross-evaluated against the unseen datasets. Additional holdout test sets included 2,531 White and 393 Asian mammograms for further validation.

Training showed significant performance differences: the Black-trained model outperforming the combined model, with RMSEs across folds of 7.53[7.16, 7.92] and 8.49 [8, 8.89] respectively. Cross-evaluation showed asymmetrical generalisation, with White-trained models underperforming on the Asian test set (RMSE 9.19[9.02, 9.38]) compared to the Asian-trained models on the White test set (RMSE 8.51[8.34, 8.67]). Combined models had the best out-of-group average performance but did not match the within-group performance levels of ethnic-specific models.

Models performed best within their own groups, but cross-group generalisation varied. These results show that accuracy and generalisability are influenced by uneven model performance across populations. Accounting for these differences during development is necessary for equitable early cancer detection. Whilst deep learning has the potential to provide reproducible and efficient breast cancer risk prediction and make early detection more accessible, attention should be given to equity control and analysis of biases within models, to ensure equal performance across all ethnic populations.

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Poster #59

Using immune biomarkers to improve early lung cancer detection during community lung health checks

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Time of diagnosis is a critical factor in lung cancer prognosis. Pre-metastatic lung cancers are often good candidates for curative surgery while treatments for metastatic lung cancer have limited success. In the UK, community lung health screening has detected of over 8000 early lung cancer cases in the last decade by utilising risk scoring to allocate low-dose CT scans using demographic and lifestyle factors. However, only 40% of people diagnosed with lung cancer meet the criteria for screening prior to their diagnosis. We reason that a pre-CT screening test could reduce the number of CT scans needed per positive diagnosis, thereby reducing the cost and increasing the reach of screening programmes. This study aims to develop immune biomarkers for community screening to allow clinicians to better stratify at-risk individuals including patients outside the current cutoffs used with PLCO and LLP scores.

We have immunoprofiled peripheral whole-blood samples from patients at community lung health checks and lung cancer clinics using CyTOF. Multiplex-ELISA assays were performed on serum samples from matched patients to investigate potential links to tissue immunology. We then utilised preliminary scRNA-seq to expand our candidate search and identify relevant signalling pathways between tumour and circulating immune cells in early cancer. Our results show a significant depletion in circulating MAIT cells in early lung cancer patients compared to control patients with similar co-morbidities from the lung health check programme. We propose these may be linked to the CXCL9-CXCR3 signalling pathway with serum CXCL9 being a strong candidate for future biomarker work. Furthermore, we detect differences in classical monocyte phenotype in early cancer patients highlighting their potential use as blood-based biomarkers of early lung cancer in the future.

Our data provides evidence of changes in the circulating systemic immune system of early-stage lung cancer patients. This work may constitute a key step towards the integration of blood-based immune biomarkers with existing risk scores. This adds to evidence that blood-based biomarkers remain a premier candidate for improving community screening programmes through broader access, better early detection power and fewer unnecessary low dose CT scans.

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Poster #60

Utilizing the B Cell Response for Early Detection of Renal Cell Carcinoma

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Background: Renal cell carcinoma (RCC) remains a significant cause of cancer mortality in the United States, with poor outcomes for advanced-stage disease and limited tools for early detection. Tumor-specific antibodies are known to develop early in other solid tumors. This study aimed to leverage Serum Epitope Repertoire Analysis (SERA), a platform for profiling B cell epitopes, and machine learning to derive a B cell epitope classifier for distinguishing between RCC and benign renal masses and healthy controls.

Methods: We analyzed 790 serum/plasma samples from 1) 289 patients with RCC, spanning all stages; 2) 25 patients with benign renal masses; and 3) 476 age-matched self-reported healthy controls. The SERA platform uses a library of 8 billion unique 12-mer peptides, each expressed on a DNA-barcoded E. coli strain. Number and type of peptides bound by an antibody are identified by next-generation sequencing. Using machine learning, a classifier was trained on 370 samples (87 RCC and 283 healthy controls) and tested in 420 samples (202 RCC, 25 benign renal masses, and 193 healthy controls). The area under the receiver operating characteristic curve (AUC) served to evaluate the classifier's performance, overall and stratified by RCC stage.

Results: Using the SERA platform, 26.4 million potential 3- and 4-mer amino acid motifs were scored based on enrichment in RCC versus controls, yielding 7,244 motifs that met the predefined thresholds for inclusion in the classifier. These features were used to train a 10,000-tree random classification forest. In validation, the model had an AUC of 0.72 (95% confidence interval [CI]: 0.68 - 0.77), while there were no significant differences (Mann-Whitney U test, alpha = 0.05) between benign renal lesions samples and healthy controls. Performance was similar across both early- and late-stage RCC, with an AUC of 0.78 (95% CI: 0.70–0.85) for stage 1, 0.72 (95% CI: 0.49–0.95) for stage 2, 0.81 (95% CI: 0.70–0.92) for stage 3, and 0.75 (95% CI: 0.68–0.81) for stage 4 RCC, each compared to controls.

Conclusions: Our findings suggest that a blood-based B cell epitope classifier can distinguish RCC from controls, with consistent performance across all RCC stages. This approach has the potential to enhance early diagnosis of RCC and to obviate the need for renal mass biopsy. Future studies will focus on refining the classifier and validating its performance in larger, multi-institutional cohorts.

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Poster #61

Detecting Early Cancer Using cfDNA Methylation and Fragmentation Signatures

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Early cancer screening enhances survival by enabling timely treatment before the disease progresses. However, in most countries, population-wide screening is currently limited to a few cancer types, underscoring the need for novel, cost-effective, and routinely deployable methods capable of detecting multiple cancers. Tumour-derived cell-free DNA (cfDNA) with distinct genetic and epigenetic alterations are released into the plasma and can be exploited for cancer screening. Here, we aim to identify precancerous and early tumour-associated cfDNA methylation and fragmentation signatures. We analyzed nanopore sequencing data from pre-diagnostic and stage II diagnostic plasma samples collected from breast cancer patients. Preliminary results revealed global DNA hypomethylation and increased within-sample methylation variability—reflected by higher coefficients of variation—in diagnostic samples. These alterations were more pronounced in younger patients. Notably, global hypomethylation was observed in both triple-negative breast cancer (TNBC) and ER+/HER2– subtypes, but not in other breast cancer subtypes represented in our cohort. Mean-based comparisons across chromosome arms indicated hypomethylation in both pre-diagnostic and diagnostic breast cancer samples, with some chromosomal regions exhibiting substantially more hypomethylation among pre-cancer and cancer samples relative to controls. To identify loci that are associated with precancerous epigenetic alterations, differentially methylated regions (DMRs) were selected across different functional elements in the genome. Using DMRs found in promoter regions, a random forest model was built within the discovery set that contains the pre-diagnostic breast cancer samples. The trained model showed moderate discriminability on the validation set that contains the rest of the pre-diagnostics and diagnostics breast cancer samples. Future work will refine feature selection and integrate fragmentation patterns and copy number alteration to enhance the performance of the model. Pathway enrichment analysis will be performed to investigate the oncogenic relevance of selected features. Success in this project will define how early cancer can be detected through liquid biopsy and advance the timeline of early detection. This project has the potential to develop a single blood test for multi-cancer detection and monitoring.

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Poster Pitch

Adapting Outreach for the Black Community: Engaging Community Champions to Boost Trial Enrollment

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Black communities face disproportionate health burdens and are underrepresented in research that shapes prevention, diagnosis, and treatment. The OHSU Knight Cancer Institute's Community Outreach and Engagement aims to build lasting partnerships with Black communities in Oregon. To do so, the team engaged key opinion leaders (via interviews), hosted community conversations, and established a Black Cultural Advisory Board (CAB). This work produced a robust, culturally specific document—a "landscape"—capturing the experiences of African American, Immigrant, and Refugee communities. The resource helps researchers and clinicians better understand these communities and includes sections titled Who We Are, How We Got Here, and Where Do We Go From Here. The latter offers three community-recommended directions: Let's Build Trust, Let's Build Health Literacy, and Let's Build Opportunity.

A follow-on health literacy project aims to replace ineffective outreach strategies promoting research participation. Originally, the focus was on creating adapted social media content as Black listening sessions reported high social media use, even for health information, but given previous enrollment data showing Latino participants were twice as likely as Black participants to join studies via social media. However, the CAB warned of growing distrust of media focusing on Black audiences, especially amid a shifting political landscape.

We shifted strategy to an in-person approach. This project embraces Let's Build Opportunity by training community members to co-facilitate and analyze data, empowering them as research champions positioned as experts in their circles to raise awareness about the importance of cultural representation in research, protections and participant rights. At the same time, we provide "gateway" opportunities to participate and learn about research like focus groups and enrollment in the Healthy Oregon Project (HOP), our cohort providing personalized health info and study invites to over 52,000 Oregonians.

Shifting plans to reflect community insights led to a 25% increase in Black enrollment in HOP, strong interest from African Immigrant communities in understanding research, and research participation training of two African American-led CHW cohorts. With a year remaining, projects like this fuel future community-driven collaboration, ensuring that the voices historically underserved communities remain central to research at the Knight Cancer Institute.

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Poster #63

Developing and Evaluating a Blood-Based Early Cancer Detection (ECD) Test for Colorectal Cancer (CRC): Insights from the PROCEED-CRC Study

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Blood-based cancer screening biomarkers have garnered much anticipation in recent years. Current CRC screening methodologies are plagued with low compliance rates. Scientific advancement calls for clinical trial recruitment from diverse backgrounds to ensure the differentiation between cancer and healthy cases in a heterogeneous population across race and ethnicity, geography, and age. Here, we describe an ongoing, decentralized, prospective sample collection clinical study, PROCEED-CRC (NCT06620627), to develop a blood-based CRC screening test in an average-risk population. In addition, the preliminary findings from a minimally invasive blood-based ECD screening test for CRC are reported. PROCEED-CRC was designed to enroll up to 3000 evaluable patients. Key eligibility criteria include participants ≥40 years old, undergoing asymptomatic colonoscopy screening, willing to provide a blood sample <120 days before a colonoscopy procedure, and providing informed consent prior to study participation. Exclusion criteria include individuals with a prior malignancy, who have undergone diagnostic colonoscopy in the past 9 years, recent CRC screening tests, precancerous findings on recent colonoscopy, or have high-risk CRC germline findings. As of June XX, 2025, there were 4675 enrolled participants and 2045 completed participants. To evaluate the performance of the CRC ECD screening test, healthy controls from PROCEED-CRC and CRC cases from the CIRCULATE-Japan GALAXY observational study (UMIN000039205) were used. Assay performance was evaluated in 2 cohorts of plasma samples: Cohort A (controls N=305, CRC N=127) and Cohort B (controls N=90, CRC N=41). Respectively, sensitivity was 95% (95% CI: 92-99%) (Cohort A) and 97% (95% CI: 86-100%) (Cohort B). Specificity was 91% (95% CI: 88-94%) (Cohort A) and 91% (76-100%) (Cohort B). Stage I sensitivity was 92% (A) and 87% (B). In Cohort A, screen-detected sensitivity, adjusted for stage, was 91%. The differentially methylated allele fraction across target regions strongly correlated with variant allele frequencies from a tumor-informed, variant-based ctDNA test (Spearman's correlation coefficient, 0.85). Using CRC-specific epigenetic markers, we developed a sensitive and specific blood-based test to detect cfDNA from early-stage and asymptomatic disease. Reported results in each cohort show the robustness of our assay. This test could increase patient adherence rates for CRC screening, thereby improving patient outcomes.

ABSTRACTS

Poster #64

Poster Pitch

CA-125 glycovariant assays improve the detection of early-stage epithelial ovarian cancer

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Objectives: Ovarian cancer is the deadliest gynecologic malignancy. The 5-year survival rate for advanced ovarian cancer is only about 30%, whereas the survival rate in early-stage disease is over 90%. Thus, the early detection of ovarian masses is an urgent clinical challenge, and resolving it is key to achieving satisfactory oncological outcomes. Current biomarkers lack the specificity and sensitivity needed for accurate cancer detection and diagnosis often requires invasive procedures like biopsy. Therefore, we aim to develop novel CA-125 glycovariant assays to improve the sensitivity and specificity of ovarian cancer diagnosis.

Methods: Blood samples of 184 patients with epithelial ovarian cancer, 127 benign ovarian tumors, and 115 unaffected controls were measured using GLYVARTM Ovarian I and II glycovariant assays (Uniogen) and the conventional CA-125 protein assay (Fujirebio).

Results: CA-125 glycovariant assays differentiated benign and malignant ovarian masses with 88% sensitivity at high 99% specificity, while CA-125 protein assay showed a sensitivity of 73%. CA-125 glycovariant assays demonstrated improved performance, particularly in patients with borderline or moderately elevated CA-125 levels at the time of diagnosis, which is a challenging group for differential diagnostics. In this patient group, CA-125 glycovariant assays showed 2.5 times greater sensitivity (33% with CA-125 vs. 83% with CA-125 glycovariants) at 94% specificity. CA-125 glycovariant assays corrected 82% of the false positive results produced by the conventional CA-125 assay. Importantly, the CA-125 glycovariant assays detected 71% of early-stage high-grade serous carcinomas, which is the deadliest type of ovarian cancer, with a very high specificity of 99%. The sensitivity of CA-125 in this patient group was only 43%.

Conclusion: This is the first study describing the clinical performance of GLYVAR Ovarian I and II assays in ovarian cancer diagnostics. The results indicate that simple and easily accessible CA-125 glycovariant assays have remarkable potential to improve ovarian cancer diagnostics without expensive equipment and data analysis resources.

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Poster #65

Minimally Invasive Collection of Dermal Interstitial Fluid via 3D-Printed Microneedles for Early Cancer Detection

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Early detection of cancer remains a major clinical challenge, and liquid biopsy is a promising tool to improve screening because it is less invasive than tissue biopsy and allows more frequent monitoring. The most common liquid biopsy specimen is blood, obtained by venipuncture, which is still invasive and requires trained personnel. Its scalability is also limited by complications in blood handling and transport, such as clotting and hemolysis. To further improve compliance and scalability, there is a critical need for minimally invasive and accessible alternatives.

Here, we propose dermal interstitial fluid (ISF) as a low-cost and painless alternative to blood for cancer biomarker detection. Dermal ISF bathes cells within the dermis and shares proteomic, metabolomic, and transcriptomic profiles highly similar to plasma while also containing unique biomarkers. Microneedle array patches (MAP) enable minimally invasive ISF collection, but clinical translation has been limited by slow sampling rates and low collection volumes. To address this, we developed a 3D-printed ISF sampling device, termed Puncture-Out-and-Press (POP), that allows rapid, consistent, and pain-free ISF collection in humans. The POP device collects an average of 15.5 mg of ISF in humans within 5 minutes with a near-zero failure rate, <1% blood contamination, and pain levels comparable to a finger prick. These improvements were achieved by optimizing a spatial pressure gradient that drives ISF flow into a perforated collection plate following MAP insertion. Proteomic analysis confirmed strong similarity between ISF and plasma and identified 149 proteins listed in the National Cancer Institute's Early Detection Research Network biomarker database.

Beyond POP, we are developing new ISF sampling devices that explore features such as absorptive materials and pre-evacuated tubes to streamline collection. We are also expanding analyses to include cell-free nucleic acids (cfNAs), which are critical for early cancer detection as they capture tumor-derived genetic and transcriptional alterations before clinical symptoms appear. Our preliminary studies demonstrate successful isolation of nucleic acids from porcine ISF, supporting the feasibility of cfNA analysis in ISF. These findings establish dermal ISF as a rich source for liquid biopsy and position 3D-printed MAPs as scalable, minimally invasive platforms for accessible early cancer detection.

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Poster #66

Lightning Talk

Early-Stage Pancreatic Cancer Detection Using Cancer-Derived Nanoparticles Recovered from Plasma by Three Electrode Cluster Dielectrophoresis

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Extracellular vesicles (EVs) released by tumors into blood carry biomarkers that can successfully differentiate patients with pancreatic ductal adenocarcinoma (PDAC) from patients with benign pancreatic disease. Despite their important biomarker cargos, nanoparticles are not used in clinical diagnostics due to the difficulty of recovering them from blood. Traditional ultracentrifugation and column chromatography are labor intensive and have low throughput. Thus, there remains a clear unmet clinical need to increase the throughput of nanoparticle-based biomarker analysis and extend the reach of these diagnostics to smaller rural clinics. Our research developing new dielectrophoresis (DEP) nanoparticle recovery technology with a three-electrode cluster design can address this challenge by enabling new instrumentation that is miniaturized for easy transport and use and also enables new high throughput designs by integration into 96 well plate formats. These three-electrode clusters are capable of changing configuration to run DEP nanoparticle collection straight from undiluted plasma in a two-electrode configuration and also perform cyclic voltammetry-based detection of electrochemically active immunostains in a three-electrode configuration. This enables system miniaturization, chip footprint expansion, and results in a high signal-to-noise ratio thereby increasing sensitivity. We applied this electrode design and our new biomarker panel of CD9, Glyican 1, and cf-DNA nanoparticles, age and sex, to a blinded 52 patient cohort consisting of pancreatic cancer patients, including 12 patients with stage 1 and 2 PDAC, and patients with noncancerous pancreatic diseases of benign cysts, pancreatitis, and precancerous intraductal papillary mucinous neoplasms (IPMNs). We show successful differentiation between stage 1 and 2 PDAC and the non-cancerous controls with an AUC of 0.94. This performs better than the traditional invasive and expensive endoscopic ultrasound-guided fine needle aspiration (EUS/FNA) diagnostic procedure (AUC 0.79). Together these results show the promise of dielectrophoresis as a technology that can recover diagnostically relevant nanoparticles from undiluted plasma samples and shows successful cancer detection and differentiation of patients with early-stage cancer from those with precancerous lesions. This technology has the necessary characteristics to bring complex nanoparticle-based diagnostics to the clinical setting.

ABSTRACTS

Poster #67

Risk-based breast cancer screening: an expert Delphi consensus assessment of evidence under the EUCanScreen initiative

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COMPANY/INSTITUTION:

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Introduction: Risk-based breast cancer screening (RBBCS) is an emerging approach aimed at tailoring screening strategies to individual risk profiles. As part of the EUCanScreen initiative—an EU Joint Action supporting high-quality cancer screening programs across Europe—a Delphi process was conducted to assess expert consensus on the current state of evidence and implementation needs for RBBCS.

Methods: A two-round Delphi survey was carried out between May and June 2025 among European experts in risk-stratified screening. Fourteen evidence-based statements covering effectiveness, acceptability, harms, feasibility, and implementation challenges were evaluated. Consensus was defined as ≥85% agreement.

Results: After 2 rounds, consensus was reached for 12 out of 14 statements. Key agreements included: •For BRCA1/2 carriers, efficacy data support standard use of MRI in addition to mammography (95%). •For carriers of high penetrance genes other than BRCA1/2, evidence is currently insufficient and more data would be needed potentially from real-world (100%). •For intermediate penetrance variants (e.g., CHEK2, ATM), the optimal screening strategy remains unclear (100%). •Ongoing trials may clarify the value of population-based RBBCS in women aged 40–74 (95%), but mortality outcomes will require complementary real-world evidence (95%). •Current trials are unlikely to support de-escalation of screening in lower-risk women (88%). •Experts agreed on the need for context-specific data to support implementation (100%), and called for more evidence on side effects (100%), socio-psychological impact (100%), equity (100%), and cost-effectiveness (94%). •New RBBCS strategies should be evaluated beyond current ongoing trials, though novel methods for assessing risk may use existing data for validation (94%).

Statements that did not reach consensus included: •Whether subanalyses from ongoing trials will be sufficient to set risk thresholds to guide screening strategies (83% agreement). •Whether available and upcoming data will be sufficient to assess the acceptability of RBBCS among women and healthcare providers (82%).

Conclusions: This Delphi process identified strong expert consensus on key aspects of RBBCS, while highlighting persistent evidence gaps in implementation, acceptability and risk threshold definition. These findings emphasize the need for real-world data and support the development of evidence-informed risk-based screening strategies across Europe.

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Poster #68

Risk-Based Breast Cancer Screening: mapping three decades of evidence under the EUCanScreen Initiative

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COMPANY/INSTITUTION:

Gustave Roussy

Risk-based breast cancer screening (RBS), which tailors screening to individual risk profiles, is a promising alternative to the current age-based model. We reviewed RBS studies from the past 35 years to foresee future developments and identify evidence gaps.

We conducted a systematic review of completed and ongoing studies on RBS worldwide. Eligible studies were identified through PubMed, ClinicalTrials.gov and a structured survey distributed within the EUCanScreen network. Data were reviewed by 3 independent investigators (PROSPERO 616967).

We identified 39 RBS studies: 25 completed (N=1.519.343), eight in follow-up (N= 243.452) and six ongoing (planned N= 133.762). Among these, 10 were randomized clinical trials (RCT), 8 non(N)RCT, 2 cross sectional (CS) and 19 observational cohorts (OC). Thirteen studies were conducted on general population and 26 on high-risk populations. Risk assessment methods included BRCA1/2 status (n=8), risk scores ± genetic markers (n=20), AI-based imaging (n=2), breast density (n=7) and single risk factors (n=2). All studies modified screening protocols: 33 imaging modalities, 10 age at start and 18 screening intervals. Primary endpoints included breast cancer (BC) survival (n=2), BC incidence (n=9), detection rates (n=12), test performance (n=12), acceptability (n=1) and recall rates (n=1). Studies examined screening escalation (E; n=29), modification (M; n=5) and de-escalation (D; n=5).

While cohort studies have demonstrated the impact of screening escalation among BRCA1/2 carriers, other RBS studies have not yet reached a sufficient level of evidence (LoE) to change practices. Major E and D studies in the general population are underway, with results expected in the coming years.

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Poster #69

Barriers to Breast and Cervical Cancer Screening Among Adolescent Girls and Young Women in Kenya: A Nationwide Cross-sectional Survey

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COMPANY/INSTITUTION:

Stony Brook University

Background: Promoting regular screening remains one of the primary preventive measures for breast and cervical cancer. The study aimed to assess the prevalence and barriers to breast and cervical cancer screening among adolescent girls and young women (AGYW) in Kenya.

Methods: The study used data from the 2022 Kenya Demographic and Health Survey (KDHS), with 12,026 AGYW who were selected by multistage sampling. The outcomes of interest were breast and cervical cancer screening. Multivariable logistic regression was used to assess factors negatively associated with the outcome variables, using SPSS (version 29.0).

Results: Of the 12,026 AGYW included in this study, only 6.0% (95%CI: 5.6-6.8) and 5.1% (95%CI: 4.8-6.0) had undertaken breast and cervical cancer screening, respectively. Low education (AOR= 0.08, 95%CI: 0.02-0.34 and AOR= 0.48, 95%CI: 0.28-0.83), not working (AOR=0.67, 95%CI: 0.46-0.97 and AOR= 0.59, 95%CI: 0.42-0.82), low wealth index (AOR= 0.55, 95%CI: 0.32-0.92 and AOR= 0.45, 95%CI: 0.25-0.81), no visit to a healthcare facility in the last 6 months (AOR= 0.48, 95%CI: 0.33-0.69 and AOR= 0.50, 95%CI: 0.35-0.71), and no birth record (AOR= 0.29, 95%CI: 0.13-0.62 and AOR= 0.58, 95%CI: 0.27-0.74), were the major barriers to both breast and cervical cancer screening, respectively. Moreover, having no access to newspaper (AOR=0.67, 95%CI: 0.46-0.97) was a significant barrier to breast cancer screening while having big problems with distance to a healthcare facility (AOR= 0.49, 95%CI: 0.33-0.73) and not using modern contraception (AOR= 0.60, 95%CI: 0.42-0.86) hindered cervical cancer screening.

Conclusions: In conclusion, more efforts are needed from both the government and cancer stakeholders to increase accessibility of breast and cervical cancer screening services, especially to those with low social economic status. More targeted education and sensitization, improving livelihoods of AGYW through various women empowerment efforts, and improving screening capacity of low-grade healthcare facilities are among the useful strategies to improve the low screening rates.

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Poster #70

Pancreatic cancer risk prediction using deep sequential modeling of longitudinal diagnostic and medication records

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Pancreatic ductal adenocarcinoma (PDAC) is a rare, aggressive cancer often diagnosed late with low survival rates, due to the lack of population-wide screening programs and the high cost of currently available early detection methods. Electronic health records (EHRs) offer a rich and generally available source of patient data, including diagnoses, medications, and laboratory results, that can support population-wide risk prediction. We developed an AI-based tool that predicts pancreatic cancer risk within 6,12, 24 and 36 months of assessment, using time-sequenced diagnostic and medication events from real-world EHR data. Trained on a large-scale US Veterans Affairs dataset with 19,426 PDAC cases and 15,906,989 controls, the tool employs a Transformer-based model that can capture and benefit from information synergy between diagnoses and medications. Our results demonstrate that incorporating medication data alongside diagnostic codes significantly improves performance. For the top N high-risk patients identified from a population of 1 million, the 3 year cancer risk is substantially higher than estimates based on age and gender alone, with standard incidence ratio (SIR) ranging from 115 for the top 1,000 patients to 70 for the top 5000 patients. We also identify the most predictive features driving the prediction, which can generate clinical hypotheses such as the role of chronic inflammatory conditions in predisposing to PDAC or the impact of specific medications on the overall health state of a patient and cancer risk. We further evaluated model performance across different socioeconomic subpopulations to quantify bias. The evaluation dataset was stratified by race and sex, revealing an AUROC of 0.901 (95%CI: 0.897-0.904) for white patients and 0.870 (95%CI: 0.860-0.880) for black patients in a 12-month prediction window. Similarly, male patients achieved AUROC of 0.892 (95%CI: 0.888-0.896), compared to 0.900 (95%CI: 0.883-0.913) for female patients. The disproportionate representation of white and male in the database likely contributes to these performance disparities, underscoring the need to address model bias arising from uneven subpopulation representation in the dataset. The risk prediction tool is intended to be the first step in a three-step clinical program: identification of high-risk individuals using AI, followed by a stratified surveillance program for early detection and intervention, aiming to benefit patients and lower health-care costs.

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Poster #71

Poster Pitch

Large language models as a decision-aid tool in lung cancer screening: An assessment of quality and feasibility

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The evolution of early detection methods may complicate screening selection. Large language models (LLMs) offer scalable decision-aid tools that may improve participation. This study systematically assesses three freely available LLMs (Meta AI (via WhatsApp), Chat GPT, Google Gemini) in supporting potential lung cancer screening (LCS) participants. Eight personas (unaware, logistically challenged, anxious, skeptical, engaged, fatalistic, comorbid and low health literacy) and associated questions (≤8 per persona) simulating LCS participants were developed from literature. Questions were entered into each LLM sequentially. Four physicians (respiratory, oncology, general practice) manually scored responses using QUEST criteria (quality, reasoning, persona, safety, trust) and decision-aid metrics (1-5, higher=desirable). Automated readability (SMOG) and sentiment (VADER, Empath) analysis used Python in Google Colab. Manual scoring showed variable LLM performance. Gemini performed best overall, despite higher question-response length ratios and SMOG indices. Meta AI performed least well, with shorter, more readable responses. In the safety domain, Gemini scored highest for bias (Average: 4.53) and falsification (4.22); all LLMs showed poor self-awareness (Gemini: 1.81, ChatGPT: 1.34, Meta AI: 1.66). Hallucinations (2 major, 5 minor) occurred in 7/24 question strings. QUEST empathy scores: Gemini 4.13, Chat GPT 2.91, Meta AI 2.38. Automated sentiment analysis did not correlate with human scoring and showed internal incongruence. Smoking cessation guidance was inadequate/absent across all LLMs. Anxious/fatalistic personas elicited higher scores; comorbid and low health literacy personas performed least well. LLMs show promise for LCS decision-making but have critical limitations. Future efforts will optimize LLMs via prompt engineering, fine-tuning, and patient feedback. Context-specific automated analysis tools are needed to support these solutions.

	QUEST (Avg/CV%)	DA (Avg/CV%)	SMOG/IQR	QRR
Gemini	3.94/28.45	3.53/38.95	13.0/1.23	53.38
Meta AI	2.31/23.40	2.18/25.14	12.17/1.95	15.16
Chat GPT	2.83/33.51	2.5/39.15	14.59/0.68	27.50

Avg = average score all raters, personas and domains. CV: Coefficient of variation (inter-rater). SMOG: Simple Measure of Gobbledygook. QRR: question-response length ratio. DA: decision-aid score.

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Poster #72

The Political Economy of Externalised Risk: A New Framework for Understanding Diagnostic Delays for Pancreatic Cancer in Primary Care

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Background: Diagnostic delays for pancreatic cancer contribute to poor survival rates, yet interventions have had limited success. Current approaches, assuming delays stem from "practice readiness," risk misattributing cause by mistaking systemic dysfunction for the disease. This paper challenges that logic, proposing a new framework for systemic drivers of delay.

Methods: This new framework developed from critical re-analysis of UK primary care qualitative data (41 multi-stakeholder interviews, co-design focus group). Data was initially analyzed via implementation science. Our analysis inverts original causal logic to re-examine the project's disruptive findings.

Findings: Patients experience diagnosis as a "Diagnostic Gauntlet," a series of arduous hurdles. This gauntlet is not practice-level deficiency but an architectural feature of a healthcare system actively externalizing diagnostic risk. The system converts internal operational, financial, and medicolegal risks into external hazards, managed by GPs and, profoundly, patients and their families. This risk-shifting compels immense, uncompensated "Diagnostic Labour"; the cognitive, emotional, and logistical tasks patients and families perform to secure a diagnosis the system is structured to defer. Our "Advocacy Burden" finding is primary empirical evidence of this extracted labour.

Interpretation: Diagnostic delays are not a technical "readiness" problem but a political-economic failure rooted in Systemic Risk Externalization. This system forces "Diagnostic Labour" to offset its deficiencies, a burden systematically and inequitably distributed, driving well-documented health disparities. Common Quality Improvement tools, while benevolent, can inadvertently function as "technologies of governance". By making practices auditable, measurable, and responsible for managing diagnostic timeliness, these tools risk depoliticizing systemic failure and reinforcing the risk-shifting they seek to mitigate. Future research must shift from optimizing localised coping to mapping the political economy of diagnostic risk and its inequitable labour distribution.

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Poster Pitch

NHS-Galleri trial: approaches to retain a diverse participant cohort across multiple trial appointments

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Introduction: A diverse clinical trial population contributes to the validity and generalisability of results. We applied approaches to support continued participation among a sociodemographically diverse enrolled cohort of ~142,000 individuals in the randomised, controlled NHS-Galleri trial (NCT05611632), assessing the clinical utility of a blood-based multi-cancer early detection test over three rounds of annual screening.

Methods: Approaches used in the trial comprised: direct communications to participants to support appointment booking and attendance (letters, emails, text messages, phone calls); supporting communications for trial awareness (leaflets, local communications campaigns, community engagement); and operational activities to facilitate appointment booking and attendance (maximising booking accessibility, offering local clinic locations and convenient appointment times). Participant feedback and appointment booking data were collected throughout and used to dynamically adjust approaches.

Cohort retention was defined as the proportion of participants returning in Year 1 (Y1) and Year 2 (Y2) relative to enrolment (Year 0), in total and by demographic groups (age, sex, ethnicity, socioeconomic deprivation). Total cohort retention targets were set at 90.5% for Y1 and 82.4% for Y2, incorporating an estimated annual dropout (8%) and attrition from cancer death or diagnosis (1.5% in Y1, 1% in Y2), to ensure statistical power for the primary outcome of reduction in late-stage (III and IV) cancers.

Results: Of the enrolled participants, >91% returned for Y1 and >88% for Y2, exceeding total cohort retention targets. Retention was consistently strong across age, sex, socioeconomic and White ethnic groups, meeting or exceeding 88% in Y1 and 85% in Y2. Retention among non-White ethnic groups met or surpassed 80% in both Y1 and Y2. Analysis of appointment booking times relative to communications indicated that most participants booked an appointment after receiving their first letter.

Conclusions: Our approaches enabled retention of a diverse participant population in the NHS-Galleri trial. Total cohort retention exceeded targets and was better than typical retention for cancer screening trials.

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Poster #74

Molecular Cancer Signal Localization in Multi-Cancer Early Detection (MCED) Testing Minimizes Radiation and Imaging Burden Compared to Whole Body Imaging Approaches

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COMPANY/INSTITUTION:

GRAIL, Inc.

Background: Blood-based MCED tests enable detection of multiple cancer types from a single blood draw. Efficient strategies for diagnostic evaluation are needed to distinguish true positives (TPs) from false positives (FPs) with minimal burden and risk. Extending a previously published model (Tyson. JNCI Cancer Spectr. 2025), we compared 2 post-positive MCED test diagnostic resolution strategies: a Cancer Signal Origin (CSO)-guided approach with repeat MCED testing to resolve FPs (CSO-Retest Strategy) vs a Whole-Body Imaging (WBI)-Only Strategy employing WB computed tomography (CT) for test-positive individuals followed by positron emission tomography (PET)/CT scans to resolve FPs.

Methods: Model parameters reflected the performance characteristics of a contemporary, commercially available MCED test: 44.4% PPV; 99.5% specificity; and a single CSO prediction of 88.7% accuracy. Analyses evaluated 3 scenarios with varying test performance characteristics and specificities. The primary outcomes were the number of imaging procedures required and radiation exposure for each clinical strategy.

Results: Across all modeled scenarios, the CSO-Retest Strategy resulted in substantially fewer (10- to 20-fold) WB CT and PET scans vs the WBI-Only strategy, thereby reducing diagnostic burden and radiation exposure. A seemingly small reduction in WBI-Only test specificity by 1% led to a 3-fold increase in FPs and a more than doubling of WBI requirements. Estimated radiation exposure for initial diagnostic evaluations for the CSO-Retest Strategy ranged from 0–26.1 mSv, while all initial diagnostic evaluations for the WBI-Only Strategy had an obligatory exposure of 28 mSv. For the 50% of CSO predictions requiring initial imaging, dose exposure ranged from 0.28 mSv (mammography) to 26.1 mSv (triple-phase renal CT), or 1–93% of the dose required for the WBI-Only Strategy.

Conclusions: A CSO-guided diagnostic strategy incorporating targeted workups and MCED retesting to resolve FPs markedly reduces radiation exposure compared to a WBI-Only approach for individuals with a positive MCED test result. Small changes in specificity lead to significantly more individuals with unnecessary workups. Molecular CSO predictions use existing diagnostic pathways and, based on modeled data, improves patient safety while minimizing healthcare resource utilization. These findings have important implications for MCED test implementation, including radiation risk, cost, and accessibility.

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Poster #75

A novel mouse model for early detection of high-risk HPV-associated head and neck squamous cell carcinoma (HNSCC)

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Human papillomavirus-associated (HPV+) head and neck squamous cell carcinoma (HNSCC) surpassed cervical cancer as the most frequently diagnosed HPV-related malignancy in 2012, and its incidence continues to rise. Despite this growing disease burden, no screening tests are currently approved for the early detection of HPV+ HNSCC. Although HPV antibodies (HPV Ab) and circulating tumor HPV DNA (ctHPV DNA) have shown promise, limitations in sensitivity and specificity have hindered their clinical implementation. A major barrier to progress is the lack of well-defined precancerous lesions for HPV+ HNSCC, which has impeded biomarker development.

To address this gap, we developed a novel HPV16 transgenic mouse model using CRISPR/Cas9 to insert the full-length HPV16 genome into the Rosa26 locus. This insertion includes the upstream regulatory region (URR) containing viral promoters, regulatory elements, and the origin of replication—allowing comprehensive study of HPV-driven transformation and host interactions.

Given the clinical association between tobacco exposure and poorer outcomes in HPV+ HNSCC, we administered 4-nitroquinoline-1-oxide (4NQO) in drinking water for 12 weeks to both HPV16 transgenic and wild-type mice. Notably, only the HPV transgenic mice developed squamous cell carcinoma, lost significant weight, and exhibited multiple malignant and benign lesions, whereas wild-type mice developed only benign papilloma. This suggests the model effectively mimics high-risk HPV-associated HNSCC.

To establish xenografts and enable biomarker discovery, tumors from two HPV mice were transplanted, and blood samples were collected. Serum from tumor-bearing HPV mice showed significantly elevated levels of multiple cytokines and chemokines compared to both tumor-free HPV mice and wild-type controls, as assessed via a protein-based quantitative array.

HPV+ HNSCC is often diagnosed at a late stage after metastasis to lymph nodes. Our novel mouse model replicates key features of high-risk HPV+ HNSCC and offers a platform for the identification of early systemic biomarkers. This could pave the way for developing effective screening strategies and improving early diagnosis.

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Poster #76

Investigating the Impact of Heterozygous BRCA2 Mutations in the Tumor Microenvironment on PDAC Progression

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COMPANY/INSTITUTION:

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Pancreatic ductal adenocarcinoma (PDAC) is a highly lethal cancer, with a 5-year survival rate under ~13%, largely due to late detection and limited treatment options. While low-grade pancreatic intraepithelial neoplasia (PanIN) lesions often precede PDAC, most do not progress to malignancy. The factors that govern their transition to high-grade PanINs and invasive cancer remain poorly understood.

Germline BRCA2 mutations are present in 5–10% of PDAC patients and confer a 3–4-fold increased risk of developing the disease. While most cancers are thought to develop due to the "two hit hypothesis", where tumor suppressive genes lose their functioning wild-type allele, BRCA2-mutant PDACs form without this. This suggests that there are other external mechanisms at play to drive increased tumorigenesis. In breast cancer, heterozygous BRCA1 mutations in stromal cells have been shown to promote a pro-tumorigenic microenvironment that accelerates malignant transformation. Whether similar effects occur in pancreatic stroma remains unknown.

This study explores how heterozygous BRCA2 mutations in the pancreatic cell microenvironment influence and promote PanIN progression. We will use our validated multi cell type organoid cocultures and transcriptomic profiling to model the interplay between epithelial and stromal compartments in BRCA2+/– versus wild-type settings. Comparative analysis of these models, along with validation in human PanIN and PDAC tissue samples, will identify stromal factors that contribute to early disease progression.

Our work will provide new insights into how inherited BRCA2 mutations shape the microenvironment to promote tumorigenesis. These findings may reveal biomarkers of progression and targets for early interception in high-risk individuals, offering a path toward improved detection and prevention strategies for PDAC.

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Poster Pitch

Multi-Cancer Screening Using AI-Enhanced Canine Olfactory Detection: Interim Results from a Multi-Center Breath Analysis Study in India

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COMPANY/INSTITUTION:

Dognosis

Background: Early cancer detection remains a critical challenge in global healthcare, particularly in resource-limited settings. Canines possess exceptional olfactory capabilities for detecting volatile organic compounds (VOCs) associated with malignancy. We developed BreathEasy, an innovative screening platform integrating biomedical detection dogs with artificial intelligence to enable non-invasive, multi-cancer detection through breath analysis.

Methods: This prospective, double-blind, multi-center study was conducted across six hospitals in Karnataka, India. We employed specially trained detection dogs equipped with wireless EEG systems, motion sensors, and video monitoring. Breath samples were collected from treatment-naïve biopsy-confirmed cancer patients (cases) and three control groups: healthy individuals, chronic disease patients, and patients with benign tumors. Multiple dogs evaluated each sample using algorithmic aggregation logic, where individual neurobehavioral AI models graded each canine assessment and results were computationally combined. We present interim analysis from 750 participants (150 confirmed cancer cases, 600 controls) representing the midpoint of our 1,500-participant test cohort.

Results: The AI-enhanced canine detection system demonstrated 93% sensitivity and 84% specificity for multi-cancer detection. Performance remained consistent across cancer types and stages. Breath samples maintained stability for three months without requiring -80°C storage, demonstrating operational feasibility for resource-limited settings. The integration of machine learning models analyzing canine neural responses improved detection accuracy compared to traditional behavioral observation methods.

Conclusions: This study establishes the clinical validity of AI-enhanced canine olfactory detection for multi-cancer screening. The BreathEasy platform addresses critical requirements for the first layer of population-level screening, improving health equity initiatives in the Global South by curating a high-risk group for standard-of-care organ-specific screening.

Clinical Trial Registration: CTRI no. CTRI/2024/10/075938 registered on 25/10/2024 with first enrollment 5/11/2024 onwards 1 year period. Study title: Evaluation of multi-cancer screening through breath samples performed by biomedical detection dogs in India.

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Poster #78

Integrated Recruitment Strategies to Enhance Representation in a Large Colorectal Cancer Screening Study

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COMPANY/INSTITUTION:

Freenome Holdings, Inc.

Background: Clinical study participation remains disproportionately low among certain racial, ethnic and rural populations, highlighting gaps in access and inclusion (Oyer et al., 2022). The PREEMPT CRC study was the largest, prospective, multicenter observational study aiming to validate a blood based colorectal cancer (CRC) screening test, using inclusive strategies to broaden demographic and geographical representation. This analysis outlines the recruitment approaches used to support a diverse study population. Methods: PREEMPT CRC used both traditional clinical sites and a decentralized clinical trial (DCT) platform. A total of 200 traditional sites participated in the study, including academic centers, regional hospitals, community clinics, and research institutes. Several community-focused institutions, including University of Chicago and Morehouse School of Medicine, implemented culturally responsive strategies such as mobile research units, home visits, and community outreach. In parallel, the study employed a DCT metasite that enabled multichannel recruitment, through direct-to-participant via digital enrollment and site-based partners supported by principal investigators and clinic-based settings. Results: A total of 48,995 participants aged 45–85 years were enrolled, 11.2% of whom identified as Black/African American, 6.8% Asian, and 11.2% Hispanic/Latino. At the University of Chicago and Morehouse sites, 68.0% and 85.3% of participants identified as Black/African American, respectively. The DCT metasite enrolled 12,137 participants across 49 states, with 60.3% from major metro areas, 30.2% from metro areas, and 7.3% from nonmetro areas. A total of 9.6% identified as Black/African American, 2.0% as Asian, and 8.4% as Hispanic/Latino. The DCT metasite had a higher rate of loss to follow-up compared to traditional sites (11.9% vs. 0.1%). Conclusion: In the PREEMPT CRC study, an integrated recruitment approach that combined traditional sites with DCT methods supported broad demographic and geographical representation. The DCT approach expanded geographical reach but showed limited racial and ethnical diversity and included participants more prone to loss to follow-up. Traditional sites played a key role in enrolling a harder-to-reach population, highlighting the complementary strengths of both models. The study underscores the importance of early diversity planning and multimodal strategies to achieve diverse representation in clinical studies.

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Poster #79

Assessing the utility of predicted mortality as a surrogate endpoint in six lung cancer screening trials.

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Clinical effectiveness of cancer screening methods is often evaluated using randomised controlled trials with a cancer-specific mortality endpoint. This requirement usually needs a large sample size and a long follow-up time. Use of accepted surrogate endpoints could accelerate the implementation of effective screening technologies. Surrogate endpoints for cancer screening trials must be effective predictors of cancer-specific mortality endpoint with a shorter follow-up. Here we evaluate the utility of predicted mortality as a surrogate endpoint using individual-participant data from six US lung cancer screening trials.

The predicted mortality screening effect at a fixed time after randomisation is the ratio of the expected number of deaths between arms. We estimate five year predicted mortality using data on cancers diagnosed to analysis time, and external reference relative survival rates from sex, age, and stage at lung cancer diagnosis. Predicted mortality relative risk between screening arms (and 95% confidence intervals) is compared to observed lung-cancer mortality and late stage diagnoses within the trials.

In trials that concluded no beneficial effect of screening on lung cancer mortality we were able to reliably identify no effect of screening up to six years and up to three years earlier, than trialists did with mortality, using predicted mortality and late stage diagnoses respectively. In trials that showed a beneficial effect of screening on mortality predicted mortality fails due to over diagnosis in the intervention arm. When over-diagnosis is adjusted for there is no benefit gained from evaluating the trial earlier using predicted mortality.

Predicted mortality is likely not an effective surrogate endpoint for cancer mortality in lung cancer trials - this is likely because lung cancer is a very aggressive cancer with short expected survival following diagnosis. However, we hope that predicted mortality based on sex, stage, and age at diagnosis will work well as a surrogate for cancer mortality in screening trials of slower developing cancers such as prostate, colorectal, and breast cancer.

The data for this project are provided by the National Cancer Institute, and the Surveillance, Epidemiology, and End Results.

This work is part of a PhD project funded by the MRC-NIHR Trials Methodology Research Partnership.

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Poster #80

MCEDsim: a simulation platform for projecting the population impact of multicancer early detection testing

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Multi-cancer early detection (MCED) tests have the potential to greatly expand the number of cancers for which screening may be possible while reducing the first-line test to a simple blood draw. Many MCED products are under development and will be made available to the public ahead of definitive answers to key questions such as who should be screened, how often, and using which products. Development of well-informed screening policy demands reliable evidence. In absence of clinical trials examining screening strategies, rigorous modeling can fill evidence gaps.

We have developed a simulation modeling framework and R package, MCEDSim, that projects both short- and long-term outcomes of MCED testing in the population. MCEDSim utilizes built-in, pre-fit natural history models that have been calibrated to sex-, age- and stage-specific SEER incidence data. The package also includes pre-fit models to project cancer survival and life tables to project other-cause morality.

Users specify the sites in the test, ages and frequency of screening, the number of screened individuals, and the site-specific sensitivity for early- and late-stage disease. The package tracks outcomes for first cancers only, including stage and age at diagnosis and age at death. The package allows for an assessment of the reduction in late-stage disease under screening, the reduction in cancer-specific deaths, and the difference in total life years with and without screening. It also tracks cumulative false positive exams throughout the course of screening.

MCEDsim will serve as an objective resource for the 1) assessing screening benefits and harms in the population given test performance 2) design of screening trials. Ultimately, we see it as a building block for projecting the long-term effects of screening given data from short-term clinical trials.

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ABSTRACTS

Poster #81

Key Risk Factors for 5- and 10-Year Relative and Absolute Multi-Cancer Risk

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Background: Cancer remains a leading cause of death globally, with both incidence and mortality expected to increase. While numerous studies explore risk factors for individual cancers, less is known about risk factors across groups of cancer. The study aims to identify common risk factors for a pre-specified set of high mortality cancers.

Methods: Data from the American Cancer Society's Cancer Prevention Study II (CPS-II) and 3 (CPS-3) were used to identify risk factors for 9 pre-specified cancers (colon, rectum, lung, esophagus, stomach, ovary, pancreas, liver, bladder). Absolute risk of developing any of the 9 cancers within 5 years and 10 years were estimated among 401,002 and 151,540 participants, respectively, with no prior history of cancer. Multivariable Cox proportional hazards models estimated hazard ratios and 95% confidence intervals for associations with different risk factors and subsequently applied to estimate individualized coherent absolute risk by age for the pre-specified cancers.

Results: Over the 5- and 10-year follow-up periods 4,541 and 6,266 cases of the 9 pre-specified cancers were identified, respectively. In multivariate adjusted models, the 4 strongest risk factors for the pre-specified cancers were (in order of highest to lowest relative risk): current smoking, history of type II diabetes, body mass index >=30 kg/m2, and family history of any cancer. The absolute 5- and 10-year risk for the pre-specified cancers were highest in those who were positive for all 4 risk factors, with an absolute 5-year risk at age 50 of 0.9% for men and 0.6% for women. The absolute 10-year risk at age 50 was 1.6% for men and 1.3% for women. The absolute risks were lowest for those that did not have any of the 4 risk factors, with a 5-year risk at age 50 of 0.1% each for men and women, and a 10-year risk at age 50 of 0.3% for men and 0.2% for women.

Conclusion: The highest 5- and 10-year absolute risk for the pre-specified cancers was observed in individuals who currently smoke, had a history of diabetes, BMI of >=30 kg/m2, and a family history of cancer. This analysis demonstrates that beyond age, considering other risk factors could be beneficial to inform who may benefit from the emerging multi-cancer blood-based tests.

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ABSTRACTS

Poster #82

Multi-omic Profiling of Localised Prostate Cancer Reveals Early Lineage and Microenvironmental Reprogramming with Potential to Inform Risk Stratification

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Prostate cancer is clinically heterogeneous, with limited genetic driver mutations and variable outcomes. To better understand early regulatory changes and identify biomarkers for aggressive disease, we performed epigenomic and transcriptomic profiling of localised prostate cancer samples and used fluorescence-activated cell sorting to resolve cell-type contributions to the tumour methylome.

Based on the methylation profile of 184 tumour-normal pairs, we identify two methylation-defined tumour subtypes ("mevotypes") that recapitulate the known genomic evolutionary trajectories – one enriched for ETS fusions and another for SPOP mutations, implying a genomic-epigenomic crosstalk during tumour evolution.

By deconvoluting the methylation changes in bulk tumours using our cell-specific methylomes as reference, we find that most tumour-specific differentially methylated regions predominantly arise in luminal epithelial cells, followed by stromal and immune cells. Interestingly, the luminal-specific methylation changes are associated with neuronal development and lineage plasticity, despite the samples being treatment-naïve adenocarcinomas. We corroborated our results with publicly available single-cell and spatial transcriptomic datasets and validate that these quasi-neuroendocrine features are associated with luminal subpopulations that are more aggressive, later pseudotime trajectory, and are spatially enriched in the tumour foci. This suggests an early reprogramming that persists in and may influence cancer progression.

Moreover, our integrated multi-omic analyses also highlight epigenetic reprogramming of the tumour microenvironment. Our results show that methylation changes originating from stromal and immune compartments map to extracellular matrix, pro-angiogenic, and immune invasion pathways and are also spatially co-located within the tumour niche.

Together, this work defines the cellular origin of epigenetic alterations in prostate cancer and suggests that early methylation events encode both tumour plasticity and microenvironmental adaptation. These features may support the development of liquid biopsy strategies for risk stratification of aggressive disease.

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Poster #83

Decomposing the Causal Chain of Cancer Screening

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Background: Cancer screening trials such as NLST, PLCO, and DANTE report mixed findings. While some trials show benefits via increased preventive therapy, others find no mortality reduction. These discrepancies may stem from differences in downstream treatment and healthcare infrastructure. However, no trials explicitly model the full causal chain from screening to mortality. This omission limits our ability to determine whether results from one setting can apply to another, known as transportability in causal inference. By comparing treatment and disease severity distributions between trial and target populations, transportability methods enable us to predict, a priori, whether a screening intervention's effect will replicate in a new setting.

Methods

We develop a novel structural framework that models the pathway from screening S to outcome Y, mediated by disease severity D, symptom burden X, and treatment T. This approach enables decomposition of the observed effect of screening into interpretable causal components.

Results

The naive estimate of the effect of screening on outcomes, E[Y=1 |S=1] - E[Y=1 | S=0], captures the average effect only under strong assumptions. Decomposing this effect yields terms like the differential treatment probability, P(T=i|(S,X,D) = (1,x,d)) - P(T=i|(S,X,D) = (0,x,d)), and prevalence-weighted outcome expectations, E[Y|(T,S,X,D) = (t,s,x,d)]. These terms illustrate that treatment behaviors, symptoms, and disease severity all impact observed outcomes even under randomized screening. Most cancer screening trials do not report these necessary variables.

Discussion

Transportable trial findings require more than randomization. Without stratified reporting of treatment and disease variables, it remains unknown whether the effects transport to new populations. Our framework provides a quantitative basis for identifying when cancer screening will deliver benefit and when it may fail to translate across contexts. To enable transportability, screening trials must move beyond reporting average effects. Instead, they should publish outcomes stratified by all causal factors linking screening to mortality, especially treatment, which is often unreported or inconsistently applied across trials. These details enable decomposition of the screening effect and estimation of how well it transfers to new populations.

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Poster #84

RECAST: A Novel Platform Trial Combining Active Surveillance and Endocrine Therapy to Investigate Alternative Strategies for DCIS Management and Breast Cancer Prevention

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Ductal carcinoma in situ (DCIS) is a biologically heterogeneous, non-invasive breast condition characterized by the proliferation of malignant epithelial cells confined within the milk ducts, with variable risk of progression to invasive carcinoma (IDC). Standard of care treatment for DCIS includes breast-conserving surgery and radiation therapy or mastectomy to prevent progression from in situ to invasive carcinoma and endocrine therapy to further reduce the risk of recurrence. However, many cases of DCIS may never progress to invasive disease and thus may be overtreated. Active surveillance (AS) is standard for GG1 prostate cancer and is emerging as an option for DCIS. Affecting 50,000-60,000 women annually in the US, DCIS is an opportunity to study preventative interventions and to determine who can be spared surgery. RECAST (Re-Evaluating Conditions for Active Surveillance Suitability as Treatment) is a Phase II platform trial studying neoadjuvant endocrine therapy as an alternative to surgical treatment of hormone receptor-positive DCIS, aiming to ascertain who is a good candidate for active surveillance with endocrine therapy alone and those who have focal disease best treated with surgery. Patients with any grade ER+ or PR+ DCIS are randomized to one of four hormonal therapies, including novel endocrine agents with the potential to increase efficacy and decrease toxicity compared to traditional endocrine therapy. Serial MRI is used to evaluate background parenchymal enhancement (BPE), lesion distinctness from BPE and change in lesion and BPE over time while on endocrine therapy. One aim is to establish MRI biomarkers to assess risk of progression to IDC. Patients at low risk based on imaging can continue on AS and be spared surgery and radiation. The trial design reorders endocrine therapy to the neoadjuvant setting, enabling investigators to identify response to endocrine therapy, characterize risk of progression to IDC, and to inform treatment decision-making before continuing with AS or proceeding with surgery. Beginning enrollment in January 2024, 50 patients have enrolled and 9 are now being screened across 11 active sites, with 10 additional sites planned for activation. RECAST is a novel trial that offers every woman a safe opportunity to determine if they are suitable for non-surgical DCIS management and serves to better understand and overcome resistance to endocrine therapy, leading to better interventions for breast cancer prevention.

ABSTRACTS

Poster #85

Poster Pitch

E.N.G.A.G.E.: A Collaborative Model for Diverse Clinical Research Empowerment, Navigation, Growth, Access, Guidance, and Equity

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COMPANY/INSTITUTION:

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Background: Just 2% of the 10,000+ NCI clinical trials achieve sufficient diversity. Early detection trials face unique challenges compared to treatment trials in achieving diversity: they are not offered in clinical settings and require large cohorts of healthy individuals.

Objective: Intentionally integrating Community Outreach & Engagement (COE) and clinical trial teams to increase geographic, racial, and ethnic diversity in early detection trial enrollment. Comparison of two sequential MCED blood-test trials at OHSU Knight Cancer Institute's Cancer Early Detection Advanced Research program (CEDAR); one conducted prior to integration and one after. Both trials returned results to participants. We demonstrate the power of bringing each group's unique skills and expertise together in collaboration for the benefit of the community.

Methods: Trial 1: Recruited patients at OHSU hospital. We exceeded enrollment goals, but the cohort lacked diversity. Trial 2: We engaged four remote health systems serving diverse communities and local metro-area partners. The COE team collaborated with longstanding community partners early using the Research in Oregon Communities Review System (ROCRS) to assess subsite feasibility and community readiness. The system facilitated community-led obstacle identification, recommendations for regionally appropriate trial recruitment and implementation, and ultimately making a trial Go/No-Go determination. The integrated trials/COE team implemented various strategies to overcome barriers to recruitment and encourage participation, including cross-training, culturally appropriate materials development, and outreach events.

Results: Collaborative problem solving with the community led to an adapted approach to recruitment and enrollment in Trial 2, which resulted in marked improvements over Trial 1:

Racial diversity increase: 6% to 26% (>4x) Ethnic diversity increase: 0.4% to 11% (>20x) Rural enrollment increase: 10% to 37% (≈4x)

Long-term community partnerships established: new clinical trials launched (e.g., two new clinical trials at Southern OR subsite) and cancer prevention education expanded.

Conclusions: Early, intentional integration of COE and trial teams is effective in diverse cohort recruitment. Early detection trials are not a fad; relying on established relationships is essential to equitable access and representative cohorts. This requires time and resources to build sustainable, long-term partnerships.

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Poster #86

Effectiveness of HPV Self-Collection for Cervical Cancer Screening in Community Outreach Programs

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Context: Nearly all cervical cancers are caused by persistent infection with high-risk human papillomavirus (HPV). HPV testing detects high-risk types earlier and more accurately than cytology. A 2014 meta-analysis in The Lancet Oncology found HPV testing has 60–70% greater sensitivity than Pap smears in detecting CIN2+ (precancerous lesions). Despite these advantages, disparities in cervical cancer screening remain. Southeast Asian women have the lowest screening rates, particularly among recent immigrants and older women. Cultural stigma, low health literacy, and language barriers contribute to under-screening. Latino, Black, and Southeast Asian women are more often diagnosed at later stages, likely due to reduced access to follow-up care. On May 14, 2024, the FDA approved self-collected vaginal samples for HPV testing in clinical settings, offering new opportunities to expand screening access.

Objective: To evaluate the feasibility and acceptability of HPV self-collection through a pathologist-led outreach initiative in Oregon.

Design: From October 2024 to June 2025, women aged 25–65 were recruited through partnerships with local organizations. Participants used pathologist-supervised self-collection kits (Copan swabs in ThinPrep media), tested via the Cobas 8800 for 14 high-risk HPV types. Surveys assessed usability and access to traditional screening.

Results: Among 156 participants (mean age 47.1), 87 identified as Hispanic or Latino, 33 as Asian, 16 as Black, and 14 as White. All samples were valid. Of these, 146 (94%) tested negative, one was positive for HPV-18, and nine for other high-risk types. HPV-positive participants received follow-up instructions. Follow-up identified one case of CIN1, two with normal cytology, and others pending. Among 129 survey respondents, nearly 90% found the kit easy or very easy to use, and a similar proportion would recommend it. While 55.8% preferred self-collection, 29.5% were neutral. Participants mentioned convenience, comfort, and privacy as main advantages.

Conclusions: HPV self-collection is an effective strategy for early cervical cancer detection and reducing screening disparities among Latino, Black, and Asian women. It improves access and acceptability, especially for those facing barriers to clinic-based care. Community-based, pathologist-led initiatives build trust and enhance outreach effectiveness.

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Poster #87

Scaling Up: A flexible framework to guide early development of biomarker-based classifiers

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The early detection and precision treatment of cancer remains one of the most critical challenges in oncology, requiring innovative approaches that integrate biomarker discovery with machine learning-based classification. Multi-marker classification models have the potential to identify individuals with preclinical early-stage cancer or precancerous conditions and, after diagnosis, to guide the selection of the most effective treatment strategies. Despite their potential, the translation of biomarker panels from the laboratory to clinically useful classification tool faces several challenges. Classifier development may take place in the context of technology development to measure the biomarkers themselves. Lack of integration of data quality assessment into classifier development inhibits identification of technical variability (low signal-to-noise) early in the process and ultimately impairs classifier performance. The development of multimarker classifiers is also hindered by small sample sizes and a lack of rigorous statistical methodologies. When training set sample sizes are too small, the classifier's performance is limited, and models trained on such datasets are more prone to overfitting. Moreover, estimates of out-of-sample performance through cross-validation can be biased due to data leakage, where the training and testing datasets are insufficiently separated. As a result, many multimarker classifiers that demonstrate initial promise in pilot studies may fail to generalize to broader, external populations. To address this challenge, we propose a framework and a set of tools designed to guide biomarker projects from the pilot phase to clinical translation. By systematically evaluating classification studies in their early phases, this framework will enhance decision-making, optimize resource allocation, and improve the overall trajectory of promising biomarker-based classifiers. Unlike existing frameworks that primarily focus on identifying individual biomarkers and overall study design, our approach explicitly provides sample size guidance for multimarker classifier development, addressing a critical gap in current methodologies. Scaling Up will be useful to the research community in interpreting signal from small studies and planning larger-scale studies to optimize classifier performance.

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Poster #88

Patient-derived Models of BRCA2 Hereditary Prostate Cancer to Inform Early Detection and Interception Strategies

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Inherited defects in DNA damage & repair (DDR) genes predispose to lethal prostate cancer. Germline BRCA2 (gBRCA2) mutations confer an 4-9 fold increased risk of developing high-risk localised prostate cancer. In cases not cured by surgery/radiotherapy, patients with gBRCA2 tumours in the M0 setting have increased mortality (5 year cancer-specific survival of 50-60% vs 90% for sporadic localised prostate cancer). Arguably, this group of patients would benefit from early detection and interception with PARP inhibition or prophylactic prostatectomy as potential control measures. Further understanding of gBRCA2 tumourigenesis & progression is required to help discriminate progressive tumours requiring intensive treatment vs those suitable for standard of care or active surveillance. As comprehensive trials in these rare localised populations is challenging, there is need for pre-clinical gBRCA2 models to study tumour evolution and evolution-blocking interception approaches. To study the earliest events of BRCA2 genetic instability and transformation, we have established immortalized prostate epithelial cell (PrEC) cultures using tissue samples taken from gBRCA2-carrier patients undergoing radical prostatectomy. CRISPR editing of BRCA2 exon 27 (which encodes a RAD51 binding domain) was then used to target the wild-type allele present in gBRCA2 carrier PrECs, thereby creating a hypomorphic allele. Compared to isogenic heterozygote controls, BRCA2-deficient clones exhibited a significant loss of RAD51 foci, increased sensitivity to Olaparib and Mitomycin C, but only a mild radiosensitive phenotype. These cells proliferate at a reduced rate with cell cycle and S-phase specific analyses suggesting ongoing DNA replicative stress. Transcriptomic and proteomic studies suggest defects in the Rad50/54 DDR pathways. BRCA2-deficient clones exhibit increased genome instability compared to isogenic controls, and acquire copy-number changes characteristic of gBRCA2 localized prostate tumours. BRCA2-deficient PrECs are non-tumourigenic in nude mice. Thus we have introduced somatic driver mutations (TP53 loss/MYC expression) to examine cellular transformation in this context.

These are the first models of BRCA2-deficient cell evolution in primary prostate cells allowing examination of heterogenous BRCA2-dependent tumour phenotypes. They will better inform chemoprevention/interception approaches married to early detection and improve outcomes in this high risk setting.

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ABSTRACTS

Poster #89

A blood-based low-cost MCED test to assist cancer diagnosis in patients with tissue masses

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COMPANY/INSTITUTION:

Research & Development, SeekIn Inc

Background: Delayed diagnosis of cancer lead to advanced-stage presentation, contributing to increased patient anxiety, healthcare costs, and mortality. Early detection enables timely intervention, improving outcomes. OncoSeek is an AI-powered multi-cancer early detection (MCED) test with a reagent cost of $25. It integrates seven protein tumor markers (PTMs) and clinical data and has previously demonstrated 58.4% sensitivity, 92.0% specificity, and 70.6% tissue-of-origin accuracy in studies involving over 15,000 individuals. This study investigates its novel application in aiding cancer diagnosis among outpatients presenting with tissue masses.

Methods: We prospectively enrolled 732 outpatients with tissue masses referred for cancer diagnosis and treatment, and recruited 355 non-cancer individuals as controls. Plasma/serum PTM levels were measured, and probability of cancer (POC) indexes were calculated using a machine learning algorithm to distinguish malignancies from benign tumors. To enhance sensitivity and reduce false negatives in this symptomatic cohort, a lower cutoff was applied, targeting 80% specificity.

Results: Among patients with tissue mass, OncoSeek correctly identified 445 of 682 confirmed cancers, with a cancer detection rate of 65.2%, comparable to the 66.3% sensitivity reported in the SYMPLIFY study, a prospective study in symptomatic patients referred from primary care. The assay detected 15 cancer types, including bile duct, breast, cervix, colorectum, endometrium, esophagus, gallbladder, head and neck, liver, lung, lymphoma, ovary, pancreas, prostate, and stomach. Sensitivity increased with cancer stage: 40.4% in stage I, 61.2% in stage II, 72.7% in stage III, and 86.0% in stage IV. Notably, POC index levels were significantly higher in cancer patients compared to those with benign tumor (n=50; $p < 0.001$), while no significant difference was observed between benign tumor patients and non-cancer individuals ($p > 0.05$), supporting the test's discriminatory capability.

Conclusion: OncoSeek demonstrated strong clinical utility in evaluating patients with tissue masses, achieving 65.2% sensitivity and robust discrimination between malignant and benign lesions. This supports its potential role in expediting cancer diagnosis and mitigating diagnostic delays.

ABSTRACTS

Poster #90

OncoSeek 2.0, an upgraded blood-based test for better sensitivity of multi-cancer early detection

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COMPANY/INSTITUTION:

Research & Development, SeekIn Inc

Background: Early cancer detection improves survival and reduces treatment costs. We previously developed OncoSeek, an AI-powered cost-effective ($25 reagent cost) multi-cancer early detection (MCED) test integrating seven protein tumor markers (PTMs) and clinical data, demonstrating 58.4% sensitivity, 92.0% specificity, and 70.6% tissue-of-origin accuracy in several clinical studies (n=15,122). This study aimed to enhance OncoSeek by incorporating three additional PTMs to improve detection in prostate, lung and various squamous cell carcinomas especially, upgrading it to version 2.0 ($31), and to validate its improved sensitivity.

Methods: The same OncoSeek algorithm was used to develop OncoSeek 2.0. A retrospective cohort was conducted to validate OncoSeek 2.0's MCED performance and assess sensitivity improvements, involving 585 cancer patients and 355 non-cancer individuals. Plasma/serum PTM levels were analyzed, and probability of cancer (POC) indexes were calculated to distinguish cancer patients from non-cancer individuals.

Results: OncoSeek 2.0 outperformed OncoSeek 1.0, achieving an AUC of 0.895 (vs. 0.849 for 1.0). At 90.1% specificity, sensitivity increased from 74.7% to 80.3% for 15 cancer types, which collectively account for accounting for 76.5% of global cancer-related mortality in the United States. Among these cancers, only five (breast, cervix, colorectum, lung, and prostate) have screening methods recommended by the United States Preventive Services Task Force (USPSTF). For the remaining 10 cancers without USPSTF-recommended screening (bile duct, endometrium, esophagus, gallbladder, head and neck, liver, lymphoma, ovary, pancreas, and stomach), OncoSeek 2.0 achieved a sensitivity of 86.4% at 90.1% specificity. Moreover, OncoSeek 2.0 showed substantial stage-specific sensitivity improvements over OncoSeek 1.0, especially for early-stage cancers: stage I sensitivity increased from 38.9% to 55.6%, stage II from 55.2% to 65.5%, stage III from 62.7% to 71.1%, and stage IV from 87.2% to 88.7%.

Conclusion: OncoSeek 2.0 achieved a 7.5% increase in overall sensitivity for all stages, with significant improvements in early-stage cancers: stage I and stage II sensitivities increased 42.9% and 20.5%, respectively. These findings suggest that OncoSeek 2.0 could become a valuable tool for multi-cancer early detection, especially for cancers lacking established screening guidelines.

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ABSTRACTS

Poster #91

A cost-effective two-step approach for multi-cancer early detection in risk-elevated populations

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COMPANY/INSTITUTION:

Research & Development, SeekIn Inc

Background : Effective population-wide cancer screening requires a careful balance between sensitivity, specificity, and cost. High false positive rates can lead to unnecessary procedures and strain healthcare resources, while high costs may hinder widespread adoption. Established two-step screening paradigms, such as prostate cancer screening with prostate-specific antigen (PSA) followed by magnetic resonance imaging (MRI), and colorectal cancer screening with fecal immunochemical testing (FIT) followed by colonoscopy, illustrate how sequential testing can optimize accuracy and resource use.

Methods : We evaluated a two-step multi-cancer early detection (MCED) approach. The initial screen used OncoSeek, a MCED test that combines a panel of seven plasma protein tumor markers (PTMs) with artificial intelligence (AI). Individuals with positive OncoSeek results then underwent an NGS-based multi-omics MCED test, SeekInCare, which offers higher performance.

Results : In a retrospective study (617 cancer, 580 non-cancer), OncoSeek alone achieved 63.4% sensitivity at 80.0% specificity. When positive OncoSeek cases were followed by SeekInCare, specificity increased to 99.0%, with sensitivity reduced to 46.2%. The two-step approach closely matched to the performance of SeekInCare alone, achieving 60.0% sensitivity at 98.3% specificity.

In a prospective cohort consisting of 1203 individuals who received the tests as laboratory-developed tests (10 cancer, 1,193 non-cancer; median follow-up time, 753 days), OncoSeek showed 50.0% sensitivity at 83.8% specificity. The two-step approach reduced the false-positive rate from 16.2% to 1.8% (98.2% specificity), while maintaining comparable sensitivity (40.0%). Although the two-step approach's sensitivity was lower than SeekInCare (70.0%), it offered higher specificity (98.2% vs. 95.2%). Importantly, due to OncoSeek's lower cost ($80 per test), the two-step approach's cost of per individual screened was reduced to $190, a 3.9-fold decrease compared to SeekInCare alone ($750). These real-world findings were consistent with the simulation results in our previous publication.

Conclusion : The two-step MCED approach using OncoSeek followed by SeekInCare substantially reduces false positives and overall screening costs, with only a modest reduction in sensitivity. This strategy offers a cost-effective solution for large-scale cancer screening, balancing accuracy with healthcare resource optimization.

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Poster #92

Reducing false positives in protein tumor marker-based cancer detection: AI-integrated and sequential testing strategies

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Research & Development, SeekIn Inc

Background: Protein tumor markers (PTMs) have been widely used in clinical practice for decades due to their cost-effectiveness and ease of implementation. However, they are primarily utilized for disease monitoring rather than cancer early detection, largely due to their high false-positive rates. While combining multiple PTMs improves sensitivity for multi-cancer detection, this often leads to cumulative false positives, as each marker is interpreted independently based on fixed thresholds.

Method: To address this limitation, we developed an artificial intelligence (AI)-based model, OncoSeek, which integrates seven PTMs into a single predictive score to reduce false positives while preserving sensitivity. To further reduce the false positives, two sequential testing strategies were evaluated: (1) repeat OncoSeek testing to exclude transient positives; and (2) a reflex testing approach using a multi-omics confirmatory test (SeekInCare) for OncoSeek-positives. OncoSeek and the reflex testing was validated in a retrospective cohort (617 cancer, 580 non-cancer; 27 cancer types). Additionally, a prospective study (n=115) was conducted to evaluate repeat testing.

Results: In the retrospective cohort, conventional PTM threshold-based method yielded 64.5% sensitivity at 65.7% specificity. In contrast, the AI-based mothed (OncoSeek) alone identified 360 individuals as positive, including 308 cancer cases and 52 false positives, achieving 49.9% sensitivity at 91.0% specificity (false-positive rate reduced from 34.3% to 9.0%). When combined with SeekInCare as a confirmatory test, 111 out of 360 positives were reclassified as negative, including 48 false positives. The reflex testing effectively eliminated 92.3% (48/52) of false positives, raising specificity to 99.3% while maintaining a sensitivity of 39.7%. In a prospective cohort of 115 individuals, 21 tested positive by OncoSeek and underwent repeat testing. Six converted to negative and remained cancer-free at 12-month follow-up. Among the remaining 15, two diagnosed with cancers, indicating that repeat testing excluded 31.6% (6/19) false positives.

Conclusion: AI-driven integration of multiple PTMs (OncoSeek) provides a cost-effective strategy for multi-cancer detection, reducing false positives to 9%. Sequential testings—via repeat testing and reflux testing—would further reduce false positives to under 1%, while maintaining sufficient sensitivity, supporting real-world clinical applicability.

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Poster #93

Poster Pitch

Baseline participant characteristics from PATHFINDER 2, a prospective interventional study of a multi-cancer early detection test in a population setting

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A blood-based multi-cancer early detection (MCED) test has demonstrated feasibility as a screening tool in large-scale clinical trials. The PATHFINDER 2 (PF2) study (NCT05155605) evaluates safety and performance of the MCED test in a diverse intended-use population. To gauge generalizability of study results, we assessed participant (ppt) baseline characteristics vs general US population data from the National Health and Nutrition Examination Survey (NHANES).

PF2, a prospective, multicenter, interventional study, enrolled ppts aged ≥50 y from diverse clinical settings in North America. Enrollment targets for sex and race/ethnicity were established from the 2019 American Community Survey (US Census Bureau). Recruitment strategies were implemented to maximize enrollment for groups historically underrepresented in clinical studies. Exclusion criteria included clinical suspicion of cancer or cancer diagnosis/treatment within 3 y. Data on baseline characteristics and key cancer risk factors were collected at enrollment. We compared the PF2 study population to a nationally representative sample of US adults aged ≥50 y from 2017-2020 NHANES data. NHANES data were weighted using complex, multistage probability sampling to generate a nationally representative sample.

There were 35,878 ppts enrolled in PF2; 35,307 clinically eligible and evaluable ppts were included in this analysis. Mean age was 64 y for both PF2 and NHANES; 56.2% were females in PF2 vs 53.6% (95% CI 52.0-55.3%) in NHANES. Race/ethnicity distribution for PF2 vs NHANES was 7.4 vs 11.0% (8.9-13.1%) Hispanic, 74.6 vs 69.7% (65.0-74.5%) non-Hispanic (NH) White, 8.6 vs 10.3% (7.6-13.1%) NH Black, and 5.8 vs 5.1% (3.5-6.8%) NH Asian. In terms of lifestyle characteristics for PF2 vs NHANES, 58.9 vs 29.2% (25.8-32.7%) had at least a bachelor's degree, 74.8 vs 63.8% (60.6-67.0%) were married/living with a partner, 69.3 vs 53.8% (50.9-56.7%) had never smoked, 66.5 vs 70.4% (68.0-72.8%) were overweight/obese, and 24.2 vs 28.4% (26.4-30.3%) reported never using alcohol.

PF2 enrolled a diverse ppt population that is reasonably reflective of the demographics of the US population aged ≥50 y. As is typical for clinical trials, a higher percentage of PF2 vs NHANES ppts reported lifestyle characteristics associated with better health. As the study population largely reflects the MCED test intended-use population, safety and performance results from PF2 are expected to reflect real-world clinical experience.

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ABSTRACTS

Poster #94

Lightning Talk

Germline Runx1 mutations in cooperation with Tet2 loss-of-function promote the fitness and self-renewal of progenitors, dysregulating hematopoiesis via cell intrinsic and extrinsic mechanisms.

PRESENTING AUTHOR:

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AUTHORS:

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COMPANY/INSTITUTION:

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RUNX1-Familial platelet disorder (FPD) from germline RUNX1 mutations present a life-long risk for platelet dysfunction and leukemia (~50%). Subsequent mutations are more common in RUNX1-FPD individuals with TET2 as the 2nd most mutated gene. It is unknown how or if TET2 mutations in FPD patients skew hematopoiesis and expand. We used Runx1R188Q/+ Scl-Cre-ERT2 Tet2fl/+ (Runx1mutTet2het) to provide a tamoxifen-inducible model of Tet2 deletion in the Runx1 germline background in hematopoietic stem and progenitor cells (HSPCs). In vivo, Runx1mutTet2het mice exhibit increased long-term hematopoietic stem cells relative to Runx1mut cells, implying a competitive fitness advantage exists. Accordingly, we observed Runx1mutTet2het outcompete Runx1mut when cocultured vitro and within an in vivo competitive transplant in the peripheral blood (PB) and BM. Mechanistically, Runx1mutTet2het HSPCs had increased colony-forming ability relative to Runx1mut HSPCs, demonstrating enhanced self-renewal capacity. We examined HSPC differentiation and found lineage bias, with Runx1mut and Runx1mutTet2het expanding absolute numbers of erythroid/megakaryocyte biased multipotent progenitor 2's (MPP2s) in the bone marrow (BM) compared to WT. Accumulation of BM MPP2s may result from impaired function, as they exhibited reduced frequency of proliferating cells as identified by BrdU uptake in Runx1mut (35.9±5.0%) and Runx1mutTet2het (47.2±13.8%) relative to wild type (WT) (76.6±6.6%). At the subsequent differentiation stages, bias persisted in Runx1mutTet2het relative to Runx1mut; CMPs, 5.83±1.30-fold, GMPs, 1.73±0.15-fold and MEPs, 5.82±1.29-fold. Competitive transplantation confirmed myeloid bias intrinsic to Runx1mutTet2het, and showed cell extrinsic myeloid bias was enhanced in Runx1mut recipients relative to WT recipients.

Despite extensive dysregulation of differentiation, Runx1mutTet2het exhibits normal PB parameters compared to Runx1mut or Tet2het mice. For example, Tet2het exhibits a neutrophil bias over WT (24.7±1.2 % vs 18.7±1.8%, q=0.004), but Runx1mutTet2het and Runx1mut do not. Similarly, Runx1mut exhibits an eosinophilic bias over WT, but Tet2het and Runx1mutTet2het do not. Similar corrections were observed in mean platelet volume, defective platelet coagulation and mean corpuscular hemoglobin. Cumulatively, these data suggest that TET2 loss-of-function expands by self-renewal and is may be detectable by the normalization of PB parameters.

ABSTRACTS

Poster #95

Poster Pitch

Multi-omic profiling of ovarian cancer serum in a population of individuals experiencing vague abdominal symptoms

PRESENTING AUTHOR:

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AUTHORS:

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COMPANY/INSTITUTION:

AOA Dx

Ovarian cancer (OC) is the fifth leading cause of cancer-related deaths in women, with most cases detected at late stages (III/IV) when five-year survival is <30%. This is due in part to vague abdominal symptoms common in non-cancerous disorders (ex. gastrointestinal, gynecological) that confound diagnosis. There is a lack of adequate clinical diagnostic assays and robust biomarkers designed for early-stage OC when symptoms present. Mass spectrometry (UHPLC-MS) offers a powerful tool for early cancer detection, but the metabolome and lipidome of OC remains understudied. We performed multi-omic profiling of serum from all stages and subtypes of OC and non-cancerous conditions representing women experiencing VAS.

We conducted multi-omics analysis of serum from a clinically annotated biomarker discovery cohort using UHPLC-MS untargeted metabolomics, lipidomics, and proteomics. Specimens were obtained from the University of Colorado Gynecologic Tissue and Fluid Bank and commercial vendors. This cohort was designed to reflect the symptomatic population: OC (N=80 early-stage, N=139 late-stage, classified as "cancer"), benign gynecological disorders (complex adnexal masses, endometriosis, etc., N=168), gastrointestinal disorders (N=50), and healthy donors (N=82), classified as "controls".

Metabolic and lipidomic profiling showed unique signatures for OC serum, with PLSDA demonstrating clear separation between cancer and controls. Lipid classes driving separation included phospholipids, sphingomyelins, and ceramides. We also observe alterations in the gangliosome, especially disialo-gangliosides GD1 and GD2, significant decreases in amino acids, and significant increases in fatty acids and acyl-carnitines. These alterations suggest OC serum reflects energetic dysregulation to support tumor cell growth.

We identified a unique multi-omic profile in OC serum compared to serum from individuals experiencing VAS. Many of the most significantly altered metabolites have previously been implicated in OC. Combining lipids, metabolites, and proteins may offer a novel diagnostic avenue that improves upon the standard of care for earlier detection of OC and improved patient outcomes. Future studies will interrogate the mechanisms behind this unique profile with the goal of understanding the metabolic underpinnings that differentiate non-cancer from OC.

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ABSTRACTS

Poster #96

Multimodal cell free DNA epigenetic sequencing for early detection of pancreatic cancer

PRESENTING AUTHOR:

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AUTHORS:

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COMPANY/INSTITUTION:

University of Oxford

Background: 80% of pancreatic ductal adenocarcinoma (PDAC) are diagnosed in late stage with <10% 5 year survival. Epigenetic modifications which regulate gene expression are promising biomarkers for cancer detection in cell free DNA (cfDNA). 5-hydroxylmethylcytosine (5hmC) is increasingly recognised to have regulatory functions and distinct patterns in cancer. We previously developed TET-assisted pyridine borane sequencing (TAPS) and chemical-assisted pyridine borane sequencing (CAPS+), a library of bisulfite-free DNA methylation sequencing technologies which detect modified cytosines with non-destructive chemistry, preserving cfDNA for combined genomic and epigenomic analysis and improving mapping rate and coverage, and demonstrated the promise of cell free TAPS in cancer detection.

Aims: We expand our approach with the first application of CAPS+ to cfDNA 5hmC sequencing and first integrated 5hmC and 5mC specific analysis of cfDNA using cfTAPS and cfCAPS+. We investigate their capability, alongside fragmentomics, in early detection of PDAC.

Methods: Plasma samples from 16 PDAC, 17 hepatocellular carcinoma (HCC), and 10 control patients underwent cfCAPS+ and cfTAPS+ sequencing. Multilayer perceptron models were trained using leave-one-out cross validation. Multimodal classifiers were constructed by averaging scores from individual classifiers.

Results: cfCAPS+ sequencing had average mapping rate of 94.5%, conversion rate of 93.7% and false positive rate of 0.13%. 5hmC signal across gene bodies could distinguish PDAC from control with AUC 0.79, with feature importance revealing genes known to be involved in tumour development. Predictive performance was robust to downsampling to 3x sequencing depth. Fragmentation profile obtained from cfCAPS+ retained expected peaks and 10bp nucleosome periodicity, with shift to shorter fragments in cancer. A multimodal classifier integrating 5hmC and 5mC across all gene bodies and fragmentomics achieved AUC 0.85, superior to individual classifiers (improved to 0.89 with pancreas specific gene bodies). A 3-way multimodal classifier integrating 5hmC across all gene bodies and fragmentomics distinguished PDAC, HCC and control with >70% accuracy for each cohort.

Conclusions: cfCAPS+ provides high quality, sensitive and specific sequencing data, preserves DNA for multiple modality analysis, and has utility in shallow sequencing. A multimodal approach using 5hmC, 5mC and fragmentation can accurately discriminate early PDAC.

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ABSTRACTS

Poster #97

Poster Pitch

Using Dielectrophoresis to Isolate Tumor-Derived Nanoparticles from Human Plasma for Biomarker Discovery and Cancer Detection

PRESENTING AUTHOR:
Sarah Mitchell

AUTHORS:
Sean Hamilton, Stuart Ibsen

COMPANY/INSTITUTION:
Oregon Health and Science University

Survivability of many solid tumor malignancies is significantly increased when diagnosed early, but early-stage diagnosis is limited by the sensitivity and invasiveness of traditional diagnostic techniques. The use of minimally invasive liquid biopsy can provide an avenue for the early detection of solid tumor malignancies, including pancreatic ductal adenocarcinoma (PDAC) which is generally metastatic at diagnosis from late-stage symptom manifestation. In early-stage PDAC tumors, necrotic regions develop from the hypoxic environment and trigger cellular lysis events, releasing cellular components directly into circulation that are fragmented by shear forces into smaller biological nanoparticles carrying disease information from the site of the tumor. Traditional isolation techniques have difficulty recovering these small, low buoyant density cellular fragments, but the recovery of these fragments from plasma for biomarker characterization is achievable with dielectrophoresis (DEP). DEP is an emerging technique where a nonuniform electric field manipulates the spatial orientation of nanoparticles. Coupled with immunofluorescent staining in a microchip system, it is possible to isolate circulating tumor material and characterize cancer-specific biomarkers for diagnostic applications. Using only 30µL of cancer plasma or cell lysates, an applied alternating electric current isolates cellular fragments while bulk material is washed away. Isolated material can then be immunostained on-chip for organelle and DNA damage proteins and imaged for quantification. The performance of antibody validation, optimization, and DNA characterization has confirmed successful on-chip isolation of fragments of mitochondria, endoplasmic reticulum, golgi apparatus, and centrosomes from cancer plasma. We have also successfully distinguished between a cohort of healthy and PDAC plasma using a mitochondria-localizing protein biomarker. Characterization of isolated cfDNA shows that cfDNA particles isolated on-chip are between 65 and 475nm in diameter and has demonstrated differing DNA damage protein expression levels in lysates of healthy and chemotherapy induced DNA damaged cells. Successful isolation of cellular fragments from cell lysates and human plasma identifies different types of biological nanoparticles in the blood of cancer patients that can be isolated using DEP, while characterization of localized biomarker cargo has applications in the early detection of cancer.

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ABSTRACTS

Poster #98

Isolating signal from noise: dynamics of CA125 in HGSOC and the ramifications for early detection

PRESENTING AUTHOR:

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University of Cambridge

Introduction: The jury is out on CA125 as an early detection biomarker for high grade serous ovarian cancer (HGSOC), owing to its lack of specificity to the disease. The UKCTOCS showed no mortality benefit from CA125-led multimodal screening (MMS), despite detecting a greater number of HGSOC cases with a reduction in incidence of advanced stage disease.

We used clinical and screening data to understand the contributions of HGSOC lesions and healthy tissue to serum CA125 levels and how long it takes for the signal from the tumour to outweigh the noise from the baseline CA125. This could shed light on why the UKCTOCS did not show mortality benefit and what conditions could ensure favourable outcomes.

Methods: We used data from 597 HGSOC patients in the OV04 study to obtain a distribution of CA125/cm3 of tumour. We isolated the CA125 signal from the tumour by choosing 101 scans that had no ascites from 32 women who had primary/interval debulking surgery; this removed sources of background CA125. We calculated the total tumour burden using a deep learning algorithm and co-registered CA125 and volume measurements using linear interpolation.

For background CA125, we obtained a distribution of the mean serum levels and the longitudinal coefficient of variation (CV) from 34,894 women in the MMS arm of the UKCTOCS study with >5 annual screens and no ovarian cancer diagnosis.

We then simulated 10,000 individuals, with HGSOC growth rates and metastases sampled from distributions estimated in previous work. The mean baseline CA125 and longitudinal variation were sampled from the distributions obtained in this study. We calculated the time at which the CA125 shed by a tumour crossed 1, 2, and 3 standard deviations past the baseline for the individual.

Results: The CA125 per tumour volume, mean background CA125 and CV were all log-normally distributed with median values of 3.7 U/mL/cm3, 12.3 U/mL and 14.1% respectively. Our simulated tumours took 12.3, 13.1, and 13.9 months before their signal superseded their background CA125 by 1/2/3 standard deviations respectively, with 47, 57, and 64% of the tumours already metastasising by this point. The tumours that had not yet metastasised provided a median window of 1.3 – 1.8 months for the signal to be detected before metastasis.

Conclusion: Our data and simulations suggest that most HGSOC tumours would metastasise before their CA125 signal becomes discernible; this makes effective early detection a challenging task.

ABSTRACTS

Poster #99

The AcceleRated community Multi cAncer Dlagnostic evaLuatiOn platform (ARMADILO)

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COMPANY/INSTITUTION:

University of Oxford

BACKGROUND Half of patients later diagnosed with cancer attend their Family Doctor with non-specific symptoms such as abdominal pain or weight loss, which can be caused by many conditions. It takes longer for these patients to be investigated for cancer, they are more likely to be diagnosed with late-stage cancer, with poor outcomes.

Multi-cancer blood tests could help to triage symptomatic patients by detecting the presence of cancer across multiple cancer sites. They could simultaneously identify patients who require cancer investigation, direct investigations to the most likely cancer site of origin, and spare many patients unnecessary cancer investigation.

Efficient primary care studies are lacking to understand the diagnostic accuracy of multi-cancer tests in patients with symptoms before cancer investigation.

OVERALL AIM To accelerate multi-cancer test evaluation in symptomatic patients attending primary care.

OBJECTIVES 1. Set-up an inclusive primary care multi-cancer test evaluation platform to meet the diverse needs of the public, health service, and commercial developers. 2. Ascertain the diagnostic accuracy of multiple multi-cancer tests in patients with non-specific symptoms attending primary care, individually, combined, and with associated clinical data. 3. Optimise inclusive recruitment processes and data capture 4. Compare patients recruited using individual GP judgement with those selected using electronic health records data

METHODS A single-arm multi-centre observational phase II diagnostic accuracy study of complementary multi-cancer tests in 9,900 patients attending up to 200 NHS primary care sites in England and Wales with non-specific symptoms, with cancer registry follow-up (Obj 1&2)

An internal pilot study to assess whether study processes are feasible and inclusive, data quality is acceptable, and that data linkages are functional. Study processes will be modified n consultation with patient representatives, community-based inclusion partners, and an independent 'council of sceptics' (Obj 3) A Study Within A Trial Data Utility Comparison Study will compare clinician-recruited participants with patients selected using electronic health records data to understand if if automated patient selection and real-time electronic health records analysis could replace clinician recruitment (Obj 4) TIMELINES: July 2025-June 2030

PLEASE GET IN TOUCH IF YOU HAVE A MULTI-CANCER TEST THAT COULD BE EVALUATED IN ARMADILO

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ABSTRACTS

Poster #100

Long-term cancer registry follow-up of false positive multi-cancer early detection (MCED) test results from the SYMPLIFY study.

PRESENTING AUTHOR:

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COMPANY/INSTITUTION:

University of Oxford

BACKGROUND SYMPLIFY was a prospective multicentre observational study evaluating the diagnostic performance of a methylation-based multicancer early detection (MCED) test in symptomatic patients referred from primary care for urgent cancer investigation to 44 National Health Service (NHS) hospital sites in England and Wales. Patients were followed until diagnostic resolution or up to 9 months by research staff at each site. MCED predictions were compared with the diagnosis obtained by standard care We aimed to follow-up the SYMPLIFY patients reported to have false positive (FP) MCED results for 24 months in the national cancer registry.

METHOD We conducted a descriptive cohort analysis for the 79 SYMPLIFY patients reported to have a FP MCED result. We accessed the National Cancer Registrations Dataset (NCRD) for 24 months following enrolment to SYMPLIFY. A line listing was prepared to detail each patient's age, sex, symptoms leading to cancer referral, referral pathway selected, and the time, site, and stage of any cancer reported.

FINDINGS 28/79 (35.4%) participants initially classified with a FP MCED were subsequently reported to have a cancer diagnosed in the cancer registry within 24 months of enrolment. Their age ranged from 36 to 94 years; 15/28 (53.6%) were female. 16/28 (57.1%) were diagnosed with cancer within 9 months of enrolment. 8 of the 16 were diagnosed with cancers that were incongruent with the diagnostic pathway chosen based on their presenting symptoms but the MCED Cancer Signal Origin (CSO) call was correct. The other 8 were referred to the correct diagnostic pathway for the cancer diagnosed, suggesting the cancer was missed by standard of care investigations or data entry errors during SYMPLIFY. 12/28 (39.3%) were diagnosed with cancer 10-24 months following enrolment. 7 of the 12 were diagnosed with pathway incongruent cancers but the MCED CSO was correct. For the remaining 5, the pathway initially chosen was appropriate for the cancer registered, suggesting the cancer was undetectable on initial standard of care investigation. Based on these data, the reduction in FPs from 79 to 51 would result in the overall MCED PPV increasing from 75.5% (95% CI 70.5–80.1) to 84.2% (80.1- 87.6).

INTERPRETATION Our results provide strong justification for proactive follow-up of positive MCED results where initial standard of care investigations do not identify cancer as one third of these patients will be diagnosed with cancer within two years.

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Poster #101

Adaptive plasticity in patient-derived precancerous organoids

PRESENTING AUTHOR:

Callum Oddy

AUTHORS:

Callum Oddy, Monika Madrova, Lauren McKenzie, Petra Vleckova, Lucia Conde, Will Waddingham, David Graham & Marnix Jansen

COMPANY/INSTITUTION:

University College London

Gastric stem cells (GSCs) sustain the gastric epithelium, ensuring its health and function. A single GSC will proliferate and differentiate to form a clonal gland. However, aberrations in genetic and epigenetic landscapes can derail this process, setting the stage for the pre-malignant phenotype, gastric intestinal metaplasia (GIM), to take over. Through staining of gastric gland serial sections, we demonstrated the sudden moment that an individual GSC deviates from their native gastric lineage to assume an intestinal-like identity, before then taking over the whole gland. Now, the question remains: How does that GSC become set up to fall to an intestinal lineage?

Leveraging a robust translational pipeline, we have cultivated patient-matched normal, GIM and duodenal organoids from clinical biopsies, culminating in a repertoire of 22 organoid lines from 6 patients. Through interrogation of these organoids lines, we aim to understand the processes pushing GSC to develop into GIM.

Utilising rt-PCR and confocal microscopy, we have demonstrated the nuanced expression patterns of gastric and intestinal markers within these organoids. Furthermore, our ongoing methylation analyses has demonstrated the epigenetic forces governing the transition from normalcy to pathology. We have shown distinct methylation signatures associated with each phenotype. Next, we hope to uncover specific differentially methylated gene sets that demonstrate the processes altered as GIM takes hold. Alongside the methylome work, sc-RNA sequencing stands to be as a powerful tool to decode the transcriptional dynamics orchestrating GSC lineage decisions hinted at in earlier analyses. Additionally, this sequencing will allow us to interrogate how the transcriptional dynamics within GSC affect the transcriptional activities of the whole cellular population. Moreover, employing novel techniques such as thiol-reactive organoid barcoding in situ (TOBis) and cytometry by time-of-flight (CyTOF), we aim to decipher the intricate post-translational signaling cascades underlying the acquisition of a cancerous phenotype in GIM.

Our comprehensive investigation should underscore the transformative potential of GIM organoids in unravelling the intricacies of metaplastic evolution. These multidimensional analyses will not only illuminate the pathophysiological underpinnings of GIM but also intimate pivotal evidence for the development of prognostic models in gastric cancer risk stratification.

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Poster #102

Real-World Evaluation of Positive Multi-Cancer Early Detection Test Results in a Dedicated Clinical Program

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COMPANY/INSTITUTION:

Dana-Farber Cancer Institute

Technological innovation has enabled the development of multi-cancer early detection (MCED) tests, which can identify a broad range of cancers through a single screening test. These tests are entering clinical practice as laboratory-developed tests, but limited data exist on their implementation. In 2023, Dana-Farber introduced an MCED Program to facilitate the evaluation of patients who have received MCED testing and to study novel MCED strategies.

We conducted a review of patients seen at the Dana-Farber MCED Program who had a cancer signal detected by the Galleri® MCED test.

Fourteen patients were evaluated for a positive cancer signal detected by the MCED test. The median age was 62.5 (54.9-81.4), 64.3% (9/14) were male, and 85.7% (12/14) were white. Following diagnostic evaluation 78.6% (11/14) had a confirmed cancer diagnosis and 21.4% (3/14) were false positives. The time from MCED test result to presentation at DFCI was a median of 28 days (6-368) and the median time to conduct the diagnostic evaluation was 20 days (5-104), which was shorter in true positive cases (15 days) compared to false positives (98 days). Among true positives, 6 had solid tumors (triple-negative breast, testicular, liver, cholangiocarcinoma, tonsillar, and lung cancer [non-smoker]) and five had hematologic malignancies (4 lymphoma, 1 myeloma). Of the malignancies detected, 10 (90.9%) have no current screening guidelines. Screening mammography was up to date in the patient found to have triple-negative breast cancer. Six cancers were diagnosed at stage I/II and 5 were stage III/IV. All false positive patients underwent repeat MCED testing at a median of 118 days (92–174); all re-tests were negative. The median number of tests/procedures to reach diagnostic resolution was 3 for true positive cases (2-7) and 5 for false positive cases (4-6). All patients required advanced imaging. The first or second cancer signal origin was accurate in 90.9% (10/11). There were no issues encountered obtaining prior authorizations for diagnostic tests and no adverse events were reported.

Most patients that presented with a positive MCED test were true positives with a diagnosis consistent with the cancer signal origin. Patients with signal detected tests were quickly adjudicated, although some patients experienced delays in finding a provider to work up their test result. These findings support a role for dedicated cancer diagnostic clinical expertise in the evaluation of MCED tests.

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Poster #103

Poster Pitch

Assessing the Usability of PSA Self-Testing to Address Prostate Cancer Disparities Among Black South African Men: A Mixed-Methods Study

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AUTHORS:

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COMPANY/INSTITUTION:

Stanford University

Background: In South Africa, prostate cancer (PCa) is a disease of disparities where uptake of PCa screening is largely based on race, class, and income. Black South African men present with higher prostate specific antigen (PSA) levels, more aggressive disease and locally advanced disease at diagnosis. Systemic barriers including financial constraints, residential location, healthcare access, guideline confusion, and stigma limit screening uptake despite notable PCa disparities. At-home PSA self-testing may reduce disparities by decentralizing access, yet evidence on usability is unknown. A novel self-test kit (Novex Pharmaceuticals), currently commercially available in South Africa, involves lateral flow chromatographic immunoassay for the semi-quantitative (<3ng/mL, 3-10, >10) detection of PSA in whole blood, using a finger prick into a small cassette.

Objective: This study assessed the usability (effectiveness, efficiency, satisfaction) of a PSA self-test kit among Black South African men aged 45–69 without a history of PCa.

Methods: In Johannesburg, 40 men engaged in a mixed-methods study. Participants first completed a think-aloud session, performing the PSA self-test while verbalizing challenges (e.g., procedural confusion, interpretation). Focus groups followed, exploring barriers to screening, test-kit experiences, trust, and promotion preferences. Baseline surveys quantified behavioral indicators (PCa knowledge, medical mistrust and stage of change using the Integrated Screening Action Model framework). Qualitative data underwent discursive analysis to identify themes; survey data were analyzed descriptively.

Anticipated Impact: This work addresses critical gaps in understanding barriers to self-test adoption. Findings will inform culturally tailored educational materials and strategies to improve screening access, with implications for reducing PCa disparities globally. Results will guide a subsequent pilot trial of screening uptake and future scale-up efforts.

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Poster #104

Unravelling fibroinflammatory and immune signatures for pancreatic cancer early detection

PRESENTING AUTHOR:

Daniel Parra-Sanchez

AUTHORS:

Authors: Kyra Fraser, Maria Rosado, Stephen P Pereira, Pilar Acedo

COMPANY/INSTITUTION:

University College London

Pancreatic cancer is associated with late-stage diagnosis and poor patient prognosis. The disease is characterised by chronic dysregulated immunity and inflammation. Moreover, chronic pancreatitis is linked with an increased risk of pancreatic cancer. Tissue remodelling during disease progression involves a complex network of cells and a crosstalk between cancer cells, stromal components and immune cells, but it remains poorly explored. Thus, to improve the outcome of patients, there is a need for better understanding of biological changes associated with the initiation and progression of pancreatic cancer at the molecular and spatial levels.

Using samples obtained from our Accelerated Diagnosis of neuroEndocrine and Pancreatic TumourS (ADEPTS) biobank, we have evaluated blood samples for the discovery of non- invasive biomarkers to discriminate patients with pancreatic cancer from symptomatic patients without cancer. In this pilot study, the transcriptome of peripheral blood mononuclear cells (PBMCs), isolated using a ficoll gradient, was explored to identify PDAC-associated mRNA signatures. Moreover, the Olink® Explore Inflammation and Oncology panels were performed in a cohort of 40 patients with early stage (I-II) PDAC, 40 chronic pancreatitis samples and 40 control patients with benign symptomatic upper GI diseases. To validate and enrich these results, a panel of inflammatory and immune markers including immunoglobulins, cytokines and chemokines was also run using multiplex techniques. Symptoms observed in our cohort were also analysed together with clinical (e.g diabetic status, biochemistry profile) and demographic data (age, sex, ethnicity, post code etc).

We have identified mRNA transcriptome signatures and differentially expressed proteins associated with inflammatory and immunological processes in PDAC compared to benign symptomatic samples (CXCL8, IL6, CEACAM). Our results offer potential diagnostic utility for early-stage disease. Additionally, our unique cohort of patient samples comprising of those with confirmed PDAC and those presenting to clinic with benign disease and similar non-specific symptoms, allows for the development of non-invasive diagnostic tests with better translational applicability. The validation of these findings in a larger patient cohort is ongoing and the use of NanoString GeoMx® Digital Spatial Profiler to perform whole transcriptome profiling in human chronic pancreatic and pancreatic cancer tissue samples.

ABSTRACTS

Poster #105

Lightning Talk

Circulating Biomarker Discovery in PSC and CCA: A Proteomic Approach to Early Detection.

PRESENTING AUTHOR:

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AUTHORS:

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COMPANY/INSTITUTION:

University College London

Introduction

Early detection of primary sclerosing cholangitis (PSC) and cholangiocarcinoma (CCA) remains a major clinical challenge, primarily due to the complex and poorly understood molecular pathways involved in disease progression. Chronic inflammation and bile duct fibrosis in PSC are known contributors to malignant transformation, while the immunosuppressive microenvironment in CCA further facilitates disease advancement. To identify systemic molecular signatures associated with these processes, we performed NGS-based serum proteomics targeting over 700 protein markers in PSC, PSC-CCA, CCA, and healthy individuals, aiming to uncover candidates for early cancer detection.

Aims and Methods

We analysed 102 serum samples from 35 PSC, 35 CCA, 12 PSC-CCA, and 20 healthy controls using two Olink proteomics panels, each targeting 368 inflammation- and oncology-related proteins. Differential protein expression was assessed using T-test or Mann-Whitney U depending on data normality, with False Discovery Rate (FDR) correction applied to control for multiple testing.

Results

Our analysis identified more than 250 differentially expressed biomarkers between each disease group and healthy controls across both panels (Adjusted p-value<0.05). These included matched interleukins such as IL-6 for both cancer groups (difference in means >2 and adj. p-value<10-3) highlighting their potential as a shared biomarker of inflammation and malignant transformation. CCA displayed the highest number of upregulated inflammatory markers, suggesting persistent immune modulation. In contrast, PSC-CCA showed moderate immune modulation but pronounced oncogenic marker expression, reflecting a shift from chronic inflammation towards malignant transformation. Furthermore, over 40 markers, many of which were proinflammatory, showed significant differential expression between PSC and CCA groups (adjusted p-value<0.05). These results suggest the existence of disease-specific circulating signatures reflective of the underlying fibroinflammatory and oncogenic mechanisms.

Conclusion

NGS-based serum proteomics revealed distinct circulating biomarkers associated with PSC and CCA. The discovery of both shared and disease-specific markers underscores their value in developing early detection tools. Further validation in larger cohorts will be essential to translate these findings into clinical practice.

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ABSTRACTS

Poster #106

Interactome Remodeling as an Early Warning System for Cancer Cell State Transitions

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COMPANY/INSTITUTION:

Oregon Health and Science University

Early cancer progression is driven by dynamic shifts in cell state, orchestrated through remodeling of protein interaction networks that often precede genetic alterations. Using our MIDAS (Mapping Interactome Dynamics and Structures) platform—which integrates multiplexed co-fractionation mass spectrometry (mCF/MS) with deep structural modeling—we generated time-resolved interactomes of progressive epithelial transitions, resolving ~9,500 interactions for over 600 dynamic multi-protein assemblies and modeling more than 1,500 binary interfaces. These assemblies uncover early regulatory network rewiring governing cell state plasticity, including epithelial-to-mesenchymal transition (EMT), and reveal structurally tractable nodes for therapeutic interception. Validation in Barrett's esophagus patient samples links specific complexes to early neoplastic progression, while pan-cancer analyses highlight their broader prognostic significance. Functional perturbation studies confirm causal roles for select complexes in transitional phenotypes. Collectively, this work, and platform, offer a generalizable framework for decoding early cell state plasticity in precancerous lesions, advancing biomarker-guided strategies for early detection and targeted intervention.

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ABSTRACTS

Poster #107

Surface glycan of small extracellular vesicles in-vitro and in-vivo increase in early-stage multiple epithelial cancers to provide novel biomarkers for potential blood biopsy

PRESENTING AUTHOR:

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COMPANY/INSTITUTION:

Oxford Brookes University

Background: Colon and breast cancer make up nearly a quarter of all diagnosed cancer, that would benefit from early stage detection. The role and release of plasma small extracellular vesicles (sEVs) in cancer is well documented. Glycoproteins are commonly used in cancer diagnosis i.e. CEA, CA125, PSA etc. Here, we show that colon and breast epithelial cancer cells and their sEVs have surface glycans that increase with cancer, which also translates to stage 1 and 2 plasma patient samples.

Method: Cancer cell lines were probed for surface glycans using lectins and analysed by confocal microscopy and flow cytometry. Imaging-flow cytometry and single particle interferometry were used for the detection using the lectins on EVs. Total plasma EVs from 1ml whole blood from healthy, stage I-II and IV metastatic breast and colon cancer patients were tested by imaging-flow cytometry for lectin binding.

Results: There were increased multiple novel glycans on cells and their EVs from metastatic and non-metastatic patient-derived cancer cell lines compared to immortalised healthy cells. In cancer patient-derived plasma sEVs, lectin binding was significantly higher in patients with stages I and II cancer than in healthy individuals. Highlighting the potential of glycans as a biomarker method for blood biopsy cancer detection.

Conclusions: This pilot research suggests that sEV surface glycans could suggest potential early diagnostic utility in breast and colon cancer for lectin-positive sEVs from 1ml blood samples.

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ABSTRACTS

Poster #108

Defining evolutionary trajectories to update subtyping schemes using lung, breast and esophageal cancer data

PRESENTING AUTHOR:

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AUTHORS:

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COMPANY/INSTITUTION:

Oregon Health and Science University

Tumorigenesis is a multistep evolutionary process that occurs within the body. Much like a canonical cancer subtype, the concept of an "evotype" expands to account for the upstream influence of molecular events that culminate to define the lineage with at the greatest evolutionary fitness at the time of detection. Here, we develop a scalable, reproducible approach for integrating diverse datasets and enabling the systematic identification of evotypes. We employ graph-embedding framework that integrates heterogeneous data sources from all cases of lung adenocarcinoma, lung squamous cell carcinoma, and breast cancer available in The Cancer Genome Atlas (TCGA) database (n=1,457), as well as data from Barett's esophagus, esophageal adenoma (=426) from both the and use our model to embed genomic, epigenomic, and transcriptomic data alongside any clinical, demographic or behavioral characteristics available. Within a given evotype, certain patterns and sequences of events are shared, and these shared features are associated with differences in severity of disease. Our pilot analysis of esophageal cancer data (n=25) showed 22,505 total omikli (diffuse clustered mutational events) with a mean of 900 events per patient and 725 kataegis (larger, denser clustered mutational events), with a mean of 33 events per patient. We hypothesize that clustered mutations play an important role in the development of evotypes, given their association with variation in disease severity. Using these and the additional data we generate for other types of mutational events, we will employ Node2Vec to generate structural embeddings that can be used as input to train a GraphSAGE model. This model will then integrate node attributes with local neighborhood information and enable to identify the molecular events and/or clinical or demographic variables co-occur and define our evotypes.

ABSTRACTS

Poster #109

Poster Pitch

Understanding the paradox of prostate cancer testing and socio-economic position for equitable early detection: Evidence from a population-based multilevel study

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AUTHORS:

Mark Clements

COMPANY/INSTITUTION:

Karolinska Institutet

Background:

Prostate cancer screening using prostate-specific antigen (PSA) is debatable. The socio-economic differences in prostate cancer incidence and survival could be partially attributed to differences in testing among the groups. This study investigated the association of SEP measures with widespread opportunistic PSA testing and quantified the extent to which measures of SEP contributed to the observed spatial variation in PSA testing.

Methods:

A population-based register study was conducted, encompassing men aged 40 years and older without a prior prostate cancer diagnosis residing in the Stockholm region. We used hierarchical Bayesian logistic regression models with spatial random effects to estimate the associations between PSA testing and SEP measures and to quantify the variation explained by SEP measures.

Results:

Men aged 70-79 years belonging to the highest income quartile had the highest proportion (35.2%) of men having a PSA test in 2016. Men who were married or in registered partnerships were more likely to have a PSA test. Adjusting for age and spatial variation, men with higher income or education had higher odds of PSA testing. The proportion of variance explained in PSA testing at the small area level was highest for income (42%). Incorporating all four SEP measures led to a higher proportion of an explained variance at the individual level (37.5%) and area-level (49.5%).

Discussion:

The findings suggest a strong association between opportunistic prostate cancer testing and SEP measures at individual and area-level. The SEP measures at the individual and area levels partially explained the spatial variation in PSA testing, where income was the strongest driver. The association of SEP with prostate cancer testing could be multifaceted with potential harms for both higher and lower SEP. The under-testing in lower SEP groups may lead to delayed diagnosis and poorer prognosis and over-testing in higher SEP group may lead to overdiagnosis of clinically insignificant cancers. Since regions in Sweden are planning to implement an organised testing program, it highlights the significant policy challenge to address the socio-economic gradient in testing to achieve more equitable prostate cancer outcomes. Future screening strategies should integrate both individual-level and contextual factors to promote a more equitable and evidence-based approach.

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Poster #110

Non-Contrast Early Detection of Breast Cancer Using High-Resolution Advanced Magnetic Resonance Imaging Models

PRESENTING AUTHOR:

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Problem: Magnetic Resonance Imaging (MRI), including dynamic contrast-enhanced (DCE) and diffusion-weighted imaging (DWI), is recommended yearly for those at high-risk for breast cancer. DCE offers high sensitivity, while DWI-derived biomarkers, such as the apparent diffusion coefficient (ADC), improve specificity. However, DCE requires intravenous Gadolinium contrast which adds cost and has been shown to accumulate in the brain with unknown long term sequelae. DWI is a non-contrast technique, though has low spatial resolution limiting its utility in detecting small lesions. Restriction Spectrum Imaging (RSI) overcomes these limitations by separating DWI signal into pools of restricted, hindered, and free diffusion without intravenous contrast. This advanced DWI technique has demonstrated improved lesion discrimination in patients with known breast cancer, helping distinguish benign from malignant lesions. Its combination with high-resolution imaging presents an innovative approach to early detection.

Methods: High-resolution DWI was collected on 122 breast cancer and screening patients and were equally separated into training and testing cohorts. Tri- and tetra-exponential (3E and 4E)-RSI models were calculated on the training set, and output maps provided spatial representation of each diffusion component. Model performances in describing diffusion signals were assessed using Bayesian criterion information (BIC) on the test set.

To assess lesion conspicuity, contrast-to-noise ratios (CNR) were measured on 28 lesions from a subset of 22 patients from the test set and compared to CNR from ADC and DCE.

Results: RSI models provided separation of diffusion contents into restricted, hindered, and free for 3E-RSI versus highly restricted, restricted and hindered, hindered and free, and flow, for 4E-RSI. The latter had the lowest BIC.

DCE had the highest CNR (median 3.21, inter-quartile range 0.92) followed by 4E-RSI C2-hindered (2.29, 1.49). Of the 28 test lesions, 7 were benign. ADC had an AUC of 0.79 while 3E and 4E-RSI had an AUC of 0.91 and 0.96 respectively. DCE had a specificity of 75%, while at 80% sensitivity ADC, 3E and 4E-RSI had a specificity of 67, 83 and 83%, respectively.

Conclusion: Though DCE achieved the highest CNR, RSI models outperformed ADC. They had the highest AUCs and specificity, highlighting RSI as a potential non-contrast method for early detection.

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ABSTRACTS

Poster #111

Early Detection of Ovarian Cancer Using Advanced Diffusion MRI

PRESENTING AUTHOR:

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COMPANY/INSTITUTION:

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Problem: Ovarian cancer is the fifth leading cause of cancer death among U.S. women, with a ~50% 5-year survival rate. Although survival can reach ~93% with early detection, over 70% of cases are diagnosed at advanced stages. Ultrasound and blood biomarker CA-125 are the most used detection tools but offer limited effectiveness for small, early-stage tumors.

Magnetic resonance imaging (MRI) offers advantages for early detection due to high soft tissue contrast, with diffusion-weighted MRI (DWI) being sensitive to microstructural changes linked to malignancy. However, standard ovarian DWI protocols use thick slices (4–5 mm), limiting detection of small lesions, and cannot reliably distinguish benign, borderline, and malignant lesions, hindering their ability to guide lesion-specific surgical management. Restriction Spectrum Imaging (RSI) is an advanced DWI technique that overcomes limitations of standard protocols by separating signals into restricted, hindered, free, and flow diffusion components.

Methods: Data was collected from 44 average- and high-risk (BRCA1/2+) patients using a high-resolution DWI sequence with 2 mm isotropic resolution, to maximize detection of small, early-stage lesions. This is the highest through-plane resolution reported for an ovarian DWI sequence to date.

Using this data, bi-, tri-, and tetra-exponential RSI models were determined by: (1) estimating compartment-specific apparent diffusion coefficients, and (2) voxel-wise signal decomposition via linear mixture modeling. Output maps (C1–C4) depicted the spatial distribution of each diffusion component. Models were assessed using fitting residuals and Bayesian Information Criterion (ΔBIC).

Results: While the bi-exponential model achieved the lowest BIC, tri- and tetra-exponential models generated maps with greater clinical utility by better separating tissue signals. Output maps revealed distinct patterns across lesion types: C1 signal was highest in malignant lesions (restricted diffusion); C3 was elevated in benign and borderline lesions (free diffusion); and borderline lesions also showed high C2 in solid components (restricted/hindered diffusion). All models showed similar fitting errors (bi: 0.49%, tri: 0.44%, tetra: 0.36%), indicating low risk of overfitting.

Conclusion: These findings support RSI as a promising approach for early detection and characterization of ovarian lesions.

ABSTRACTS

Poster #112

Poster Pitch

A Multimodal AI Biomarker for Early Detection of Cancer Cachexia Integrating Clinical, Radiologic, and Laboratory Indicators

PRESENTING AUTHOR:

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COMPANY/INSTITUTION:

Moffitt Cancer Center

Cancer cachexia is a multifactorial metabolic syndrome marked by progressive skeletal muscle wasting, metabolic dysfunction, systemic inflammation, and weight loss, contributing to poor quality of life and increased mortality in cancer patients. Despite its clinical importance, no definitive biomarker exists; commonly used serum indicators for malnutrition and inflammation, skeletal muscle metrics from radiologic data, and anthropometric measures often provide information overlapping with other conditions, limiting diagnostic specificity. Existing composite indices, including the Cancer Cachexia Index (CXI), modified CXI, and Cachexia Score, integrate multiple symptomatic factors but lack standardized thresholds and are rarely scalable for routine clinical use.

This study presents a multimodal AI-based biomarker for early cancer cachexia detection, integrating diverse mechanistic signals from routinely available patient data. These include basic clinical data (demographics, anthropometrics, disease status), inflammatory and nutritional laboratory markers, skeletal muscle metrics from CT imaging, and structured cachexia symptoms extracted from unstructured clinical notes using open-source large language models (LLMs). Unlike prior models trained on curated research datasets, this framework is developed using real-world clinical data, enhancing generalizability and feasibility.

The AI framework incorporates confidence estimation to flag uncertain predictions when heterogeneous data modalities present conflicting signals, enabling expert review. The framework dynamically adapts to patient-specific factors, including age, ethnicity, cancer type, and stage, offering a flexible, threshold-free early detection approach. Preliminary results show stepwise improvements in prediction accuracy at diagnosis: 77% with basic clinical and imaging data, rising to 81% with laboratory values, and 85% when structured clinical notes are included. Survival analysis supports these findings, with the concordance index improving from 0.638 using clinical data alone to 0.656 with skeletal muscle measurements, 0.670 with laboratory values, and 0.722 when clinical notes are added.

This multimodal AI biomarker advances mechanistic insight by combining diverse biological and clinical signals into a scalable, reliable, and clinically actionable early detection tool that supports timely, personalized interventions to improve patient outcomes.

ABSTRACTS

Poster #113

Lightning Talk

HybridSybil: Integrating 3D-CNN and Vision Transformer for Longitudinal Lung Cancer Risk Prediction from LDCT

PRESENTING AUTHOR:

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Background and Motivation: Lung cancer remains the leading cause of cancer mortality, emphasizing the need for accurate early detection from LDCT screening. This study introduces HybridSybil, comprising two deep learning architectures combining 3D-CNNs and Vision Transformers for longitudinal lung cancer risk prediction.

Methods: The first model, TemporalSybil, addresses the challenge of variable-length patient sequences through absolute temporal positioning. The second model, MaskedSybil, employs attention masking to handle missing timepoints in a structured manner. Both architectures utilize a hybrid feature extraction strategy combining global spatial context through Vision Transformers with aggregated local features achieved through a CNN backbone, addressing the multi-scale nature of lung nodule characteristics. The models employ cumulative probability layers for risk prediction across six-year follow-up periods, optimizing early cancer detection. Hyperparameter optimization is performed using Bayesian search across 10-fold cross-validation, ensuring robust model selection and generalization.

Results: HybridSybil architectures outperform the original Sybil model in predicting lung cancer risk over a six-year horizon. TemporalSybil, achieved the highest AUC in Year 1 (0.94 [0.87, 1.00]) and maintained superior performance across subsequent years, culminating in the highest overall concordance index (0.76 [0.70, 0.81]). MaskedSybil, also demonstrated consistent performance improvements over Sybil, especially in early prediction years, with a Year 1 AUC of 0.90 [0.80, 0.98] and C-index of 0.74 [0.68, 0.80]. In contrast, Sybil, which relies on a single scan timepoint, exhibited lower AUCs across all years with Year 1 AUC of 0.80 [0.69,0.90] and C-index of 0.72 [0.67, 0.78], highlighting the importance of leveraging longitudinal scan information for robust risk stratification.

Conclusion and Future Work: An end-to-end Transformer-based model that directly learns temporal progression from raw imaging data of longitudinal embeddings significantly improves Sybil's ability to predict long-term lung cancer risk from LDCT scans. Future work will focus on developing models that adapt to different patient risk factors including age, smoking history, family history, and environmental exposures to provide more personalized risk assessments.

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Poster #114

Electron Microscopy Reimagined for Cancer Early Detection and Interception

PRESENTING AUTHOR:

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COMPANY/INSTITUTION:

Oregon Health and Science University

Modern electron microscopy (EM) has moved beyond single 2-dimensional high-magnification images of select cellular organelles. Today's EM offers the highest resolution imaging possible and can catch the very smallest, earliest anomalies in tissue, making it an ideal technology for cancer early detection and interception studies. Furthermore, Scanning Electron Microscopy (SEM)-based techniques offer large-format, high-resolution imaging of cancer biopsies in both 2D and 3D, providing unmatched detail of cancer phenotypes at disease stages.

Our work utilizes Focused Ion Beam-Scanning Electron Microscopy (FIB-SEM) to map samples at 4-nm resolution over hundreds of microns, allowing for the preparation of targeted "nanobiopsies" for 3D reconstruction. Deep learning models rapidly detect, classify, and segment organelles with minimal manual annotation. These nanobiopsy image stacks are rendered into detailed 3D models, revealing ultrastructural features such as nuclear invaginations, aberrant nucleoli, mitochondrial structure and organization, and cell-cell interactions. Additionally, the Extracellular matrix (ECM) organization can be viewed in full context with adjacent cancer tissue. We will show FIB-SEM datasets highlighting phenotypic differences between normal and early cancerous prostate, breast and pancreas tissues, providing insight into early tumor development and potential sub-cellular vulnerabilities for targeted therapy.

When complementary data, such as Immunohistochemistry (IHC), cyclic Immunofluorescence (cycIF) or multi-omics analyses, are available from the same specimens, structure-function relationships can be directly explored. However, most patient tissues are preserved in formalin-fixed paraffin-embedded (FFPE) blocks, which traditionally have been incompatible with EM due to fixation and embedding differences. To overcome this hindrance between clinically important modalities and EM correlation, we are reimagining novel sample preparation methods for SEM to enable our high-resolution 3D workflow on adjacent sections of FFPE tissue sections. This innovative imaging workflow will assist identification of meaningful targets for 3D EM by leveraging the other data modalities for targeted nanobiopsy collection. These 3D data will provide mechanistic information otherwise unattainable.

ABSTRACTS

Poster #115

Lung Cancer Screening Knowledge and Its Association with Adherence to Annual LDCT

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COMPANY/INSTITUTION:

Oregon Health and Science University

Introduction: Lung cancer screening (LCS) adherence rates are low in routine clinical settings (1). Research indicates a potential association between higher health literacy and better adherence to cancer screenings (2). Our study aimed to assess how knowledge of LCS influences adherence to recommendations of annual low-dose computed tomography (LDCT) scans.

Methods: We conducted an analysis of data from a longitudinal, prospective observational study of patients enrolled from three health care systems after an LCS shared decision-making interaction with their clinician (3). The study sample included patients who completed a baseline survey and underwent their initial LDCT. The primary outcome was adherence to recommendations for the annual LDCT (measured at 12 months). To assess LCS knowledge at baseline, we asked participants, "which of these conditions do you think that the CT scan screens for?" (3). To assess change in LCS knowledge at 12 months, we asked participants "Has your knowledge changed regarding lung cancer screening?". We used adjusted logistic regression to detect an association between LCS knowledge and adherence adjusting for age, race/ethnicity, reading difficulty, income, and study site.

Results: A total of 201 participants were included. Overall adherence rate to 12 months follow up guidelines was high at 80.1%. Adherence rates were similar in regards to age, gender, race, smoking status, employment status, income, reading difficulty and study site. Only approximately half of the participants answered the baseline knowledge question correctly (49.1% correct). Most participants (82.8%) reported no change in their LCS knowledge at 12 months. Adherence rates for patients without knowledge change was 79.0% versus 86.5% for patients with knowledge change (p=0.36). After adjusting for potential confounding variables, correctly answering the primary question was not significantly associated with higher adherence to LCS at 12 months following the initial LDCT (odds ratio 1.5, 95% CI [0.61, 3.85], p=0.37).

Conclusions: Our results suggest that knowledge about LCS does not influence adherence to follow-up recommendations. A core component of shared decision making is to increase patient knowledge about LCS. However, increased knowledge about LCS alone appears to be insufficient to improve adherence. This finding suggests that other strategies are necessary to address barriers to adherence for patients eligible for lung cancer screening.

ABSTRACTS

Poster #116

Diagnostic accuracy of exogenous D5-Ethyl-β-D-glucuronide (OWL-EVO1) as a probe for detection of lung cancer using exhaled breath – a phase 2 study

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COMPANY/INSTITUTION:

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Introduction: Earlier diagnosis of lung cancer improves treatment outcomes. Breath analysis offers a non-invasive method for early lung cancer detection. We have previously presented in-human safety, tolerability and proof-of-principle data using an Exogenous Volatile Organic Compound (EVOC®) probe, D5-Ethyl-β-D-glucuronide (OWL-EVO1), for targeting extracellular β-glucuronidase for the detection of lung cancer through exhaled D5-ethanol on breath [1]. Here, we present initial findings of a case-control phase 2 study in participants with biopsy-proven lung cancer and co-morbidity/risk factor matched controls.

Methods: The primary objective was to evaluate diagnostic accuracy (sensitivity and specificity) of intravenous OWL-EVO1 and secondary objectives included optimising testing parameters and further profiling safety and tolerability (through adverse event reporting). Up to ten breath samples from pre-dose to 180min post dose, were collected from 187 lung cancer patients (all stages), or controls, across seven sites and analysed using gas chromatography mass spectrometry.

Results: Breath samples using 2mg/kg doses of OWL-EVO1 (40 cases vs 47 controls) showed no case-control separation at early time points, with modest performance at later timepoints; likely compounded by off-target cleavage. To minimise off-target cleavage, the dose was lowered to 0.8mg/kg (50 cases vs 50 controls). Peak performance for stage 1 and 2 lung cancer in this cohort was a 67% sensitivity and 70% specificity for breath samples taken at 130 minutes post-dose. There were 29 adverse events; 10 (in 6 participants) were possibly or probably related to OWL-EVO1 and resolved without sequelae. There were no serious adverse events or reactions, or suspected unexpected serious adverse reactions.

Conclusion: This study presents initial diagnostic accuracy data for IV OWL-EVO1 and supports further development of OWL-EVO1 as a probe to diagnose lung cancer using breath. Future work will utilise an inhaled form of OWL-EVO1 allowing for more practical administration in a clinical setting, while aiming for higher probe concentrations at the tumour site, thereby reducing off-target cleavage to improve sensitivity and test performance.

1. https://www.owlstonemedical.com/media/uploads/files/2023-08_Evolution_Poster_for_IASLC_Compressed.pdf

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ABSTRACTS

Poster #117

Breast Cancer Genetic Risk Prediction in Young Women

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COMPANY/INSTITUTION:

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Introduction: ~10,000 women <50 years are diagnosed with Breast Cancer (BC) annually in the UK, meaning 1 in 6 BCs occur before screening. Young women are more likely to be diagnosed with advanced stage disease and aggressive subtypes, leading to a worse prognosis than those identified through screening. Polygenic Scores (PGS) can enhance risk stratification; however, there are substantial differences in PGS distributions across ancestries and the PGS distributions have not been widely investigated in younger women.

Methods: We are conducting a prospective case-control study on 1000 women (250 cases;750 controls) to assess the well-validated SNP313 PGS, developed in European ancestry populations, in women aged 30-39-years in Greater Manchester, UK. All women were genotyped on the Illumina Global Screening Array (GSA). We investigated the distributions of SNP313 PGS z-score (with expected population mean of 0.0) on the whole cohort and by self-reported ethnicity. We are also investigating novel techniques to identify Pathogenic Variants (PVs) in 9 BC risk genes using the GSA and Illumina's GenomeStudio software. We are assessing 68 'common' PVs in Greater Manchester, seen in ≥1.0% of ~920 families within Manchester Center for Genomic Medicine (MCGM).

Results: In the whole cohort to date (n=681) mean SNP313 z-score in young BC cases (mean age 37.0-years) was higher than in controls (mean age 35.4-years), although the mean PGS in controls was slightly above zero (cases [n=104] 0.46;controls [n=577] 0.08). When only self-reported White European participants were considered, SNP313 was well calibrated to the expected values with good discrimination between cases/controls (cases [n=83] 0.35;controls [n=492] 0.01). The highest mean z-scores were seen in the self-reported Black participants (cases 1.81;controls 1.01). The GSA/GenomeStudio approach identified PVs with high sensitivity for small base changes (94%) and large rearrangements (87.5%), and with 100% specificity.

Conclusion: This case-control study confirmed SNP313 can identify young women (30-39-years) at increased breast cancer risk, but ethnicity/ancestry adjustments are required for implementation to avoid overprediction of breast cancer risk. The GSA can be adapted to identify BC PVs, and the combined approach may be more feasible for risk assessment of ethnically diverse populations with ancestry adjustment.

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ABSTRACTS

Poster #118

Cancer-Based Mutation Detection Utilizing Dielectrophoresis and PCR On a Single Microfluidic Device

PRESENTING AUTHOR:

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AUTHORS:

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COMPANY/INSTITUTION:

Oregon Health and Science University

Introduction:

Genetic-based diagnostics often requires multiple time-intensive steps, including cfDNA isolation and amplification. To improve this process, we developed an electrokinetic microfluidic platform that enables direct cfDNA isolation from untreated plasma using dielectrophoresis (DEP). This was followed by on-chip PCR amplification facilitated through a custom thermal cycling system, representing a significant step toward simplified, rapid genetic diagnostics in clinical settings.

Methods:

A 20µl plasma sample was loaded into the microfluidic device and a DEP force was applied for 10 minutes. A 100µl was buffer was then loaded to remove the excess plasma. Immediately after a PCR master mix was introduced into the device and a custom thermal cycling system was utilized to achieve accurate temperatures with our DEP chip. On-chip isolation and amplification were confirmed using gel-electrophoresis and ddPCR.

Results/Discussion:

To validate the feasibility of our approach, we isolated and amplified L1PA2, a common housekeeping gene, from undiluted and unaltered human plasma samples. The platform successfully achieved DEP collection and on-chip PCR amplification of our target gene. By utilizing this method and limiting fluid transfers and sample loss, we observed 5 times more DNA copies and a lower limit of detection that was 3 times lower, when compared to isolating with DEP and eluting the solution to perform off-chip PCR. This method was then utilized to successfully detect a cancer related KRAS mutation in pancreatic cancer patient plasma samples, which is seen in approximately 85% of individuals with pancreatic ductal adenocarcinoma (PDAC). These results show a successful integration of both DEP isolation and on-chip PCR amplification on a microfluidic device that can detect cancer-based mutations.

Conclusion:

This work demonstrates a novel platform with the ability to collect and amplify nucleic acids on a single microfluidic chip from unaltered plasma. Our detection of KRAS mutations show the possibility that this method can be utilized on other genomic mutations. The clinical use of this device can improve bedside and rural diagnosis by condensing the multiple steps of isolation and amplification into a single device, which is an important advancement for point-of-care diagnostic devices.

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Poster Pitch

Improving the Consistency of Cancer Biomarker Detection Using Dielectrophoresis-Based Nanoparticle Recovery from Plasma via an Internal Standard Approach

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Mehrzad Sasanpour

AUTHORS:

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COMPANY/INSTITUTION:

Oregon Health and Science University

Extracellular vesicles (EVs), such as exosomes, are nanoscale particles enriched with tumor-specific cargo and offer significant potential for the early detection of pancreatic cancer through protein-based biomarkers. Despite this promise, standard isolation techniques like ultracentrifugation are time-consuming, and technically demanding. To overcome these limitations, we established a label-free dielectrophoresis (DEP)-based method using microelectrode array chips that enables rapid, efficient, and direct isolation of EVs from whole plasma, offering a robust alternative to conventional, labor-intensive extraction techniques.

To improve the sensitivity and consistency of DEP-based biomarker detection, particularly given the variability in plasma conductivity among human samples, we implemented an internal standard method. This involved spiking plasma samples with a known concentration of reference particles, either 100 nm fluorescent polystyrene beads or fluorescent liposomes. During DEP processing, both the internal standards and the target extracellular vesicles were simultaneously captured. By comparing the raw CD9 signal from EVs to the normalized ratio of CD9 signal relative to the internal standard, we were able to evaluate how effectively this approach reduced signal variability. We demonstrated that incorporating fluorescent polystyrene bead internal standards significantly reduced the variability of the EV biomarker CD9 signal, lowering the coefficient of variation (CV) by an average of 57% compared to unnormalized values across three replicates. Furthermore, DEP effectively recovered beads with diverse characteristics, including variations in size, surface functionalization, and dye localization, highlighting their potential as alternative internal standard candidates.

To further address signal variability in EV biomarker detection, we explored the use of 10–15% w/v of the non-ionic detergent Tween 20. Preliminary experiments combining Tween 20 with fluorescent bead internal standards showed a reduction in signals from protein aggregates, such as human serum albumin (HSA). However, this also led to a marked decrease in the EV biomarker CD9 signal. This dual effect suggests that Tween 20 may disrupt both protein aggregates and EVs, thereby interfering with DEP-based capture. To counteract this, we investigated the use of additional additives in combination with Tween 20 to enhance DEP collection efficiency.

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Poster #120

Poster Pitch

Barriers to participation in Pancreatic Cancer Early Detection in the Community

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There are substantial disparities in access to and participation in cancer screening and early detection across communities. In many regions of the country, including Oregon, participation in cancer screening is lower among residents of rural and frontier areas (compared to urban) and among minoritized populations, particularly members of the Black, Indigenous, Hispanic and Latino communities. Understanding and addressing these disparities is imperative if we hope to effectively implement pancreatic cancer screening among those at-risk. To address this, we completed focus groups and patient engagement studios (interviews) to discuss patient perspectives of pancreatic cancer, screening principles, and the concept of early detection (n=86). The first groups included: 1) three rural counties in Oregon with the highest incidence of pancreatic cancer; 2) Black/African Americans; 3) Hispanic/Spanish speaking. We completed thematic analysis using the four priorities of the Health Belief Model: perceived susceptibility, perceived severity, perceived benefit, and perceived barriers to participation. We abstracted data from a total of 6 focus groups (2 conducted in Spanish) and 10 interviews. In addition to observations related to knowledge, facilitators and barriers to screening, two common themes were identified, the first emphasized starting with the most accurate test. The second focused on invasiveness, with a preference to start with a minimally invasive test and then pivoting to a more definitive test if necessary. These results informed the development of a 10-item survey that is undergoing validation testing with over 100 completed surveys and will be incorporated into the Healthy Oregon Project cohort to learn from a population sample of over 50,000 individuals the key barriers to pancreatic cancer screening and early detection uptake in communities.

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ABSTRACTS

Poster #121

Hypothesis-free machine learning reveals novel predictors of colon cancer risk from 3,342 features in UK Biobank

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Colon cancer is a major contributor to cancer-related morbidity and mortality worldwide. Early detection has the potential to alleviate this burden, with 5-year survival rates improving from ~10% when diagnosed at stage IV to ~90% at stage I. Risk prediction tools can facilitate earlier diagnosis and improve outcomes. Existing risk models are typically built on predefined variables, which may overlook unanticipated predictors. Machine learning can complement this approach by exploring thousands of features and their interactions, enabling the discovery of novel risk factors.

We trained gradient-boosted decision trees (XGBoost) with a Cox proportional hazards loss to predict incident colon cancer (n=5,563) in UK Biobank. A total of 3,342 features were included, spanning questionnaire data, biochemical markers, and prior diagnoses/medications. SHAP (SHapley Additive exPlanations) values were used to assess feature importance. To stabilise SHAP estimates, we implemented an ensembling strategy at two levels: 50 bootstrap samples to capture population variability, each with 5 randomly initialised models to account for XGBoost stochasticity. Top-ranked features were then evaluated in multivariable Cox models alongside known risk factors.

The SHAP-stabilised ensemble achieved an average concordance index (C-index) of 0.75 in the training set and 0.70 in a held-out test set, indicating good generalisability. SHAP values successfully recovered known colon cancer predictors, including age, polygenic risk score, anthropometric factors, alcohol consumption, smoking, family history of bowel cancer, and physical activity. The Cox model achieved a C-index of 0.73 in the training set 0.70 in the test set. Significant novel predictors included blood biomarkers (red blood cell distribution width [HR 1.08, 95% CI 1.03–1.13], plasma urea [HR 0.95, 95% CI 0.91–0.99], total protein [HR 0.97, 95% CI 0.96–0.99]), prior medical conditions (varicella infection [HR 0.55, 95% CI 0.41–0.73], 'other arthrosis' [HR 0.70, 95% CI 0.60–0.83]), and employment status [HR 1.37, 95% CI 1.00–1.87].

Hypothesis-free machine learning applied to large-scale biobank data can recover established colon cancer risk factors while identifying novel predictors with potential biological and clinical relevance. While further validation of these novel predictors must be undertaken, integrating these features into risk models has the potential to improve early identification of individuals at increased risk of colon cancer.

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Poster #122

Cancer early detection using cfDNA fragmentomics in Li-Fraumeni Syndrome

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Li-Fraumeni syndrome (LFS) is a very high risk cancer predisposition syndrome (80% by 70 years of age). Current early detection strategies rely on imaging surveillance. Studies have shown cell-free DNA (cfDNA) fragment length (FL) and inferred tumour fraction (TF) as potential biomarkers of early cancer in LFS.

We performed shallow whole-genome sequencing and fragmentomic analysis of cfDNA samples collected between May 2022 and April 2025 from 52 adults with LFS [43 with >1 sequential sample]. Cancer status determined by imaging (and pathology where indicated clinically) at the time of sampling was as follows: cancer naïve=61 (G1); current cancer (stage 1/2)=6 (G2a); current cancer (stage 3/4)=5 (G2b) [combined active cancer, stage 1-4, G2all (G2a+G2b)]; and previous cancer, currently cancer free =90 (G3) [total samples=162].

There was a statistically significant reduction in mean of median FLs (bp) in G2all (161.5) compared with G1 and G3 (168.8, Mann-Whitney U (MWU)=190, p=0.0197 and 168.3, MWU=282, p=0.0174 respectively) but not when G1 and G3 were compared with G2a (167.0, MWU=139.5, p=0.3429 and MWU=214.5, p=0.4079 respectively). No significant difference in median FLs was demonstrated between G1 and G3 (MWU=2702, p=0.868). FL ratio analysis (20-150bp:151-220bp) between sample groups demonstrated no significant difference between G1 (0.23) and G3 (0.24) (MWU=2682, p=0.8132) or between G1 and G3 individually compared to G2a (0.28; MWU=124, p=0.2045 and MWU=190, p=0.2354 respectively). However, a statistically significant difference in FL ratio was seen between both G1 and G3 when individually compared with G2all (0.68; MWU=189, p=0.0208 and MWU=286, p=0.0216 respectively). Inferred tumour fraction analysis demonstrated a statistically significant difference between G2a (0.08) and G2b (0.06; MWU=0, p=0.0043) but no significant difference was demonstrated between other groups.

Our results show a significant reduction in median cfDNA FLs and an increased ratio of smaller cfDNA fragments (<150bp) in individuals with active cancer at the time of sampling compared with those who were healthy, with or without previous cancer history. Further data and additional downstream analytical methods are required to develop these findings further, particularly in the early cancer group. Our data supports cfDNA FL being a biomarker of cancer in LFS patients for whom there is an urgent need for new cancer early detection strategies.

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Poster #123

An engineered high-precision microphysiologic model to investigate early interactions of squamous cell carcinoma with the bone microenvironment

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Early detection of cancer-associated bone remodeling is critical for improving patient outcomes, particularly in diseases like oral squamous cell carcinoma (OSCC), where bone invasion is a hallmark of aggressive progression. Bone homeostasis relies on tightly regulated interactions among osteoclasts, osteoblasts, and osteocytes, yet replicating these dynamic interactions in vitro has been challenging. Here, we present a bone-on-a-chip model designed to mimic the nanostructure and biological functions of native bone, utilizing a rapid biomimetic mineralization method. This platform enables osteoblast encapsulation in a matrix that calcifies, mimicking the process in real bone, and promotes osteocyte differentiation and paracrine regulation of osteoclastogenesis, thereby facilitating in vitro bone remodeling. The system demonstrated sensitivity to matrix-dependent osteoclast formation and function, outperforming conventional receptor activator of nuclear factor-κB ligand (RANKL) and macrophage colony-stimulating factor (M-CSF) treatments. Critically, the bone-on-a-chip model recapitulated tumor-bone interactions and reproduced patient-specific responses to anti-resorptive therapies, such as alendronate and denosumab, correlating with in vivo and clinical observations. By offering real-time interactions of cancer cells with the cellular and extracellular complexities of bone, this platform offers unprecedented potential for the early detection of cancer-induced bone changes, providing a transformative tool for understanding cancer-bone interactions and refining therapeutic strategies.

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ABSTRACTS

Poster #124

Protease Activity Level for Blood-Based Detection of Ovarian Cancer from Non-malignant Disease

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Proteases and their inhibitors can become dysregulated during ovarian cancer tumorigenesis and invasion, causing an excess of activity relative to healthy tissues or non-cancerous ovarian diseases. Increased activity does not necessarily directly correlate with genetic expression levels of proteases since proteases are transcribed in their inactive form and require intermediary processes to reach activation. Measuring protease activity directly could be a valuable biomarker to indicate the presence or progression of cancer. Many of these dysregulated proteases are released into circulation making it possible to monitor protease activity directly from blood. Protease activity can be monitored using synthetic peptide substrates designed with amino acid sequences specific to certain proteases. These peptides can be designed to create a fluorescent signal upon cleavage that is easily quantifiable. Proteases can cleave hundreds to thousands of peptides, and this results in signal amplification and highly sensitive assays. We investigated protease activity in ovarian cancer by performing a pilot study using a small cohort of patients with high-grade serous carcinoma (n=7) and benign ovarian disease (n=4) using a high-throughput substrate assay to screen 360 unique substrates for protease activity in albumin depleted plasma. The signal of fluorescent cleavage products was measured overtime and quantified for fluorescence intensity. We identified 28 peptides that showed a statistically significant increase in activation between cancer and non-cancer conditions. We then used sparse logistic regression and Student's t-test to select for 5 peptides and performed a blinded investigation of protease activity in albumin depleted serum from an expanded cohort of patients with ovarian cancers (n=48) and non-malignant ovarian diseases (n=27). We identified subsets of the 5 peptide candidates that are highly activated in ovarian cancer serum compared to benign cysts ($p<0.05$) and borderline tumors ($p<0.01$). Using inhibitors and purified enzymes, these peptides show evidence of specificity for matriptase-like proteases and metalloproteases. These cohort results have allowed us to identify peptide candidates that we aim to further investigate as a panel in a larger cohort study with healthy controls.

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Poster #125

Label-free Raman spectroscopy integrated with machine learning for the cancer early detection.

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COMPANY/INSTITUTION:

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The development of new methods with high sensitivity and specificity for early cancer detection is in high demand. Some methods focused on analyzing a tissue (e.g., cyclic immunofluorescence) require complex sample preparation or the introduction of additional labels or staining that can modify a sample in an unknown way. Conventional Raman spectroscopy is a well-established method that provides precise information about the sample composition without the need for additional labels or sample modification. The goal is to identify a cancer cell in a tissue without introducing labels or applying aggressive treatment to the sample will benefit the current cancer diagnostic methods.

Because of the nature of the effect, Raman provides information about all bond vibrations present in the sample and ultimately reveals the chemical composition of the studied material. The Raman method is widely used in industry, for example, in material or medicinal fields as a quality control measure. Currently, Raman is used as an analytical tool and focused on the analysis of strong signals of interest. Unfortunately, the application of Raman for biological samples is not straightforward and requires additional investigations due to inherently complex and low signals, the primer focus of our study.

At present, we are working on the integration of Raman spectroscopy with machine learning. We have a significant progress in sample preparation and data collection of the cell culture on the easily accessible benchtop Horiba Xplora instrument. We were able to detect a spectral difference of cells in different states, apoptosis vs non-treated cells. There is a clear change in the spectra with the change in the state of the cell. Also, the difference in the Raman signal corresponding to the separate parts of the cells (nucleus vs cytoplasm) is identified using clustering methods, opening the door for advanced machine learning methods. The acquired data is used for model training for the final goal of distinguishing cancerous and healthy cells and future implementation in cancer screening.

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Poster #126

Structure of extrachromosomal DNA revealed by super-resolution microscopy

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Extrachromosomal DNA (ecDNA) has increasingly been recognized as a hallmark of cancer (Weiser, 2025). A key function of ecDNA is to harbor and drive the over-expression of known oncogenes such as EGFR and MYC. The mechanisms through which ecDNA achieves gene over-expression are only partially understood, and a complete understanding of these mechanisms require analysis of both the sequence and the structure of ecDNAs, including the associated proteins and regulatory elements. Currently, most ecDNA detection methods rely on either sequencing or fluorescence in situ hybridization (FISH). Sequencing-based methods (Pecorino, 2022) offer high specificity and complete characterization of the complex gene content of ecDNAs but provide limited insight into the corresponding 3D organization. DNA-FISH (Dong, 2023) allows sequence-specific detection of ecDNA but is not designed to resolve the complete 3D organization of these small (100-300 nm) particles. In addition, recent studies (Bailey, 2024) have revealed that the genetic content of ecDNA can be heterogeneous. We hypothesize that ecDNA particles are also structurally heterogeneous. This structural heterogeneity may reflect both the intra-molecular topological associations and the compositional heterogeneity. To test this hypothesis, we use an optimized super-resolution microscopy approach to resolve the DNA backbone of individual ecDNA molecules with <20 nm spatial resolution, which can be combined with FISH and other histone marker imaging strategies. Through quantitative image analysis, we show how ecDNA is structurally heterogeneous and how the organization of DNA and associated proteins is different from the well-studied chromosomal DNA. These structural changes may confer high levels of gene expression through a variety of mechanisms, some of which are specific to the unique structural composition of ecDNA nanodomains. Our work provides new insight into the physical organization of ecDNA, complementing prior studies that primarily utilize sequencing and biochemical methods.

References:

Bailey, C. et al. (2024), Nature 635, 193–200.

Dong, Y. et al. (2023), Frontiers in Oncology 13, 1194405.

Pecorino, L.T. et al. (2022), Biochemical Society Transactions 50, 1911–1920.

Weiser, N.E. et al. (2025), Cancer Discovery 15, 1105–1114.

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Poster #127

hla2vec: Embedding based clustering of HLA alleles

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The genes in the major histocompatibility complex (MHC) that code for the Human Leukocyte Antigen (HLA) protein complex are some of the most diverse genes in the genome. HLA class I typing for TCGA tumor RNA-seq data, comprising 33 cancer types, resulted in over 300 HLA alleles, this is only a fraction of the large landscape, with the IMGT/HLA database reporting nearly 20 thousand HLA class I alleles. Each one of these alleles can have major alteration into the peptides that are selected for antigen presentation, and thus alter T Cell Receptor (TCR) selection and immune response to neo-antigens. TCR profiling via cfDNA is one of the methods being researched for early cancer detection, but to understand TCR response, we must understand the HLA alleles that are modulating it. This research project seeks to quantify the actual space of HLA alleles by using deep learning based methods to create an embedding space for HLA data. Using the BigMHC dataset, with almost 15 million tested HLA binding assays, we looked for pairs of HLA alleles that were tested against the same peptides. Then using a new algorithm derived from the word2vec method, we trained a deep learning model to recognize these pairs of HLA alleles that had similar binding patterns. This gave us an encoder that could be used to place HLA alleles into an embedding space for analysis. In this embedding space, alleles that have similar binding patterns are placed near each other. This deep learning based distance metric can then be used to cluster HLA alleles into subtypes, grouping together patients likely to have similar immune MHC binding patterns.

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Poster #128

Developing 3D Tumor Model Systems to Investigate Early Cancer Progression Using Multiplexed Spatiotemporally-Controlled Genetic Manipulation

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Tissue-engineered in-vitro 3D model systems using hydrogel matrices are a promising tool to study early cancer progression by replicating important aspects of cell-cell and cell-matrix interactions. However, there is a need to temporally and spatially control genetic manipulation to probe how mutated cell populations interact with the surrounding healthy cells and how this contributes to tumor formation. In particular, there is increasing evidence supporting that many cancers have a polyclonal origin, with multiple mutated populations contributing to tumor formation. Modeling polyclonal cancer progression will require controlled delivery of different genetic payloads to different cells at different times. This is challenging to achieve with traditional gene delivery vehicles, such as viruses or lipid particles, due to the diffusional barriers presented by the matrix. To address this challenge, we have developed a technology to achieve spatial and temporal control of gene delivery through the integration of gas-core lipid-shell microbubble particles that facilitate delivery of their DNA payloads to nearby cells when exposed to focused ultrasound. Our objective is to develop a technique to selectively activate different size populations of gene delivery particles within 3D tumor models, enabling the sequential delivery of multiple genes. Our approach is to fabricate different size populations of particles (small, medium, large) that each is activated at different ultrasound intensities. Here we show the first steps of successful multiplexed DNA delivery based on particle size, concentration, and ultrasound intensity. Hydrogels containing medium-sized particles showed higher transfection levels at 100% ultrasound intensity at a concentration of 10^9 particles/mL. Small microparticles showed higher transfection at 25% ultrasound intensity and 10^10 particles/mL. Multiplexed particle experiments utilized hydrogels containing a 50-50% ratio between small and large microparticles. Optimal ultrasound conditions for the small particles were applied and showed small particles preferentially transfected cells twice as much as the large particles. This technique paves the way for future multiplexed ultrasound-triggered delivery within hydrogel tissue models, which can enable activation of multiple genetic manipulations relevant to early disease progression and lead to identification of new biomarkers that will be critically important for early detection applications.

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Poster #129

Elucidating the Relationship Between Pancreatic Cancer and the Liver during Early and Pre-Cancer Progression

PRESENTING AUTHOR:

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Pancreatic Ductal Adenocarcinoma (PDAC) is known for its asymptomatic early stages and metastatic late stages. While the overall 5-year survival rate is ~13%, the rate increases dramatically to ~80% when diagnosed early. The majority of cases are found at the late stage, but even when diagnosed early, 70% of patients will experience recurrence after surgical resection—most often arising as liver metastases. Despite the mutational progression from pancreatic intraepithelial neoplasia (PanIN) precursor lesions to PDAC being fairly well described, early diagnosis remains elusive. However, while seeking more effective diagnostic methods using blood biopsies, our team discovered that liver-specific cell free-mRNA was upregulated in early-stage PDAC patients regardless of metastatic status. Further supporting this observation of a close communicative relationship during early disease progression, work using a PDAC mouse model showed liver premetastatic niche formation (PMN) was initiated during the development of low grade PanINs. These observations have led to the hypothesis that liver PMN formation is initiated during PanIN development in humans.

In order to elucidate this PDAC-liver relationship leading to liver PMN formation, we are using patient-derived organoids (PDOs) as a representative model. PDO cultures have been shown to secrete cell free-RNA similar to that found in human plasma, and the ability of in vitro liver organoid cocultures to recapitulate aspects of PMN formation has been demonstrated. To recapitulate the effects seen in our patient cohort, PDAC cell lines and late stage PDAC PDOs will be co-cultured with complex, multi cell type liver organoids. To model pre-PDAC development, we have developed a number of normal pancreas PDOs that will be sequentially CRISPR-engineered with mutations known to be associated with PDAC progression. Analyzing the changes in cellular and cell-free RNA and protein expression between these cocultures will generate a stepwise timeline of pre- to advanced cancer progression that would otherwise be infeasible in a patient cohort.

This project seeks to validate a novel co-culture method and enhance our understanding of pre-PDAC development in the context of the liver and clarify the inter-organ relationship leading to liver PMN formation during pre-PDAC progression. Ultimately, this work will support further endeavors in identifying early PDAC detection markers.

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Poster #130

External validation of the Full BLOOD count trends for colorectal cancer detection (BLOODTRACC) risk prediction models in English primary care

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Background: Colorectal cancer is common in the UK. Around 55% of patients are diagnosed late-stage, where likelihood of survival is low (five-year survival: 90% at Stage 1; 10% at stage 4). To facilitate earlier detection, we developed the sex-stratified BLOODTRACC models, dynamic prediction models utilising age and patient-level trends over repeat full blood count (FBC) tests in primary care for two-year risk of colorectal cancer.

Aim: To externally validate the BLOODTRACC models in a primary care dataset.

Methods: We performed a cohort study using primary care patient data between 01/01/2000 and 31/12/2018 from the Clinical Practice Research Datalink, linked to the National Cancer Registration and Analysis Service. Eligible patients had at least one FBC test and no history of colorectal cancer before their current FBC (baseline). Trends over historical FBCs taken over five years prior to the current FBC informed risk of diagnosis in two years (+/- 3 months). Co-occurring symptoms at baseline FBC were extracted. Model performance was assessed using the area under the curve (AUC) and calibration statistics, with 95% confidence intervals (CIs).

Results: We included 2,956,977 males and 3,561,349 females, with 0.5% (n=13,423) and 0.4% (n=12,919) diagnosed in two years following their current FBC, respectively. Mean (standard deviation (SD)) age at current FBC was 60.8 (13.5) years for men and 62.2 (15.0) years for women. The AUC (95% CI) of the models was comparable for both men and women (0.75 (0.74-0.75)) and between patients with and without colorectal cancer-related symptoms for both men (with 0.75 (0.73-0.78); without 0.74 (0.74-0.75)) and women (with 0.71 (0.69-0.74); without 0.74 (0.74-0.75)). Combining blood test trend with presence of co-occurring change in bowel habit gave the highest AUC (men 0.81 (0.75-0.87); women 0.76 (0.67-0.85)). The calibration slope (95% CI) was 0.97 (0.95-0.99) for men and 0.98 (0.96-0.99) for women. We will present further results, including predictive performance by stage at diagnosis.

Conclusion: The dynamic BLOODTRACC prediction models identify patients with undiagnosed colorectal cancer with good discrimination. We developed an evidence base for incorporating blood test trend into primary care clinical guidance for improved colorectal cancer detection. Further work is underway to enhance performance of the models and investigate the role of blood test trend for detection of other cancers.

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Poster #131

Lightning Talk

Blood test trends for cancer detection in patients presenting with non-specific symptoms in primary care: a diagnostic accuracy, longitudinal cohort study

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Background: Non-specific symptoms (NSSs), such as constipation and reflux, result in diagnostic delays in primary care. Our recent work found that monitoring temporal changes (or trends) over repeat blood tests in patients with unexplained weight loss identifies high-risk patients prior to blood test abnormality, such as thrombocytosis (raised platelets). We compared the predictive performance of blood test trend to abnormality in 18 NSS cohorts.

Methods: We performed a multi-cohort study (18 cohorts). Each cohort included the first presentation of that NSS over 01/01/2000-31/12/2018 from the Clinical Practice Research Datalink. Patients were aged 18+ years and had at least two blood tests over five years pre-NSS. Blood tests commonly performed in primary care were studied: liver function test, full blood count, and inflammatory markers. Repeat blood tests over five years pre-NSS derived trends. Blood test abnormality was defined using established reference ranges, such as albumin <35g/L, on blood tests co-occurring with the NSS. The outcome was cancer diagnosis within six months post-NSS (yes/no). To model the association with cancer risk, we used joint models for trend and Cox models for abnormality (yes/no), with adjustment for age and sex. A two-sided 5% significance level was used. The area under the curve (AUC) with (95% confidence interval (CI)) was derived.

Results: The cohort size ranged from 121,948 with bloating to 3,432,338 with back pain. A declining trend in red blood cell-related tests and rising trend in others tests was associated with cancer diagnosis in each NSS cohort, except haemoglobin in patients with constipation (HR=1.00, 95% CI=1.00-1.00, p=0.313), bilirubin in patients with venous thromboembolism (HR=1.01, 95% CI=1.00-1.02, p=0.080), and haemoglobin, mean corpuscular volume, and bilirubin in patients with a fever. Blood test trend gave a higher AUC (95% CI) than abnormality for most blood tests in each NSS cohort, except comparable (overlapping CIs) AUCs for haemoglobin in most NSS cohorts. For example, haemoglobin trend 0.70 (0.70-0.72) and abnormally low 0.72 (0.71-0.73) in patients with constipation and trend 0.65 (0.64-0.66) and abnormally low 0.66 (0.65-0.67) in patients with appetite loss. We will present the positive and negative predictive value of trend.

Discussion: Monitoring temporal changes in some commonly used blood tests may enhance cancer risk stratification in patients presenting with NSSs in primary care.

ABSTRACTS

Poster #132

Investigating the effectiveness of a chatbot in promoting National Health Service Bowel Cancer Screening Intentions: a randomised survey

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Introduction: Across the United Kingdom, colorectal cancer (CRC) screening uptake remains low. Barriers include miscomprehension about screening processes. We have developed a chatbot that aims to support informed decision-making about screening participation through personalised, supportive dialogue. This study aimed to test the chatbot's impact on screening intentions compared to a static website.

Methods: A three-arm online randomised survey (n = 1,046) was conducted in which participants were allocated to either a static website with a chatbot, standard screening information with a chatbot, or a static website alone. Participants were either pre-eligible (ages 34-49, n = 559) or eligible (ages 50-75, n = 487) for bowel cancer screening.

Results: The majority of respondents who were given standard information and a link to a chatbot, actively interacted with the chatbot (pre-eligible = 64.36%, eligible = 55.95%). Users agreed that the chatbot provided relevant (44.87%) and effective replies (40.85%). Less than 31.92% were worried about privacy or security. All arms showed increased likelihood of future screening participation with no significant between-group differences. Importantly, chatbot satisfaction significantly predicted future likelihood to participate in screening ($\beta = 0.46$, $p = 0.01$) ($R2 = 0.031$, $F(1, 186) = 6.035$, $p = 0.01$). In open-ended responses users suggested providing more personalised and specific responses as an improvement for future iterations.

Conclusion: Having a satisfactory user experience with a chatbot was positively associated with intended CRC screening participation. Work to increase satisfaction with chatbot use should focus on further personalisation and improving the library of chatbot responses.

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Poster #133

Poster Pitch

FTIR Imaging and Machine Learning for Early Detection of Oral Cancer in Precancerous Lesions

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Oral squamous cell carcinoma (OSCC) is a very aggressive cancer with a poor five-year survival rate of 50%. Oral epithelial dysplasia (OED) is a precancerous lesion carrying an increased risk of malignant transformation (MT) to OSCC. Unfortunately, the gold standard histopathological diagnosis of OED relies on subjective morphological evaluation of the biopsy tissue and is inaccurate in predicting their MT risk, making oral precancer management one of the biggest challenges for clinicians. We propose using Fourier transform infrared (FTIR) spectroscopic imaging combined with machine learning (ML) as a novel approach to address the medical gap in OED diagnosis, with the goal of enabling early detection of oral cancer in precancerous lesions.

FTIR provides comprehensive and non-destructive biochemical profiling of tissues, known as "biomolecular fingerprinting". Building on our previous finding that FTIR imaging combined with ML achieved 100% accuracy in distinguishing OSCC from benign tissues, we hypothesized that the FTIR-ML approach can also predict MT in OED. In this study, we tested this hypothesis using 30 OED biopsies, including 12 with and 18 without MT. Formalin-fixed-paraffin-embedded biopsy blocks were cut into two consecutive sections for H&E staining and FTIR analysis respectively. Six regions of interest (ROIs) were selected from each biopsy and were imaged using a Perkin Elmer FTIR Spectrum Spotlight system in transmission mode. The Eigenvector PLS_Toolbox software was used to preprocess and analyze the FTIR images. Average epithelial spectrum was extracted from each ROI image, generating an OED dataset of 180 spectra with corresponding MT labels. We used the OED dataset as a test set for the previously trained OSCC-Benign PLS-DA model and also trained a new PLS-DA model using cross-validation. Both models demonstrated strong performance, achieving accuracies of 81.7–83.3% and F1 scores of 0.77–0.80 in predicting MT in the 30 OED biopsies—substantially outperforming the 24–40% accuracy of the conventional histopathological approach.

Our findings present exciting evidence supporting the feasibility and clinical translation of the FTIR-ML approach in assessing the MT risk in precancerous oral patients. This innovative approach holds significant promise in providing objective, quantitative, and reliable risk evaluation for precancerous oral lesions, facilitating their treatment and management and enabling early detection of oral cancer.

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ABSTRACTS

Poster #134

Distinguishing Early Stage Pancreatic Cancer from Benign Pancreatic Disease via Electrokinetic Separation and Electrochemical Sensing of Liquid Biopsy Samples

PRESENTING AUTHOR:

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AUTHORS:

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Early detection of pancreatic cancer remains a critical unmet need, as current diagnostic tools lack the sensitivity and specificity required for effective intervention. Circulating extracellular vesicles (EVs) offer a rich source of tumor-derived biomarkers but are notoriously difficult to isolate and analyze from complex biological fluids such as whole blood or plasma, limiting their clinical utility. We present a novel microfluidic device that leverages dielectrophoresis (DEP) for rapid, label-free isolation and electrochemical quantification of EVs directly from undiluted plasma and whole blood. The device features engineered electrode geometries that generate sufficient electric field gradients to isolate EVs, even from undiluted plasma and whole blood samples without requiring hydrogels or insulative coatings. Unlike traditional EV isolation by ultracentrifugation, which can take up to 24 hours, our method achieves isolation in just 8 minutes. By applying a 14 kHz, 5 Vpp AC signal, the system captures EVs via positive DEP while simultaneously repelling red blood cells through negative DEP, reducing nonspecific background. EV presence was validated via immunofluorescence and electron microscopy. Following isolation, we performed on-chip quantification of tumor biomarkers using square wave voltammetry and electrochemically-labeled antibodies. This approach yielded a 10-fold improvement in signal-to-noise ratio and a 2% enhancement in coefficient of variation compared to fluorescence-based methods. Notably, the device achieved a limit of detection of 0.95 µg/mL for EV-bound CD9—outperforming commercial ELISA assays by an order of magnitude. In a blinded study of 52 patient samples (pancreatic cancer vs. benign pancreatic disease), quantification of a three-biomarker panel yielded an area under the ROC curve (AUC) of 0.93, representing an 85% improvement over the only FDA-approved liquid biopsy for pancreatic cancer. This technology offers a fast, portable, and cost-effective platform for EV-based liquid biopsy, supporting high-sensitivity cancer detection and enabling earlier intervention in clinical settings.

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ABSTRACTS

Poster #135

Deciphering the Role of the Immune Microenvironment in DCIS Progression Risk

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Ductal carcinoma in situ (DCIS) is a non-obligate precursor to invasive breast cancer (IBC). Only 10–15% of patients who do not undergo locoregional treatment develop IBC within 5.5 years, yet almost every woman diagnosed faces breast-conserving surgery (BCS), often with adjuvant radiotherapy, and many undergo endocrine therapy or even mastectomy. This widespread overtreatment drives an urgent need for reliable biomarkers of progression risk. Given the pivotal role of the immune microenvironment (IME) in the progression of many cancers, we hypothesized that spatial interactions in the DCIS IME, alone or in concert with the genomic profile of the DCIS epithelium, could unmask hidden risk signals.

We performed multiplex immunofluorescence (mIF) to identify B cells, macrophages, helper, cytotoxic and regulatory T cells on 141 tissue slides from surgical resections of DCIS patients (77 progressors, 64 non progressors) from a Dutch population-based cohort. All were treated with BCS alone. In parallel, RNA Seq (n=361; 126 matched) and targeted Panel Seq (n=103 matched) data enabled integrated immune–genomic analyses.

We computed first nearest neighbour (1NN) distances across all 36 possible cell phenotype combinations. While none were associated with progressor status, ER status, HER2 status and Ki67 score were all clearly associated with immune to DCIS cell distances. HER2 was independently associated with distances to B cells while Ki67 was associated with distances to regulatory T cells. TP53 mutant lesions exhibited higher stromal density of all T cell types and was associated with all immune to DCIS distances.

Clustering by gene co-expression on 361 RNA-Seq samples yielded 38 gene modules; immune related and hormone signaling modules showed the strongest correlations in samples matched to mIF (n=126) with IME spatial metrics. Notably, a hormone signaling module had markedly differential expression in a mostly HER2+, immune hot subset, with SOX11—an embryonic mammary transcription factor previously linked to faster progression—clearly overexpressed in these samples.

While no link could be made between the spatial distribution of the DCIS IME at surgical resection and the risk of later progression to IBC, this study reveals clear interactions between the DCIS IME and hormonal and genomic features of the DCIS epithelium that may work in tandem to influence the progression journey to IBC.

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ABSTRACTS

Poster #136

Metabolic risk is an important determinant of adipocyte hypertrophy beyond age, BMI and breast density in patients with ductal carcinoma in situ

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Background

Ductal carcinoma in situ (DCIS) is a non-obligate precursor to invasive breast cancer, but distinguishing patients with harmless from potentially hazardous ductal carcinoma in situ (DCIS) remains a challenge. A recent biomarker that was found to be prognostic of invasive breast cancer is adipocyte hypertrophy. However, little is known about the correlation between adipocyte size, clinical factors and mammographic breast density.

Methods

Archival hematoxylin and eosin- stained breast biopsy and excision specimens were retrieved from 669 women diagnosed with primary DCIS between 2000 and 2020 treated at the Netherlands Cancer Institute. These slides were digitized whereafter a machine-learning algorithm using HALO®, was applied to retrieve adipocyte size. Radiology reports were obtained to extract mammographic BI-RADS density. Age at diagnosis, body mass index (BMI), menopausal status and information on comorbidities were extracted from electronic patient records. A composite metabolic risk score was created using comorbidity data. Associations between adipocyte size, clinical factors and density were investigated using univariable and multivariable linear regression models.

Results

Significant positive correlations (p= <0.0001) were found between adipocyte size and age, BMI and all metabolic comorbidities with the exception of smoking. Strong negative correlations were found between adipocyte size and density categories C and D (p= <0.0001). In univariable linear models with age and BMI, the metabolic risk score was able to further differentiate between patients with and without adipocyte hypertrophy beyond age and BMI using a clinically relevant cut-off. In multivariable analysis, age, density, BMI and metabolic risk remained statistically significant in association to adipocyte hypertrophy.

Conclusion

BMI is the strongest predictor of adipocyte hypertrophy in DCIS patients, however metabolic risk further differentiates between patients with and without adipocyte hypertrophy. Future work should investigate metabolic risk in combination with clinical factors in the progression of DCIS.

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ABSTRACTS

Poster #137

The effect of ECM composition and stiffness on pancreatic cancer organoid behavior

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Pancreatic ductal adenocarcinoma (PDAC) is the most common form of pancreatic cancer and has a five-year survival rate of ~13%, which is further decreased to <4% when diagnosed at an advanced stage. Therefore, it is important to understand how PDAC progresses from premalignancy to malignancy and to identify interventions to inhibit this progression. Pancreatic cells gain genetic mutations over the course of development into cancer that drive their malignant behavior. KRAS mutations, especially KRASG12D, are found in greater than 90% of PDAC cases and arise in low-grade PanIN lesions. TP53 mutations occur in around 75% of PDAC cases and are found in high-grade PanIN lesions. Together, these mutations have been shown to be sufficient to drive PDAC development in mouse models and confer a cancerous phenotype to organoids.

It has been shown that the composition of the extracellular matrix (ECM) changes during the progression from normal tissue to premalignant PanIN lesions to PDAC. It is also known that the pancreas becomes stiffer and more fibrotic during tumor progression. However, it is not known how these changes in composition and stiffness affect specific aspects of cancer cell behavior, such as proliferation, invasion, and epithelial to mesenchymal transition. We aimed to determine how cancer cell behavior differs between normal and tumor microenvironments, focusing specifically on the composition and stiffness of the ECM.

We optimized a protocol to decellularize tissue which leaves matrix proteins intact while removing cellular content. We cultured normal organoids and organoids with KRASG12D and TP53 mutations (KPC) on these decellularized ECM scaffolds to determine the effect of normal vs tumor matrix composition on cancer cell behavior. To isolate the effect of stiffness on cancer cell behavior, we cultured normal and KPC organoids in soft and stiff PEG hydrogels whose stiffness can be controlled by increasing cross-linking without changing composition. We then validated the use of live cell dyes to visualize changes in the mitochondria, cell membrane, and F-actin cytoskeleton over time.

Analysis of live cell imaging of these dyes revealed distinct morphologies between organoids plated on normal versus tumor decellularized ECM scaffolds and on soft vs stiff PEG hydrogels. By taking a systematic approach to these experiments, we determined how mutations and properties of the microenvironment affect cancer cell behavior.

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ABSTRACTS

Poster #138

Turning Indocyanine Green (ICG) into a Tumor Targeting Dye for Cancer Early Detection and Therapy

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Indocyanine green (ICG) is a near-infrared (NIR) fluorescent dye approved by the FDA and widely used in clinical imaging due to its favorable optical properties and safety profile. However, its clinical utility in tumor imaging is limited by poor aqueous solubility, aggregation-induced fluorescence quenching, short circulation time, and nonspecific tumor accumulation via the enhanced permeability and retention (EPR) effect. To overcome the limitations, we developed a series of peptide-conjugated ICG derivatives by attaching short hydrophilic peptide chains composed of hydrophilic amino acids such as aspartic acid or lysine residues. These modifications were designed to enhance aqueous solubility, prevent aggregation, and reduce non-specific plasma protein binding. Our leading candidate (SP-ICG) demonstrated the greatest improvement in solubility, maintaining over 80% of the dye in an unbound state following plasma incubation. Upon intravenous injection, all peptide-ICG conjugates exhibited extended circulation times, with prolonged blood circulation over 24 hours. The enhanced solubility also enabled renal clearance. In vivo live animal imaging revealed that SP-ICG began accumulating in tumors as early as 4 hours post-injection, with a significantly high tumor-to-background ratio (>7) 24 hours post-intravenous injection. SP-ICG was also capable of detecting early-stage lesions, as evidenced by strong fluorescence in sub-millimeter 4T1 mammary tumors formed only 2 days after injection. SP-ICG demonstrated broad tumor-targeting capability across multiple models of colon, breast, lung, skin, and cervical cancers, including HCT-116, A375, HeLa, MC38, YUMM, LLC, and TRAMP-C2 models. Additionally, the modularity of the peptide scaffold allows for the conjugation of therapeutic payloads, such as chemotherapies, positioning SP-ICG as a dual-function platform for both imaging and targeted drug delivery. These findings establish SP-ICG as a highly promising agent for tumor-targeted delivery of contrast agents and therapeutic molecules for the detection and therapy of early cancers.

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ABSTRACTS

Poster #139

High-throughput image-based phenotypic profiling of immune cells with germline PALB2 variants for pathogenicity prediction

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Individuals with germline variants in the homologous recombination repair gene PALB2 are at significantly higher risk for breast, as well as ovarian, pancreatic, and prostate cancers. However, approximately half of the reported PALB2 variants are classified as variants of uncertain significance (VUS), complicating cancer risk stratification and patient management. While deficiencies in DNA damage repair (DDR) pathways have been shown to alter immune responses and immunoregulatory processes, most studies have focused on tumors and cancer cells, leaving the impact of germline variants on immune cell functionality largely unexplored. In this study, we employed a high-throughput image-based phenotypic profiling (HIPP) method to characterize cellular morphological, immunological, and DDR-related phenotypes in immune cells. Peripheral blood mononuclear cells (PBMCs) from a total of 26 individuals, including 13 carriers of germline pathogenic PALB2 variants and 13 non-carriers, were studied and ~200 phenotypic features were automatically quantified from each single cell. Our findings reveal that PBMCs from pathogenic PALB2 variant carriers exhibit a distinct phenotypic profile, suggesting the influence of germline pathogenic PALB2 variants on immune cell morphology and function. The identified discriminative features were subsequently used to develop computational models for pathogenicity prediction and classification of VUS, offering a potential tool for enhanced clinical interpretation. This approach may be extended to other genes of interest, helping to address the clinical challenges associated with VUS.

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ABSTRACTS

Poster #140

Lightning Talk

Leveraging proteomics and deep learning for non-invasive head and neck cancer detection through passive saliva monitoring (SensOrPass)

PRESENTING AUTHOR:

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Background: Early detection of Head and neck cancer (HNC) has the potential to substantially improve survival outcomes for HNC patients. There are currently no HNC biomarker tests used for early detection in routine clinical practice. Case-control studies that could be used to derive diagnostic biomarkers tend to be underpowered. Recent evidence suggests that we may be able to address this challenge by leveraging pan-cancer variation in data from large population studies using approaches from deep learning.

Methods: We compare a range of machine learning approaches and model training scenarios to use proteome data to distinguish between HNC cases and controls. Models were trained using blood plasma proteomes from the UK Biobank (UKB) with n = 13,208 pan-cancer cases. Prediction performance was assessed in a cross-tissue comparison using an independently collected sample, the SensOrPass HNC case-control study (n = 175), with proteomes obtained from saliva rather than blood plasma.

Results: We obtain best performance (AUC=0.87 versus AUC < 0.75 for others) from a transfer learning approach we call CNN-Synth, a convolutional neural network trained in UKB to distinguish between profiles from a set of controls and cases including synthetic profiles generated by a pretrained variational autoencoder. Post-hoc explainability using SHapley Additive explanations identified IL6, CXL17, CXCL13, IGF1R and FASLG as the top five proteins contributing to predictor performance.

Discussion: Our findings underscore the potential for deep learning and explainable AI to leverage data from large population datasets to advance early cancer detection and improve clinical outcomes.

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ABSTRACTS

Poster #141

Poster Pitch

Multiplexed super-resolution imaging of mitochondria in clinical tissue sections reveals systematic structural rearrangements during pancreatic cancer progression

PRESENTING AUTHOR:

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AUTHORS:

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Pancreatic ductal adenocarcinoma (PDAC) ranks among the deadliest cancers, largely due to the absence of effective early detection methods and limited treatment options at advanced stages. This disease often arises from pancreatic intraepithelial neoplasms (PanINs) with increasing cell proliferation and progressive stromal thickening. The progression is accompanied by structural reorganizations within the tissue at molecular to cellular scales. Direct analysis of these molecular and structural changes is essential for revealing mechanisms of malignancy and discovering diagnostic markers but has been difficult with conventional imaging methods due to limitations in spatial resolution and field-of-view (FOV). To address these challenges, we have recently developed PRIME-PAINT (PRism-Illumination and Microfluidics-Enhanced DNA-PAINT), a super-resolution fluorescence microscopy platform designed for large-scale, multiplexed imaging of cell populations and tissue sections. Leveraging large field illumination and on-stage microfluidics, PRIME-PAINT achieves 25–40 nm lateral resolutions across FOVs up to 0.5 mm x 0.5 mm and is compatible with formalin-fixed paraffin-embedded (FFPE) tissues. We have used PRIME-PAINT to examine changes in mitochondria, an important organelle involved in metabolic reprogramming during PDAC progression in patient biopsies. Using an optimized sample preparation workflow, we were able to clearly resolve the fine structures of mitochondria in the tissue sections, allowing us to detect alterations in mitochondria abundance, structure, and spatial distribution in low- and high-grade PanINs and in PDAC regions. Our findings provide new insights into changes in mitochondrial function during PDAC progression and demonstrate the utility of PRIME-PAINT in analyzing a wider range of cellular structures during cancer progression.

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ABSTRACTS

Poster #142

Integrated epidemiological and genomic data yields insights into the relationship between precancer and cancer states of the oesophagus

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Cancer generally takes years to evolve, and early diagnosis can prevent life-threatening cancer. Symptomatic, advanced cancers often lack evidence of a precancer at diagnosis and yet, if the link between a precancerous state and cancer can be proven, the opportunity arises for screening and prevention. Oesophageal adenocarcinoma (EAC) is an increasingly prevalent, poor outcome cancer and its presumed precursor, Barrett's oesophagus (BE) is only evident in around half of cases. To test the hypothesis that BE is not a pre-requisite to EAC we classified a prospective cohort of 3,100 EAC patients for any evidence of BE and compared the epidemiological, clinical and genomic characteristics. Our findings demonstrate that the specific demographic and genomic features observed in BE also correlate strongly with EAC, regardless of the presence of a BE phenotype. Further we found evidence for the earliest features of BE evolution in both BE-negative and BE-positive EAC phenotypes. Advanced tumour stage was the only variable that corresponded with increased likelihood of BE-negative EAC, including in some patients with a prior diagnosis of Barrett's. Phylogenetic analysis of multiregional cancer samples further demonstrated that BE-negative and BE-positive EAC share similar evolutionary trajectories. The role of a single BE-mediated pathway to EAC has implications for early diagnosis strategies. We anticipate that our methodology combining large epidemiological and genomic datasets with respect to phenotype could help establish the significance of other precancer states.

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ABSTRACTS

Poster #143

Deconvolving the Patterns of Copy Number Alterations in Barrett's Esophagus Progression from Multi-Regional Sequencing

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Introduction The progression of Barrett's Esophagus (BE) to malignancy is accompanied by increasing copy number alterations (CNAs). However, the timing of CNAs events during evolution remains unclear. This study leverages multi-regional, longitudinal sequencing of BE to map CNA temporal dynamics, identify key drivers of BE progression, and improve risk stratification.

Methods Two BE cohorts were analyzed. The discovery cohort included shallow whole-genome sequencing (sWGS, 0.4X) from 777 BE samples across 88 patients, while the validation cohort included 256 BE samples from 95 patients. We refined the bioinformatics tool RASCAL1 to improve absolute CNA analysis by automatically selecting high-quality samples. Phylogenetic trees were generated by MEDICC22 to classify CNAs along an evolutionary timeline. Risk scores were computed based on the probability of CNA occurrence in non-progressing vs. dysplastic BE samples. A random forest model was trained to predict dysplasia based on risk score and validated in an independent cohort.

Results In the discovery cohort, 52.3% (260/497) of NDBE and 75.2% (124/165) of dysplastic samples were high-quality, with 16.9% (21/124) of dysplastic samples exhibiting whole genome doubling (WGD). In the validation cohort, 79.4% (181/228) of NDBE and 86.2% (25/29) of dysplasia/cancer samples were high-quality, with WGD in 24.0% (6/25) of dysplastic cases. Early-stage CNAs in non-progressing BE showed specific chromosomal gains and losses, whereas later-stage CNAs in dysplasia were more widespread and less commonly shared. Risk scoring of known drivers revealed that SMAD4 losses and CCND3/GATA4 gains were linked to dysplasia. Our model with divergent evolutionary patterns predicted dysplasia with an AUC of 0.89 (Sensitivity: 80.6%, Specificity: 95.7%) in the discovery set and AUC of 0.84 in the validation set (Sensitivity: 73.1%, Specificity: 93.9%).

Conclusion This study maps CNA evolutionary trajectories in BE, demonstrating selective constraints in early evolution and stochastic processes in dysplastic progression. CNA-based risk scores offer a promising tool for lesion risk stratification.

Agenda »

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