HYBRID EVENT

ScitechSeries

2ND INTERNATIONAL CONFERENCE ON

INNOVATIONS AND ADVANCES IN CANCER RESEARCH AND TREATMENT

VENUE

DoubleTree by Hilton Boston Logan Airport Chelsea
Address : 201 Everett Ave, Chelsea, MA 02150,
United States

NOVEMBER 06-07, 2024

Contact Us:

info@scitechseries.com

+44 2045874848

https://www.scitechseries.com/

+44 2045250803

Table of Contents

Our Keynote Speakers

Jianhua Luo
University of Pittsburgh
USA

Johnathan Whetstine
Fox Chase Cancer Center
USA

Eric Scheinbart
Immunity Redefined
USA

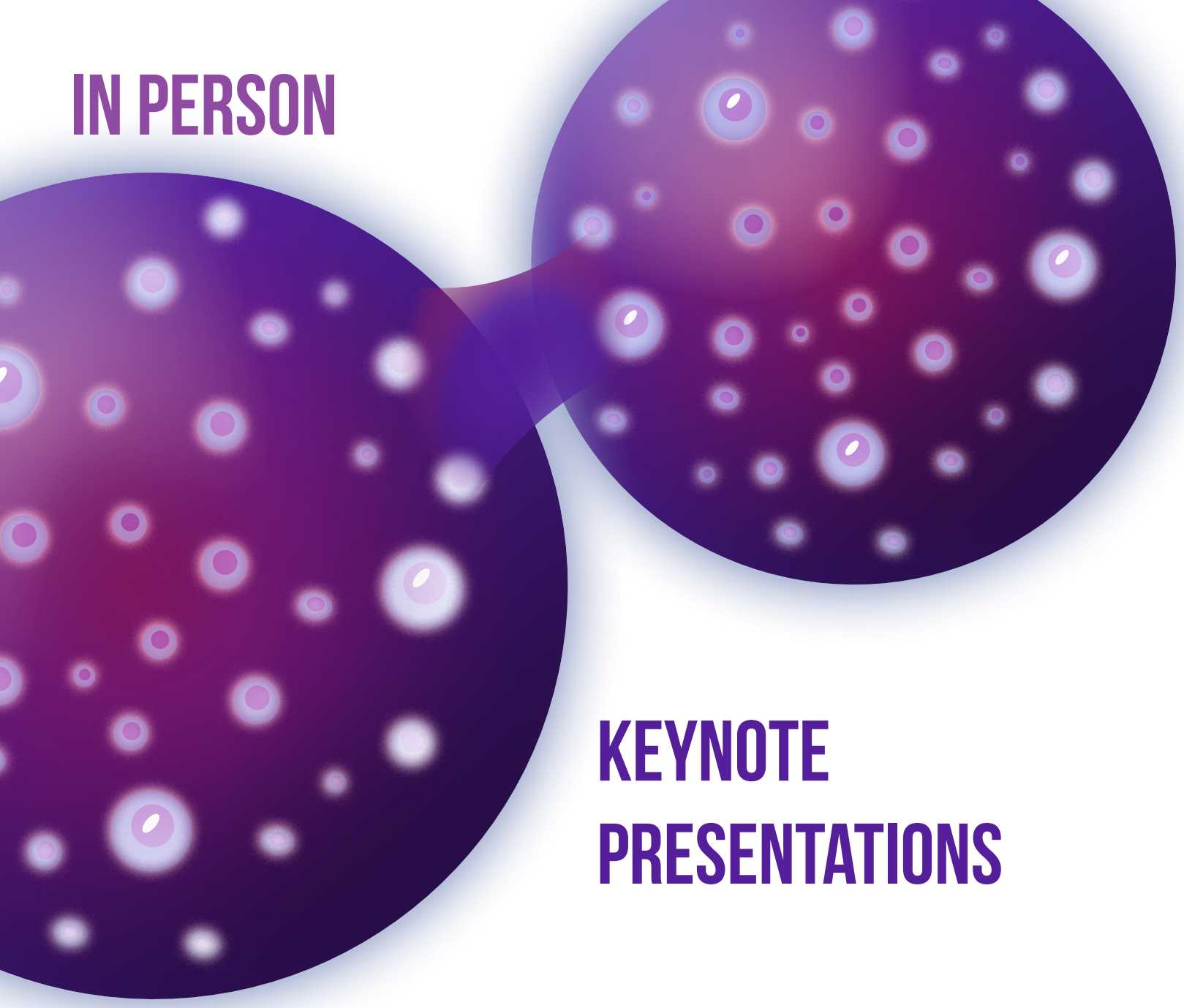
Mandip Sachdeva
Florida A&M University
USA

Nitin T. Telang
Cancer Prevention
Research Program
USA

Rachna Chhachhi
Rachna Restores
India

Thank You All

IN PERSON



KEYNOTE
PRESENTATIONS

NOVEMBER
06-07, 2024

Jianhua Luo

University of Pittsburgh School of Medicine
USA

Serum fusion transcript markers to predict liver cancer and monitor the treatment impact through machine learning

Abstract:

Hepatocellular carcinoma (HCC) is one of the most lethal malignancies for human. Early diagnosis of HCC is crucial in reducing the mortality of the disease. In this study, a panel of 9 fusion transcripts in the serum samples from 136 individuals using TaqMan qRT-PCR was analyzed. Seven fusion genes were frequently detected in the serum samples of HCC patients, including MAN2A1-FER (100%), SLC45A2-AMACR (62.3%), ZMPSTE24-ZMYM4 (62.3%), PTEN-NOLC1 (57.4%), CCNH-C5orf30 (55.7%), STAMBPL1-FAS (26.2%) and PCMTD1-SNTG1 (16.4%). Machine learning models were constructed based on serum fusion gene levels to predict HCC occurrence in the training cohort using leave-one-out-cross-validation approach. One of the machine learning models called 4-fusion genes logistic regression model (MAN2A1-FER<40, CCNH-C5orf30<38, SLC45A2-AMACR<41, PTEN-NOLC1<40) produced a 91.5% accuracy in the training cohort. The same model generated an accuracy of 83.3% in the testing cohort. When serum α-fetal protein (AFP) level was incorporated into the machine learning model, a 2-fusion gene+AFP logistic regression model (MAN2A1-FER<40, CCNH-C5orf30<38, AFP) was found to generate an accuracy of 94.8% in the training cohort. The same model generated 95% accuracy in both the testing cohort and the combined cohorts. Cancer treatment reduced most of the serum fusion transcript levels. Serum fusion gene machine learning models may serve as important tools in screening HCC and monitoring the impact of HCC treatment.

Biography

Luo has been studying molecular mechanisms of human malignancies in the last 36 years. Currently, he is a Professor of Pathology and Director of High Throughput Genome Center at University of Pittsburgh. In the last 30 years, Dr. Luo has been largely focusing on the genetic and molecular mechanism of human cancers such as prostate cancer. He is one of the pioneers in utilizing high throughput gene expression and genome analyses to analyze field effects in prostate cancer and liver cancer. He is also the first in using methylation array and whole genome methylation sequencing to analyze prostate cancer. He and his colleague helped to develop an ultra-low error synthetic long-read sequencing technology called LOOPSeq that can be utilized to quantify mRNA isoforms and mutation isoform distributions in single cell level. His group has discovered 21 novel fusion genes in prostate, liver and colon cancers. Subsequently, his group discovered that many of these fusion genes are recurrent in many other types of human cancers. His group also developed a genome intervention strategy targeting at the chromosomal breakpoint of fusion gene to treat cancers. Recently, his group has been focusing on machine learning prediction of prostate and liver cancers. Overall, these findings advance our understanding of how cancer develops and behaves, and lay down the foundation for better future diagnosis and treatment for human malignancies.

Johnathan Whetstine

Fox Chase Cancer Center
USA

Epigenetics: A gatekeeper to DNA amplification & rearrangements

Abstract:

DNA amplification and rearrangements are associated with pathological states such as neurological disorders, cardiac disease and cancer. Our laboratory aims to define the principles regulating selective DNA amplification and rearrangements so we may control these events in disease. By resolving general mechanisms governing selective amplifications and rearrangements, we will build a framework to further understand the molecular basis by which these abnormalities occur in neoplasia and other diseases. The unanswered question remains as to whether distinct mechanisms control DNA copy gains and rearrangements within cells, leading to diseases such as cancer. Recent studies have begun to uncover the importance of epigenetic states in regulating amplification. The question remained as to whether selective extrachromosomal amplification could give rise to inherited genomic rearrangements. Therefore, we set out to test these relationships. We have identified specific methyl-lysine modifiers that controls site-specific DNA amplification, and in turn, rearrangements. These studies leveraged genetic and chemical treatments coupled to cytological approaches and epigenomic profiling to resolve this question. While interrogating the factors controlling the local chromatin, we have also begun to appreciate its impact on inherited genomic rearrangement events. Furthermore, we have been able to establish relationships between the pathways we uncovered and these type of amplification and rearrangements in cancer. Taken together, we have established the key methyl-lysine modifiers generating and preventing DNA copy gains and rearrangements. The most recent studies addressing this observation will be presented at the meeting.

Biography

John Whetstine, also known as John W, discovered his passion for science while attending Bolton Agricultural High School in Tennessee, where he earned his high school degree. Despite moving frequently as a child, Bolton became the place where he delved into the world of science, particularly captivated by Punnett squares. Although unsure about the path of a scientist, his high school teacher's influence ignited a love for discovery. Pursuing undergraduate degrees in recombinant genetics and chemistry at Western Kentucky University, he later obtained his PhD in the Pharmacology Department at Wayne State University in Michigan, combining his interests in gene control and chemistry. His postdoctoral fellowship at Harvard Medical School in Massachusetts led him to become part of the team that discovered histone lysine demethylases, a subject he continues to study

at the molecular and translational levels. Dr.Whetstine then joined Massachusetts General Hospital and Harvard Medical School, rising to the position of associate professor and Tepper Family Scholar, as well as vice chair of the epigenetics center. Recruited to Fox Chase Cancer Center in December 2018, he is now the Jack Schultz Basic Science Endowed Professor, Director of the Cancer Epigenetics Institute, Co-leader of the Nuclear Dynamics and Cancer Program, and Director of the Genomics Resource. His research has unveiled the role of chromatin factors in driving extrachromosomal DNA amplification, linking these regions to aggressive tumors and drug resistance. Dr. Whetstine's lab has significantly impacted our understanding of DNA replication regulation and copy number control, identifying new biomarkers and therapeutic targets. He has mentored and contributed to the development of the next generation of scientists at various academic levels, with his traines achieving success at prestigious institutions and in leading pharmaceutical companies. The accomplishments of his trainees stand out as the most cherished stories of his career.

Mandip Singh

Florida A&M University
USA

Overcoming resistance in lung cancer using natural killer cell derived exosomes

Abstract:

We evaluated IL-15 stimulated natural killer cell-derived exosomes (NK-EVs) as therapeutic agents in vitro and in vivo in Osimertinib resistant lung cancer (H1975R) with EGFR mutations (L858R) in combination with carboplatin (CBP). NK-EVs were isolated by ultracentrifugation and characterized by nanoparticle tracking analysis and atomic force microscopy imaging revealed vesicles with a spherical form and sizes meeting the criteria of exosomal EVs. Further, western blot studies demonstrated the presence of regular EV markers along with specific NK markers (perforin and granzyme). EVs were also characterized by proteomic analysis which demonstrated that EVs had proteins for natural killer cell mediated cytotoxicity (Granzyme B) and T cell activation (Perforin and Plastin-2). Gene oncology analysis showed that these differentially expressed proteins are involved in programmed cell death and positive regulation of cell death. Further, isolated NK-EVs were cytotoxic to H1975R cells in vitro in 2D and 3D cell cultures. CBP's IC 50 was reduced by approximately 2 folds in 2D and 3D cell culture when combined with NK-EVs. The EVs were then combined with CBP and administered by i.p. route to H1975R tumor xenografts and significant reduction in tumor volume in vivo was observed(P<0.001). Further NK EVs were encapsulated with miR 593 and mIR 149-5p based on our gene ontology studies and further studied in PDX lung cancer models. Our findings show for the first time that NK-EVs target the PD-L1/PD-1 immunological checkpoint, induce apoptosis and anti-inflammatory response by downregulation of SOD2, PARP, BCL2, SET, NF-κB and TGF-ß. The ability to isolate functional NK-EVs on a large scale and using them with platinum-based drugs may lead to new clinical applications and suggest the possibility of the combination of NK-cell-derived EVs and CBP as a viable immunochemotherapeutic strategy for resistant cancer

Biography

Mandip Singh Sachdeva is a Professor of Basic Sciences and Pharmaceutics Section Leader at Florida A&M University's College of Pharmacy and Pharmaceutical Science. He also serves as the Editor in Chief of Critical Reviews in Therapeutic Drug Carrier Systems. Based in the Dyson Pharmacy Building, Dr. Sachdeva is recognized for his contributions to pharmaceutical sciences, with a particular focus on drug delivery systems and therapeutic innovations. His work fosters advancements in pharmacy education and research.

Eric Scheinbart

Immunity Redefined
USA

The Naturopathic treatment of cancer and chronic diseases

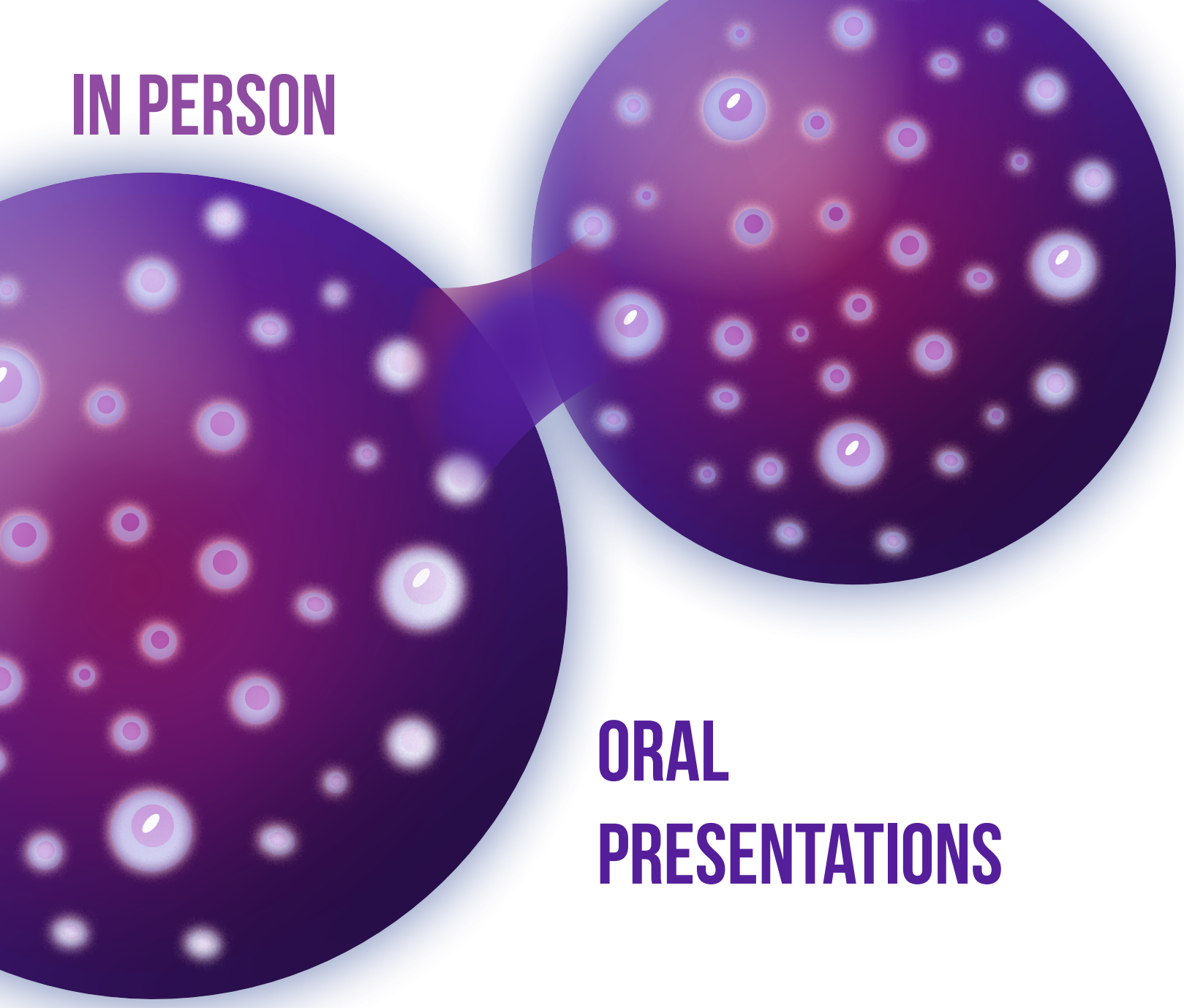
Abstract:

These days, more and more people are seeking alternative, integrative natural therapies to complement their traditional medical care OR in place of their conventional medical treatment. The immunotherapeutic stimulation of the patients own immune response is an important and integral factor for fighting cancer at it's optimum to "seek out" and destroy the malignant cells through immunomodulating properties activating macrophages, natural killer {NK} cells and T cells to attack the tumor cells along with lymphokines, interleukin 1 and 2, CD$ and CD8 to activate the cell mediated response. The research being clinically evidenced based, reveals an effective, organic, sustainable and safe naturopathic plant-based product, a proprietary compounded blend, physician formulated, that has shown great success with cancers, chronic diseases and the COVID=19 virus, with a successful track record for more than twenty years. It is my pursuit to help as many people as possible with this innovative, revolutionary and unique product by improving the outcomes for patients with a better chance to live longer and thrive with this natural plant-based immunotherapy.

Biography

Eric A. Scheinbart, MD practices Integrative and Alternative medicine for cancer and chronic diseases. For more than twenty years, with the conviction to improve health, longevity and the quality of life with Naturopathic Immunotherapies of plant based, organic compounded proprietary blend that stimulates the patient's natural immune system to heal itself. Dr. Scheinbart is a board-certified physician and Mahareshi Ayurvedic trained physician, a board-Certified diplomat of the American Academy of Anti-Aging and a Fellow of the American College of Nutrition. He has successfully improved the health, longevity and quality of life of patients with prostate, breast, ovarian and pancreatic cancers as well as many other cancers, chronic diseases such as diabetes, and neurodegenerative diseases like MS, Parkinson's disease and dementia and viruses, such as Herpes, EBV and Covid-19. He has been recognized by the NIH/NCI for his work and presented in Bethesda at the NIH. He has spoken at the Cancer Control Society, the A4M and Society of Integrative Oncology in Shanghai, China the World Medical Conference in Dubai, UAE, European Medical Society in Frankfurt, Amsterdam, Paris and London as well as Canada and USA. Most recently as the keynote speaker in Bangkok, Thailand.

IN PERSON



ORAL PRESENTATIONS

NOVEMBER

06-07, 2024

Nur Aimi Aliah Zainurin

Aberystwyth University
UK

Towards a home companion diagnostic test for the early detection of Breast Cancer: The potential of the urine metabolome

Abstract:

Breast cancer is one of the deadliest cancers with 685,000 deaths and 2.26 million cases reported in 2020. Early detection is crucial for better treatment outcome. Mammography is the gold standard screening modality for breast cancer diagnosis but use of a cost-effective companion diagnostic with a high sensitivity and specificity is required to reduce the mortality rates; especially in group perceived to be low risk, e.g., younger women. This study aims to discover the novel biomarkers in liquid biopsies by direct infusion high resolution mass spectroscopy (DI-MS) to facilitate the development of low-cost and high throughput biomarker assay (or panel of biomarker profiles) that could be exploited such as ELISA. Metabolite profiling focused on urine samples from breast cancer (BC; n=9), benign breast disease (BBD; n=31), symptomatic control (SC; n=35) and age-matched healthy control (HC; n=24) groups, using DI-MS. Multivariate statistical analyses used the R-based Metaboanalyst platform. Data mining revealed 185 urinary metabolites that significantly ($p<0.05$) different across the sample groups. Heatmap depicted the expressions (up or down-regulated) of the urinary metabolites were consistent with the high frequency clinical breast tissue metabolic biomarkers related to breast cancer from previous published studies. Partial least squares discriminant analysis (PLS-DA) showed a clear separation between (1) groups (BC vs HC, BC vs BBD and BC vs SC. Based on pairwise analysis between BC and HC groups, the volcano plot revealed 150 metabolites were significantly up-regulated while 273 were down-regulated. Receiver operator curve (ROC) analysis identified m/z 430.19974, 369.17542 and 370.1783 with accuracies of 0.949, 0.921 and 0.926 respectively with the potential as the diagnostic biomarkers for breast cancer. In conclusion, the encouraging preliminary finding from this study illustrates that urinary metabolites can be a promising adjunct tool to the current breast screening programme which warrant further analysis with larger patients' cohorts.

Biography

Miss Aimi Zainurin is a doctoral student (PhD) in Department of Life Sciences, Aberystwyth University, UK, working on breast cancer project under research group of Prof. Mur, Clinical Hub Aberystwyth (https://www.clinicalhubaberystwyth.com/). She graduated with Biochemical-Biotechnology Engineering (Hons) and MSc Biotechnology Engineering in 2017 and 2019 respectively from International Islamic University Malaysia (IIUM). She worked as a scientist trainee in one of the top Asian biopharmaceutical companies and followed as a researcher at National Institute of Health (NIH) in Malaysia before decided to further her study. Her research interests in omics sciences focus on identifying the biomarkers and understanding the underlying relationship between the biomolecules, their molecular processes, and biological pathways to gain insights into disease mechanisms.

Je-Hyun Yoon

University of Oklahoma
USA

Metabolic regulation by noncoding RNAs

Abstract:

Accelerated glycolysis is the main metabolic change observed in cancer, but the underlying molecular mechanisms and their role in cancer progression remain poorly understood. Here, we show that the deletion of the long noncoding RNA (lncRNA) Neat1 in MMTV-PyVT mice profoundly impairs tumor initiation, growth, and metastasis, specifically switching off the penultimate step of glycolysis. Mechanistically, NEAT1 directly binds and forms a scaffold bridge for the assembly of PGK1/PGAM1/ENO1 complexes and thereby promotes substrate channeling for high and efficient glycolysis. Notably, NEAT1 is upregulated in cancer patients and correlates with high levels of these complexes, and genetic and pharmacological blockade of penultimate glycolysis ablates NEAT1-dependent tumorigenesis. Finally, we demonstrate that Pinin mediates glucose-stimulated nuclear export of NEAT1, through which it exerts isoform-specific and paraspeckle-independent functions. These findings establish a direct role for NEAT1 in regulating tumor metabolism, provide new insights into the Warburg effect, and identify potential targets for therapy.

Biography

Je-Hyun Yoon has completed his PhD in 2011 from University of Arizona and postdoctoral studies in 2015 from National Institutes of Health. He is an Associate Professor on Oncology Science in University of Oklahoma. He has published more than 60 papers in reputed journals and is an expert of RNA biochemistry.

Joseph Larsen

Harvard Medical School
USA

Multimorbidity and its impact in older united states veterans newly treated for advanced non-small cell lung cancer

Abstract:

U.S. veterans with cancer often have multiple comorbidities, or multimorbidity, but the nature of these comorbidities is poorly understood. Here we define patterns of multimorbidity and their impact in older United States veterans with non-small cell lung cancer (NSCLC). Latent class analysis (LCA) was applied to identify patterns among 63 chronic conditions in 10,160 veterans aged 65 years and older newly treated for stage IIIB or higher NSCLC in the national Veterans Affairs health-care system from 2002 to 2020. Five patterns emerged, with metabolic diseases (24.7% of all patients; HR [95% CI], 1.10 [1.04 -1.16]), psychiatric and substance use disorders (16.0%; HR [95% CI], 1.17 [1.10-1.24]), cardiovascular disease (14.4%; HR [95% CI], 1.22 [1.15-1.30]), and multisystem impairment (10.7%; HR [95% CI], 1.36 [1.26 -1.46]) having a higher hazard of death compared to veterans with minimal comorbidity beyond their NSCLC (34.2%, reference), controlling for age, gender, race, days between diagnosis and treatment, date of diagnosis, and NSCLC stage and histology. Associations held after adjusting for the count-based Charlson Comorbidity Index. Multimorbidity patterns were also independently associated with emergency department visits and unplanned hospitalizations. These findings demonstrate the need to move beyond count-based measures of comorbidity, which are unlikely to capture the complexity of multimorbidity in older adults with lung cancer, and to consider cancer in the context of multiple chronic conditions.

Biography

Joseph Larsen, Ph.D. is a post-doctoral research fellow at the Veterans Affairs (VA) Boston Healthcare System in the Big Data Scientist Training Enhancement Program (BD-STEP) with an appointment at Harvard Medical School and the Division of Aging at Brigham and Women's Hospital in Boston, Massachusetts. His research focuses include modeling human evolution and the progression of diseases (e.g., cancer and COVID-19) as well as his current work on the impact of multimorbidity patterns in patients with non-small cell lung cancer. His research background during his education at UCLA and USC to now his postdoctoral work at the VA Boston and Harvard Medical School has garnered him skills in mathematical modeling, statistical analyses, large database acumen, electronic health records (EHR) utilization, survival analysis, and machine learning, which he uses to study disease progression and its impact on patient outcomes and care utilization

Miral Mashhour

King Fahad Specialist Hospital Dammam
Saudi Arabia

Challenging cases in breast cancer pathology

Abstract:

Breast cancer is the most common cancer among females in Saudi Arabia. The eastern province has the highest incident rate up to 29%. The usual cases are of high grade, Late-stage, and among the younger age group. Five challenging breast neoplastic cases will be presented including Gross, Microscopy, Radiology, Treatment and Literature review

Biography

Miral Mashhour is a consultant pathologist specializing in breast, gynecology, and liver pathology. She completed three fellowships at Toronto University's Sunnybrook Hospital and Toronto General Hospital in 2011. Currently, she serves as the Director of Pathology and Laboratory Medicine at King Fahad Specialist Hospital in Dammam. Dr. Mashhour has numerous publications in highly indexed journals and is a frequently invited speaker at both national and international symposiums.

Salvador Martinez

Miguel Hernandez University
Spain

Induced immunosuppression by brain pericytes helps in glioma genesis and progression

Abstract:

Direct interaction between perivascular cells, termed pericytes (PC), and glioblastoma multiforme (GBM) cells is essential for inducing changes in the pericytes' antitumoral and immune phenotype. Starting from the early stages of carcinogenesis in GBM, GBM-conditioned PC (GBM-PC) undergo proliferation, acquiring a protumoral and immunosuppressive phenotype. They secrete elevated levels of antiinflammatory cytokines, express immunosuppressive molecules, and substantially impair the activation capacity of immunocompetent T cells, thereby promoting tumor growth. Blocking the conditioning mechanisms of PC in the GBM tumor microenvironment (TME) results in tumor eradication due to immunological activation. This indicates that PC are a pivotal cell type within the TME responsible for the tumor-induced immunosuppression facilitating GBM cells' evasion of the immune system. Other cells within the TME, such as tumor-associated macrophages (TAM) and microglia, have also been identified as contributing to this immunomodulation. However, the cellular heterogeneity of immunocompetent cells within the TME can lead to misinterpretation of different stages of PC cellular responses as TAM. Hence, novel therapies can be formulated to disrupt GBM-PC interactions and/or PC conditioning.

Biography

Salvador Martinez (MD, PhD and Professor of Anatomy) is analyzing the role of pericytes (perivascular cells) in the control of the immune response against glioblastoma multiforme. This study is describing the cellular and molecular mechanisms underlying the immune tolerance of this type of cancer (Valdor et al., Oncotarjet, 2017, PNAS, 2019; Molina et al., Cancers 2019, Front Cel Biol 2022; Pombero et al., 2023), demonstrating the cellular mechanisms underlaying tumor immunosuppression.

Shrestha Ghosh

Dana-Farber Cancer Institute
USA

Identification of RIOK2 as a key transcriptional regulator of human blood cell development and telomere biogenesis

Abstract:

Anemia is a predominant comorbidity in blood cancer patients, such as acute myeloid leukemia (AML) and myelodysplastic syndrome (MDS). On the other hand, telomere shortening is a characteristic feature of aging individuals and patients diagnosed with idiopathic pulmonary fibrosis (IPF) and MDS. Although telomerase activity tightly controls telomere length homeostasis to prevent malignancies and other disorders, the upstream regulation of telomerase holoenzyme subunits remains largely elusive. Also, the intriguing association between telomere shortening and anemia is poorly understood. We have previously reported that RIOK2 (right open reading frame kinase 2) functions as a master transcription factor in human blood cell development1, and loss of RIOK2 impairs erythropoiesis, thus causing anemia1,2. RIOK2's expression significantly correlates with its targets (GATA1, KLF1, RUNX3) in MDS and AML patient-derived cells1. Here, we show that RIOK2 transcriptionally regulates key telomerase subunits (TriC and Dyskerin complexes) to maintain telomere biogenesis in various cell types using gene expression analyses, fluorescence in situ hybridization, and chromatin immunoprecipitation3. Interestingly, RIOK2's expression is downregulated in aged individuals and IPF patients, and its mRNA levels significantly correlate with TriC and Dyskerin complex subunits in MDS and IPF patients as well as aging individuals. Importantly, ectopic expression of RIOK2 significantly alleviates telomere shortening in primary lung fibroblasts isolated from IPF patients3. Collectively, our findings demonstrate that RIOK2 governs both telomere biogenesis and blood cell development, highlighting it as an unprecedented connecting link between anemia and telomere shortening. Thus, RIOK2-driven transcriptional programs have potential therapeutic implications in aging, IPF and blood cancers.

Biography

Shrestha Ghosh completed her PhD from The University of Hong Kong in 2017 and joined Dana-Farber Cancer Institute (DFCI)/Harvard Medical School (HMS), Boston for postdoctoral studies in 2018. She is now an Instructor at DFCI/HMS. She is a gold medalist in her undergraduate studies and received the best doctoral thesis award in medicine faculty of HKU in 2018. Her thesis was published as a book by Elsevier in 2019. She has now co-founded a start-up to find novel therapeutics in blood-related disorders. She has published several papers in reputed journals, such as Nature Immunology, Nature Communications, Cell Metabolism, Cell Reports.

Chandraditya Chakraborty

Dana-Farber Cancer Institute
USA

HIF-1a molecular stress pathway associates with the development of cervical carcinoma

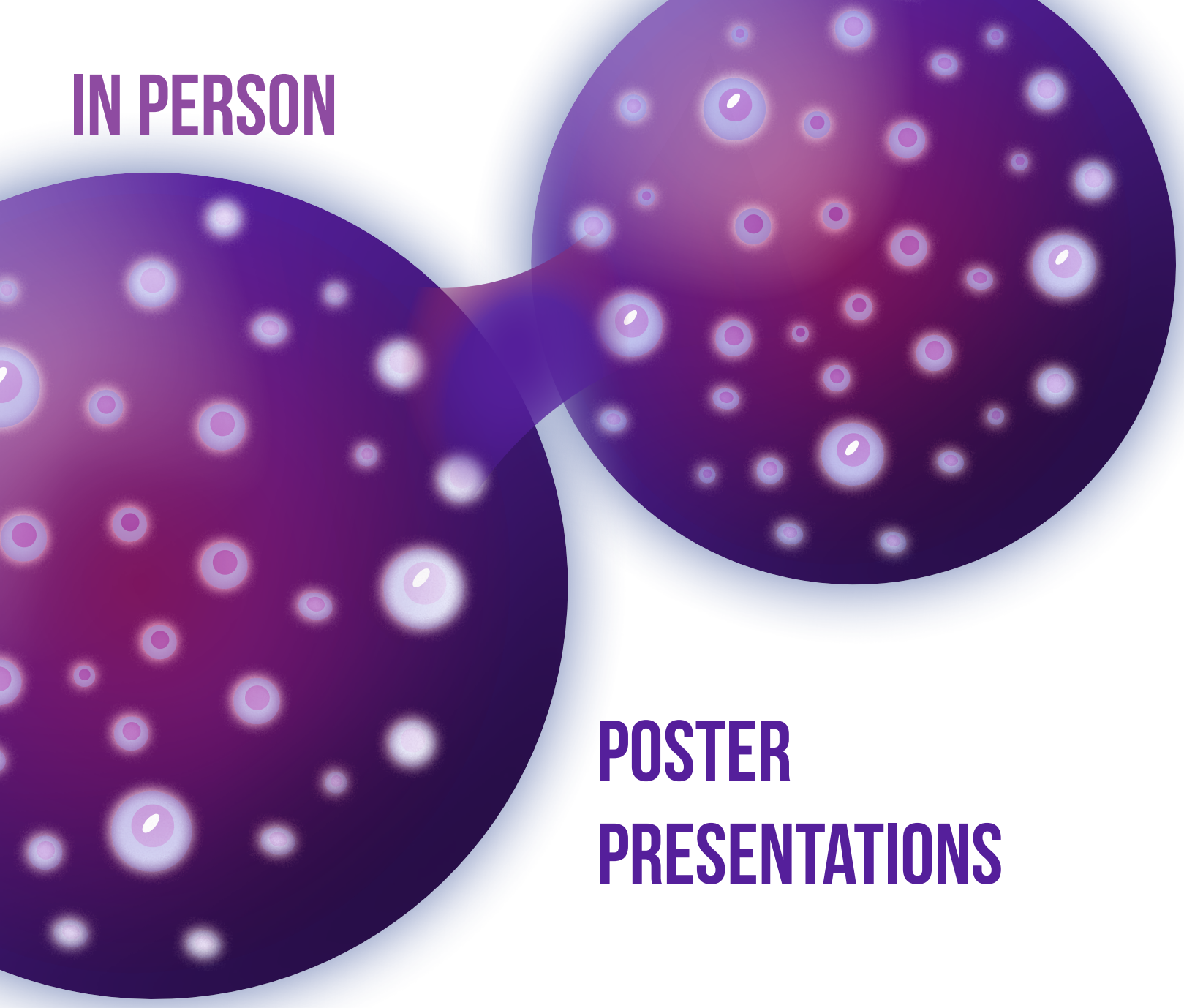
Abstract:

To understand the mechanism of cellular stress in different cell types of normal cervical epithelium and during different stages of cervical carcinoma, we analyzed the expression/methylation/copy number variation/mutation of HIF-1a and its associated genes LIMD1, VHL and VEGF in disease-free normal cervix, adjacent normal cervix of tumors, cervical intraepithelial neoplasia, cancer of uterine cervix samples and CACX cell lines. Interestingly, in basal-parabasal layers of normal cervical epithelium, LIMD1 showed high protein expression, while low protein expression of VHL was concordant with high expression of HIF-1a and VEGF irrespective of HPV-16 infection. Furthermore, there was significant concordance with the low promoter methylation of LIMD1 and high in VHL in the basal-parabasal layers of normal cervix. LIMD1 expression was significantly reduced while VHL expression was unchanged during different stages of cervical carcinoma. In different stages of cervical carcinoma, the expression pattern of HIF-1a and VEGF was high as seen in basal-parabasal layers and inversely correlated with the expression of LIMD1 and VHL. Additional deletion of LIMD1 and VHL in CIN/CACX provided an additional growth advantage during cervical carcinogenesis through reduced expression of genes. We found that overexpression of HIF-1a and its target gene VEGF in the basal-parabasal layers of normal cervix was due to frequent inactivation of VHL by its promoter methylation. Thus, it was evident that molecular signature of key regulatory genes of the HIF1-a molecular stress pathway affecting cell fate and cell survival in the proliferating basal-parabasal layers of normal cervical epithelium is maintained during the development of cervical carcinoma through additional methylation/deletion/sequence variation leading to poor prognosis of CACX patients.

Biography

Chandraditya Chakraborty has completed his PhD from Calcutta University in 2017 followed by postdoctoral studies from Dana-Farber/ Harvard Cancer Center and is presently a scientist at Dana-Farber Cancer Institute, Harvard Medical School. He is a recipient of NCI SPORE Career Enhancement Award and IMW Young Investigator Award and published several papers in impactful journals like Blood, gastroenterology etc.

IN PERSON



POSTER PRESENTATIONS

NOVEMBER
06-07, 2024

Catherine L. Ingram

Dana Farber Cancer Institute
USA

Targeted degradation of NTAQ1 using a cereblon molecular glue to study the N-degron pathway

Abstract:

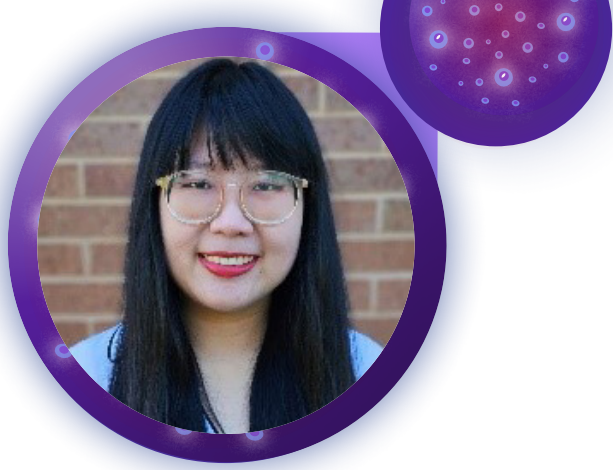
The N-degron, or N-end rule, pathway facilitates selective proteolysis determined by N-terminal residues, known as degrons. As a critical part of the ubiquitin-proteasome system, this pathway affects numerous cellular processes including protein quality control, regulation of gene expression and DNA repair, and response to environmental stress. Its ability to regulate these processes makes it an attractive target for anti-tumor therapies.

N-terminal glutamine amidase 1 (NTAQ1) is a key component of the N-degron pathway. It hydrolyzes Nterminal glutamine to glutamate, enabling subsequent arginylation by ATE1. This modification results in recognition by E3 ligases, leading to ubiquitination and proteasomal degradation. Although previously deemed undruggable, we identified a selective cereblon (CRBN) based molecular glue degrader of NTAQ1, called EM12-FS. In this study, we explore the effects of NTAQ1 degradation by EM12-FS on cellular viability and function.

Using cell-based assays, proteomics, and genomic approaches, we demonstrate that EM12-FS-mediated degradation of NTAQ1 leads to increased levels of RAD21 and p21. Furthermore, combining EM12-FS with certain targeted cancer therapies, including Palbociclib and Olaparib, enhances cellular response to these treatments. Targeted degradation of NTAQ1 by EM12-FS serves as a useful strategy for chemically probing the N-degron pathway. Advancing our understanding of this pathway may present new therapeutic opportunities.

Biography

Catherine Ingram is a fourth year student at Northeastern University (Boston, MA), where she majors in Cell & Molecular Biology and is a coxswain on the Women's Rowing Team. She completed her first coop at Takeda Pharmaceuticals in the fall of 2023 and is currently working at Center for Protein Degradation at Dana Farber Cancer Institute. As the Biology Co-op, she studies therapeutically relavent degrader and non-degrader molecular glues.



Wariya Nirachonkul

Chiang Mai University
Thailand

The enhanced cytotoxic effect of curcumin on leukemic stem cells via CD123-targeted nanoparticles

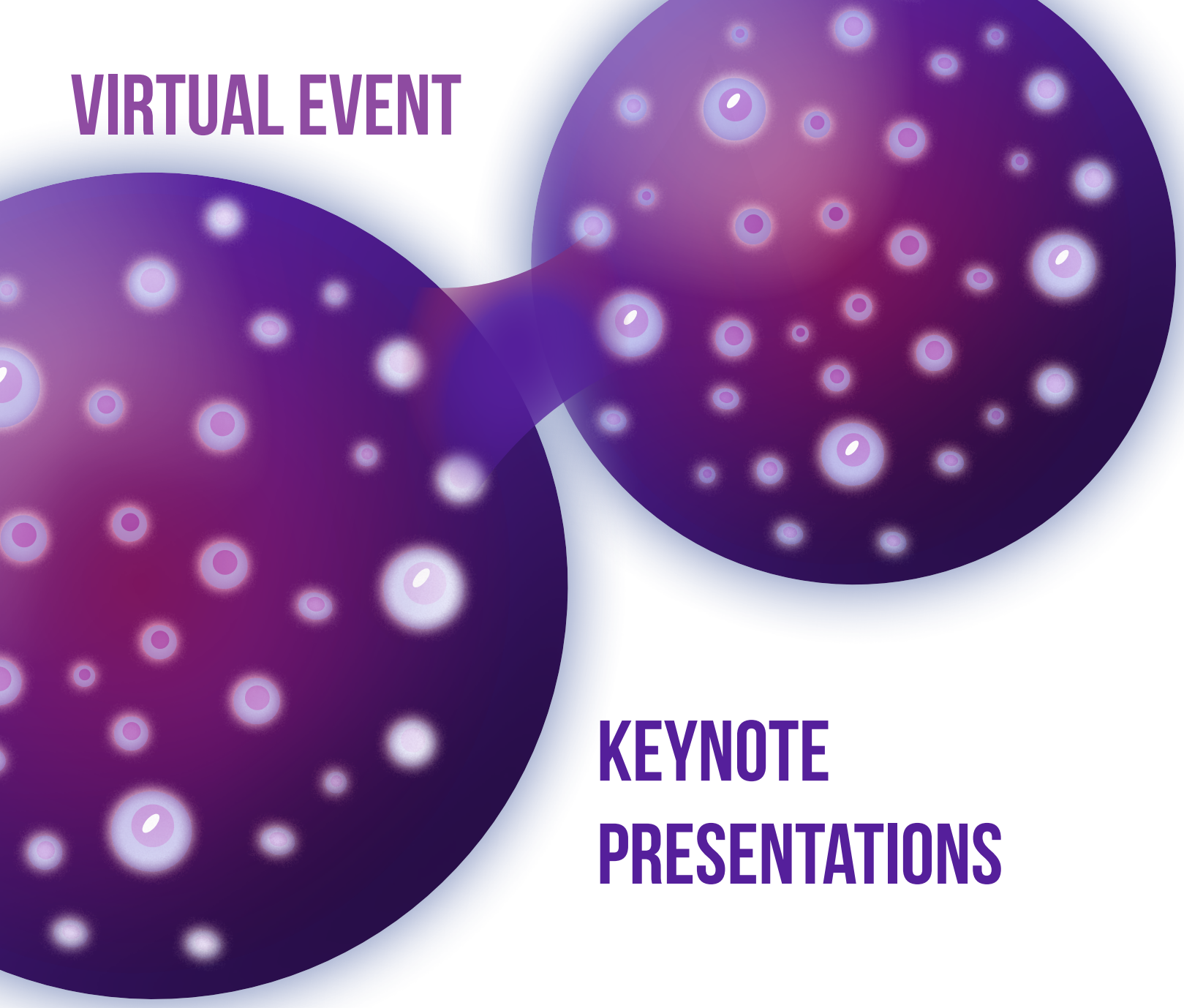
Abstract:

Treating acute myeloid leukemia (AML) is challenging due to drug resistance and high relapse rates. A key factor in relapse is the presence of leukemic stem cells (LSCs) in the bone marrow, which remain in a quiescent state and evade chemotherapy due to high P-glycoprotein expression. Targeting these LSCs is crucial, and CD123, which is overexpressed in LSCs but not in normal stem cells, presents a promising therapeutic target. This study aimed to enhance the targeting and elimination of LSCs using CD123 and curcumin. Curcumin, a compound from turmeric known for its anti-leukemic properties, suffers from poor bioavailability and rapid clearance. To improve the limitations, curcumin was encapsulated in nanoparticles (nanocurcumin) and conjugated with an anti-CD123 antibody (anti-CD123-Cur-NPs). The cytotoxicity of anti-CD123-Cur-NPs and curcumin-loaded nanoparticles (Cur-NPs) was tested on KG-1a cells, a model for LSCs. Results showed that both Cur-NPs and anti-CD123-Cur-NPs were cytotoxic, with IC50 values of 74.20 ± 6.71 µM and 41.45 ± 5.49 µM, respectively. Importantly, neither formulation affected normal peripheral blood mononuclear cells (PBMCs). Anti-CD123-Cur-NPs increased apoptosis in KG-1a cells compared to Cur-NPs and demonstrated higher uptake in KG-1a cells as confirmed by flow cytometry. In conclusion, anti-CD123-Cur-NPs effectively improve curcumin's bioavailability and target LSCs specifically, offering a promising approach to enhance therapeutic efficacy against AML

Biography

Wariya nirachonkul is a Ph.D. candidate in Biomedical Science at Chiang Mai University, Thailand. She earned a B.S. in Medical Technology with first-class honors from Chiang Mai University in 2017. From 2021 to 2023, she served as a visiting scholar at the Department of Pharmaceutical Chemistry, School of Pharmacy, University of Kansas, gaining valuable international research experience. Their work has been supported by the Royal Golden Jubilee Scholarship from the Thailand Research Fund.

VIRTUAL EVENT



KEYNOTE PRESENTATIONS

NOVEMBER

06-07, 2024

Rachna Chhachhi

Rachna Restores
India

Oral cancer and treatments that increase survival rate

Abstract:

The incidence of different kinds of Oral Cancers has increased by 34% in the decade. The different types of oral cancers that exist are Lymphoma minor salivary gland, including Adenoid cystic carcinoma (ACC), Mucoepidermoid carcinoma, Polymorphous low-grade adenocarcinoma, Carcinoma ex-pleomorphic adenoma. There is also Mucosal melanoma, Sarcomas, Squamous cell carcinomas. In my abstract I will specifically talk about squamous cell carcinomas and survival treatments that work. 25% people do not survive, cell carcinoma of the mouth. The trigger for this kind of cancer can we tobacco but I have also treated nontobacco cancers successfully. Even in the late stages, there are survival tactics that can be utilised to reduce the cancer activity, side-effects of chemotherapy and radiation and increase chances of recurrence in the future. As a cancer metastasis, nutrition and mental health expert, my focus is to help with recovery by a nutrition and reduce metastasis over a three-year period as well as secondary cancers induced by radiation over a 9–12-year period.

In my abstract and speaker presentation, I will be presenting three mouth cancer cases, two of which survived and one which did not. My presentation will go into clinical details of patient reports, inflammation levels, age, tobacco use, stress levels, lifestyle habits all of which can impact patient recovery.

Methods:

- Documenting the role of nutrition, stress reduction in recovery.
- Reduction of side-effects of chemotherapy and radiation via nutrition, stress reduction. These need to be documented and normalised much more than is the current scenario as they increase patient lifespan and survival rates beyond five years. 3. The role of chronic stress in increasing susceptibility to squamous cell carcinoma (SCC) by suppressing protective immunity and increasing regulatory/suppressor T cells within the tumour microenvironment.
- The role of malnutrition as a risk factor for the onset of oral cancer.
- My treatment methodology (Methods) in addressing the above, and clinical impact on patient recovery process.

- 3 case studies.

Results:

- Summary of treatments that have worked.
- Summary of reduction in side-effects to increase survival rate and quality of life.
- Summary of addressing the triggers to reduce cancer activity – specific focus on tobacco, stress and malnutrition.

Conclusion:

The role of nutrition, stress reduction on survival rate of squamous cell carcinoma of the mouth.

Biography

Rachna Chhachhi specialises in reversal of chronic lifestyle diseases without medication and is a certified Cancer Coach, Nutritional Therapist, Certified International Yoga Teacher and WHO certified in Malnutrition for infants & children. Founder of RachnaRestores®, Unhurry® and registered e-learning platform, RachnaRestores School – Rachna's purpose in life has been to help those suffering with a poor quality of life understand the power of holistic nutrition to heal themselves.

Nitin T. Telang

Cancer Prevention Research Program
USA

Colon cancer stem cell models for drug discovery

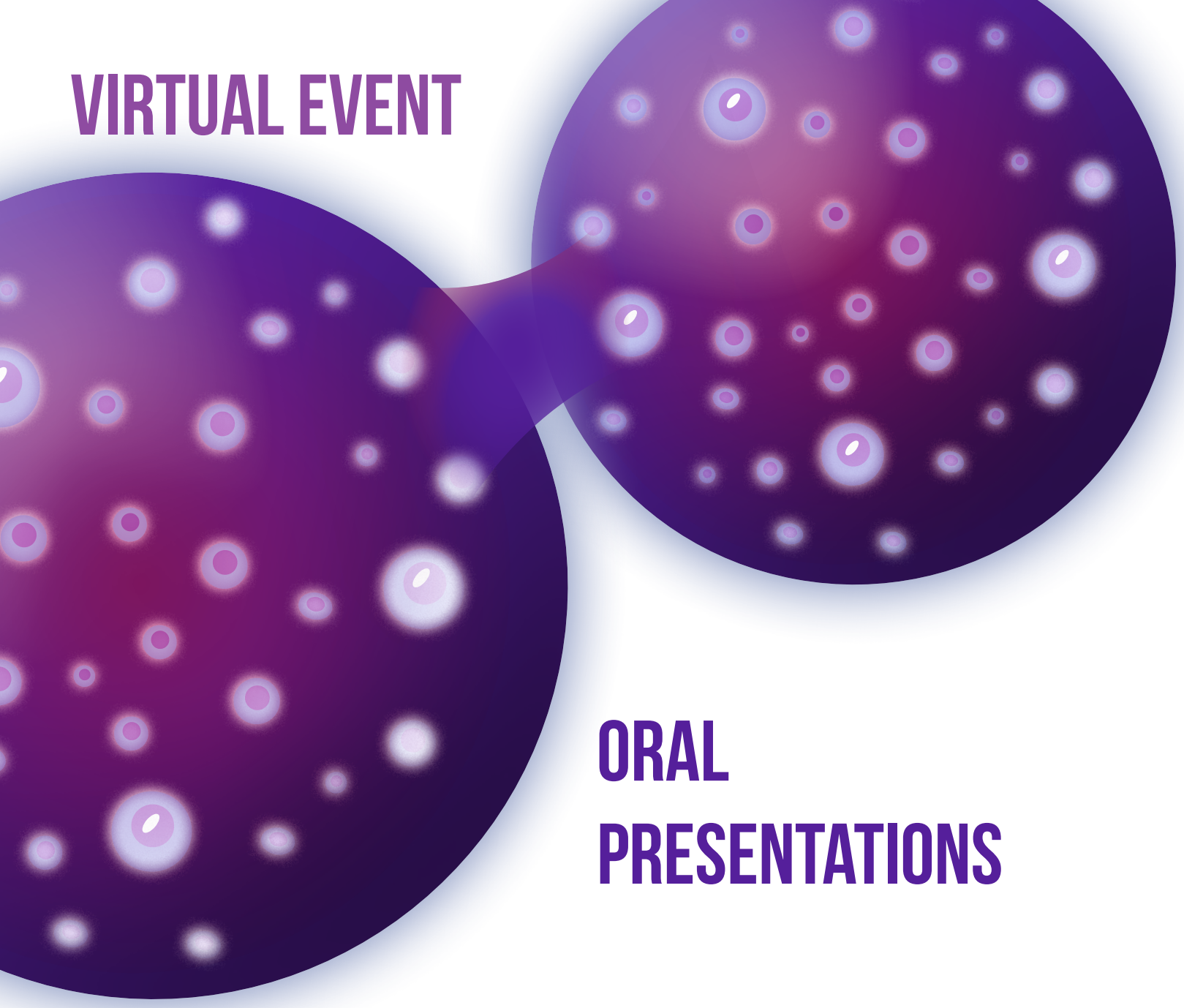
Abstract:

Pharmacological chemotherapeutic agents represent mainstream treatment options for colon cancer. Conventional and targeted therapeutics are associated with systemic toxicity, acquired therapy resistance and chemo-resistant cancer initiating stem cells. These limitations emphasize identification of stem cell targeting bioactive agents as testable drug candidates. Natural products exhibit low toxicity, preclinical efficacy and are unlikely to be associated with phenotypic resistance. These agents may represent new drug candidates. Reliable drug-resistant cancer stem cell models facilitate investigations to identify potential drug candidates. Cellular models for genetically predisposed early onset colon cancer provided a means to isolate and characterize drug-resistant phenotypes for familial adenomatous polyposis and hereditary non-polyposis colon cancer subtypes, respectively. Treatment with non-steroidal anti-inflammatory agent sulindac (SUL) and DNA synthesis inhibitor fluoro-uracil (FU) selected SUL resistant 850MIN COL and FU- resistant Mlh1/1638N COL tumorigenic colonic epithelial cells, respectively. Drug resistant cells exhibited increased tumor spheroid formation and upregulated expression of CD44, CD133 and c-Myc, representing cancer stem cell markers. Treatment of SUL-R cells with mechanistically distinct dietary phytochemicals inhibited tumor spheroid formation. Treatment with curcumin, a bioactive agent from turmeric, inhibited tumor spheroid formation and downregulated CD44, CD133, and c-Myc expression. Collectively, these data provide mechanistic leads for future investigations to examine the effects of bioactive agents on Apc and DNA mismatch repair gene expression, cancer stem cell specific telomerase expression, epigenetic modification and epithelial-mesenchymal transition. These future research directions also provide a basis for future investigations on patient derived tumor explants and organoids to extend clinically relevant translational potential of the preclinical evidence.

Biography

Telang is the research director at palindrome liaisons consultants. He earned Ph.D. Degree in1974, and obtained post-doctoral training at university of Nebraska, American health foundation, New York and memorial Sloan Kettering cancer center, New York. Faculty appointments: memorial Sloan Kettering cancer center, New York, Weill Cornell medical college of Cornell university, New York and Strang cancer prevention center, New York. Grant review study sections: us national cancer institute and us department of defense. Editorial boards: oncology reports, international journal of oncology, world academy of sciences journal and international journal of molecular sciences. Awards: national cancer institute first award, department of defense idea award and a.m. marquis lifetime achievement award. Peer-reviewed publications: carcinogenesis, cancer prevention, and cancer stem cell biology. Past funding: us national cancer institute and us department of defense breast cancer research program.

VIRTUAL EVENT



ORAL PRESENTATIONS

NOVEMBER

06-07, 2024

Anurag Mishra

University of Allahabad
India

Exploring the impact of hyper homocysteine mia in cancer management

Abstract:

Homocysteine (Hcy) is a sulfur-containing toxic amino acid derived from the metabolism of Methionine (Met). Hcy levels are broadly categorized as moderate (16 to 30 µmol/L), intermediate (31 to 100 µmol/L), and severe (over 100 µmol/L) [1]. Chronic elevation in Hcy concentration or its metabolites may cause Hyperhomocysteinemia (Hhcy) and Homocystinuria. Age, gender, family history of stroke, serum folate, vitamin B12 deficiencies, and serum creatinine are important determinants of Hcy concentrations in the body [2, 3]. Hhcy is associated with an increased risk of diabetes, osteoporosis, cardiovascular disease, hip fracture, cognitive decline, chronic kidney disease, hypothyroidism, neurodegenerative disorders, oxidative stress, cancer, and dislocation of lenses [4, 5, 6]. In vitro study shows Hhcy modulates the blood sugar levels in circulation [7, 8]. Hhcy is closely associated with the abnormality of Diabetes [9, 10, 11]. Vitamins B, Folate, and Choline are the key factors that regulate Hcy metabolic pathways. The supplementation of vitamins B6, B12, and folic acid has been clinically proven to lower Hcy levels in the circulation while the deficiencies in any of these vitamins might lead to an increased risk of Hcy concentration [12, 13, 14]. Hcy metabolism is also found linked to the genetic polymorphism of genes Methylene Tetrahydrofolate Reductase (MTHFR), Methionine Synthase (MTR), and Cystathionine β-Synthase (CBS) [15, 16, 17]. This study aims to establish the association of Hcy metabolism with Cancer management.

Biography

Anurag Mishra has completed his Ph.D. from the Department of Biochemistry, University of Allahabad, India. Currently he is working as a researcher in the same Department. He is Assistant Professor at the Department of Biochemistry, ISD College, University of Allahabad, India. He has more than 6 years of teaching and 10 years of research experience in Cancers, Osteoporosis, Oxidative Stress, Nicotine, and Genetic Polymorphism. He has over 15 publications in prestigious journals including book chapters and has been serving as an editorial board member in repute journals. He has also presented many papers in national and international conferences.

Eleni Petsalaki

University of Crete
Greece

A novel mechanism for chromatin bridge sensing by the abscission checkpoint in human cells

Abstract:

Chromatin bridges are DNA strings that link anaphase poles or daughter nuclei and are associated with carcinogenesis. DNA bridges occur from the separation of twisted, linked chromatin that is caused by problems in DNA replication or incomplete DNA decatenation. In response to chromatin bridges, cells delay abscission by activating the abscission checkpoint which delays completion of cytokinesis in order to prevent chromatin breakage or tetraploidization by furrow regression. Here, we show that spontaneous or replication stress-induced chromatin bridges derived from catenated DNA exhibit "knots" of tangled, overtwisted DNA next to the midbody. Topoisomerase IIα (Top2a), an enzyme that relaxes supercoils and untangles catenated DNA forms irreversible Top2-DNA cleavage complexes (Top2ccs) on DNA knots. Inhibition of Top2a results in diminished localization of Rad17, MRN, ATM, Chk2 and CPC complex to the DNA bridges and induces chromatin bridge breakage. Furthermore, proteolytic degradation of Top2ccs is required for localization of Rad17 to the bridge DNA. In turn, Rad17 promotes recruitment of the MRN complex to DNA knots and downstream abscission checkpoint signaling to delay abscission and prevent chromatin bridge breakage in cytokinesis. In contrast, chromatin bridges generated by dicentric chromosomes do not exhibit DNA knots or Top2ccs next to the midbody, and fail to recruit Top2a, Rad17 and other downstream proteins and are unable to induce an abscission delay. Our results describe a novel mechanism by which the abscission checkpoint detects chromatin bridges in human cells, through generation of irreversible Top2ccs on DNA knots. Because chromosomal instability is a major cause of cancer, identifying new genes that protect genome integrity is very important for cancer research.

Biography

Eleni Petsalaki is a Post Docroral Research Scientist in Dr George Zachos' lab at University of Crete, Greece. She completed her PhD in 2014 in Molecular Biology and Biomedicine at the Department of Biology. Her main interest is mitotic cell division and mechanisms that monitor mitotic progression called the mitotic spindle checkpoint and the abscission checkpoint. She is an author of 16 publications including Journal of Cell Biology, Nature Communications, Journal of Cell Science and others. Her publications have received 305 citations so far. She is currently a member of FEBS, AACR, and Royal Society of Biology.

Anne Catherine Heuskin

University of Namur
Belgium

Exploring UHDR irradiation parameters and flash effect occurrence on c. elegans and tumor spheroids

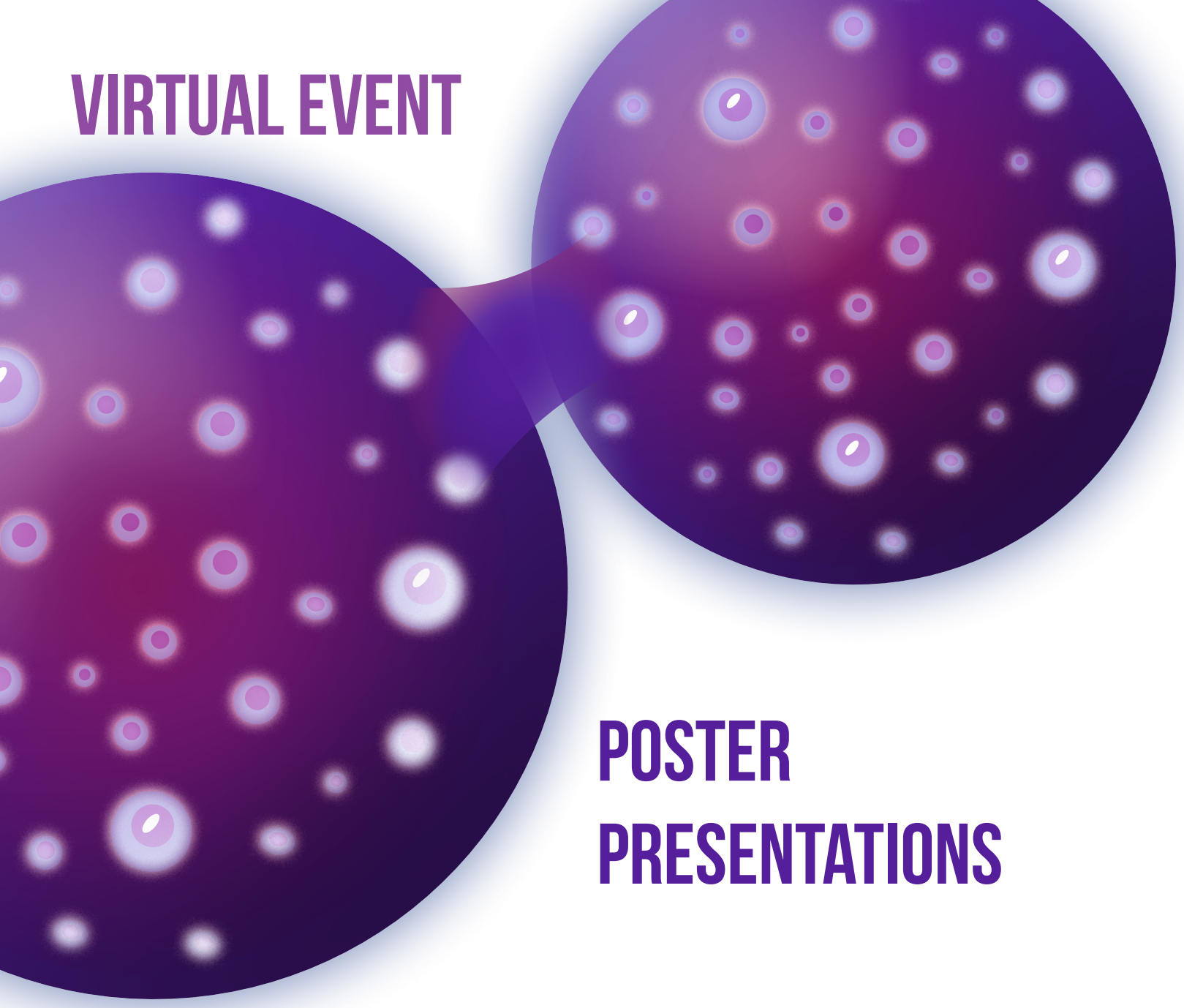
Abstract:

UHDR irradiations show healthy tissue sparing effect known as the FLASH effect. Since 2014, the FLASH effect has been investigated worldwide to understand how to trigger it. At the LARN laboratory, a chopper system allowing to mimic the beam structure of clinical proton accelerators, with tunable LET and instantaneous dose rate up to 1000 Gy/s, was developed. Parameters can be set up independently allowing the screening of numerous beam structure. Mono-pulses were used to expose wild type C. elegans embryos, a high throughput healthy-tissue in vivo model, and colon cancer 3D spheroids, as a surrogate for tumor tissue. The UHDR irradiations were performed by delivering one single pulse for total doses from 2 to 20 Gy, with a 4 MeV proton beam (LET = 10 keV/µm) in CONV (2 Gy/min) and UHDR (1000 Gy/s). Worm length was measured 96 h after exposure and the growth delay of cancerous HCT-116 spheroids was monitored over 18 days. All groups of irradiated worms showed a significant growth delay at 10 and 20 Gy compared to the control group ($p < 0.0001$), regardless of the dose rate. However, the UHDR group growth delay was significantly less severe at both doses, suggesting a sparing effect ($p < 0.001$). On the other hand, UHDR was more potent to reduce proliferation in the 3D cancer model. These results suggest that different mechanisms are at play in healthy and tumor tissue models. Other beam structures and various LET will be tested in the future.

Biography

Anne-Catherine Heuskin is a physicist with expertise in the field of radiobiology and nanotechnology. Together with Prof. Stephane Lucas and Prof. Carinne Michiels, she set up an experienced interdisciplinary radiobiology team, composed of physicists and biologists. Ultimately, their research activities seek to optimize cancer radiation therapy, in particular using high-LET particles such as protons or alpha particles. Current projects focus on FLASH therapy, macrophages reprogramming, mitochondrial dynamics, intrinsic or induced radio resistance and lipid-ROS.

VIRTUAL EVENT



POSTER PRESENTATIONS

NOVEMBER
06-07, 2024

Maksym A. Jopek

Medical University of Gdansk
Poland

Optimizing RNA normalization techniques in platelet RNA-based liquid biopsies for improved ovarian cancer detection using machine learning

Abstract:

Introduction: The reliability of machine-learning (ML) integrated platelet RNA-based diagnostic tests is heavily influenced by the sample processing methods used during model training. In this study, we assessed the impact of three RNA normalization protocols and their impact on classification accuracy.

Materials and Methods: Data were collected from two distinct cohorts. The first cohort included publicly available samples (390 healthy donors - HD, 144 ovarian cancer – OC, 1484 samples from patients with 17 other cancer types) from In't Veld et al. 2022 [1] and served as a training and validation dataset. The second cohort consisted of samples from HD (n=7), benign controls - BC (n=25), and OC patients (n=32) served as a test set. Gene counts from the test cohort were normalized using three different approaches: 1) normalizing the test samples independently, 2) normalizing the test samples alongside the training data, and 3) normalizing each test sample separately with the training data.

Results: The logistic regression model scored 68.63% sensitivity, at a 100% specificity threshold on the validation set. Using the first normalization method for the test samples, the model scored 66.3% balanced accuracy while classifying the HD, BC, and OC samples. The second approach resulted in 79.9% balanced accuracy. The third approach resulted in the highest balanced accuracy of 81.3%.

Conclusion: This study highlights how normalization protocol affects the diagnostic process of RNA sample classification using ML models. Minimizing batch effects by normalizing each test sample with training data separately proved to be the most accurate approach.

Biography

Maksym Jopek is currently a 3rd year PhD student at the Intercollegiate Faculty of Biotechnology at the University of Gdansk and Medical University of Gdansk, specializing in the Division of Translational Oncology. Their research is focused on the applications of artificial intelligence in liquid biopsy for cancer detection. In addition to their PhD studies, Maksym Jopek consults on medical research projects at the Centre of Biostatistics and Bioinformatics Analysis at the Medical University of Gdansk and works as a bioinformatician at the Clinic of Arterial Hypertension and Diabetology at the University Clinical Centre in Gdansk.

Martin Porebski

Wake Forest University School of Medicine
USA

Genetic, immune and metabolic endpoints as biomarkers of immune checkpoint therapy response

Abstract:

The development of immunotherapies represents a significant advance within clinical oncology, but its efficacy is confined to a subset of patients, and the emergence of acquired resistance is increasingly apparent. Unlike conventional chemotherapy, which often results in measurable changes in tumor size, evaluating responses to immune checkpoint inhibitor therapy proves challenging due to its unique mechanism and the frequent occurrence of disease progression before tumor regression. Consequently, identifying biomarkers of therapeutic response becomes pivotal in formulating strategies to enhance overall response rates. In our current investigation, we conducted a retrospective analysis of peripheral blood mononuclear cells (PBMCs) and plasma obtained from patient blood draws before initiating treatment and then three weeks after the first cycle of therapy for those with metastatic non-small cell lung cancer undergoing immune checkpoint inhibitor therapy; participants are enrolled in an ongoing Wake Forest Phase II clinical trial (NCT04253964) that is evaluating the impact of ECOG Performance Status on outcomes in advanced lung cancer. This analysis builds on methodology from a recently published study centered around patients with metastatic melanoma. To determine biomarkers of response we employed single-cell RNA sequencing (scRNAseq) to study the identity and transcriptional profiles of involved cells within patient PBMCs. Transcriptomic clustering consistently identified the major immune cell populations expected in PBMCs: monocytes, natural killers, B cells, and T cells. Graph-based cluster analysis further uncovered transcriptional variations, allowing the identification of multiple immune cell subpopulations within these major clusters. Pathway enrichment analysis of the T cell population revealed that one of the top regulated pathways is oxidative phosphorylation which includes genes related to the mitochondrial electron transport chain and mitochondrial membrane integrity. To determine whether response is related to regulation of this pathways PBMCs were subjected to cellular respiration analysis. Our data demonstrates that patients that respond to immunotherapy have a 2-fold ($p<0.001$) increase in respiratory capacity when compared to non-responders suggesting that mitochondrial function is associated with response. We further validated these observations in our cell population and observed that patients that do not respond to immunotherapy have lower mitochondrial membrane potential relative to patients that respond. In summary, our research introduces a novel set of tools for integration into clinical practice. These tools enhance clinical decision-making, enabling the prediction of therapeutic responses and facilitating the implementation of personalized treatment approaches to enhance the outcomes of cancer immunotherapy.

Biography

Martin Porebski resident physician in Internal Medicine training at Atrium Health Wake Forest University Baptist Medical Center. My interests include global health as well as medical-entrepreneurship. Ultimately, I hope to specialize further through fellowship and combine my life experiences to bring about comprehensive, empathetic, evidenced-based care and develop a career where my impact is felt on more than one patient at a time. Always looking for new and interesting opportunities to diversify my career outside of purely clinical medicine!

Kimiya Shirbacheh

Nickan
Iran

A novel therapeutic approach for metastatic Breast Cancer: Glucose deprivation of tumor cells

Abstract:

Background: Metastatic breast cancer remains a critical challenge due to the tumor cells' metabolic adaptability and resistance to current therapies. We propose a novel therapeutic strategy focused on depriving tumor cells of glucose while selectively delivering nutrients to normal cells.

Methods: The approach involves depleting glycogen stores in normal tissues via a crash diet and prolonged fasting, followed by the administration of Total Parenteral Nutrition (TPN) supplemented with essential ingredients encapsulated in liposomes for 30 days. These liposomes are designed to selectively target normal cells by leveraging their unique metabolic environment.

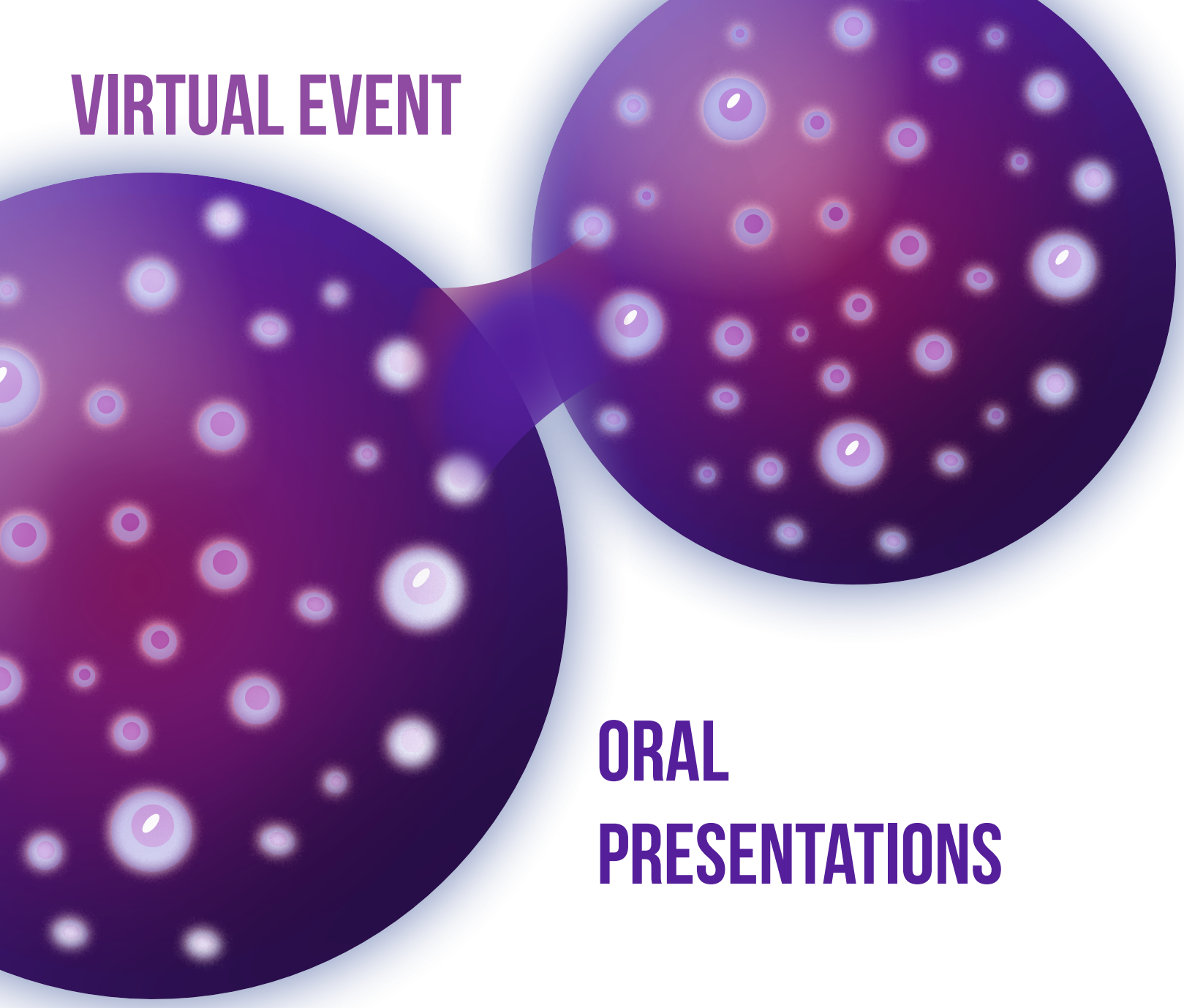
Results: The liposomes are coated with a pH-sensitive copolymer, Polyethylene glycol-Poly-L-histidine (PEG-PLH), designed to bind with glucose transporters (GLUTs) on all cells to release the nutrient material. The Poly-L-histidine (PLH) component is engineered to undergo conformational changes in the acidic microenvironment of tumor cells, which prevents the copolymer from binding to the GLUTs on tumor cells while maintaining its functional structure in a normal tissue environment. This selectivity is further enhanced by using superhydrophobic fluorinated compounds conjugated with trastuzumab, which specifically binds to HER2+ tumor cells. The superhydrophobic structure creates a repulsive surface in response to the hydrophilic PEG coating on the liposomes, effectively deterring the liposomes from accumulating in metastatic sites. Additionally, zwitterionic modifications of the liposome surfaces in the low-pH microenvironment of tumor cells create a hydration layer around the liposomes. This prevents their passage through the capillary walls and accumulation in tumor tissues. Consequently, this strategy facilitates the targeted delivery of nutrients to healthy tissues.

Conclusion: These three strategies effectively reduce glucose availability to tumor cells while maintaining normal cellular metabolism in normal tissues. The reviewed scientific evidence suggests that this method has the potential to improve therapeutic outcomes and decrease the likelihood of metastasis in HER2+ breast cancer especially in combination with the conventional methods. Further in vitro and in vivo studies, followed by clinical trials, are essential to validate this approach and explore its applicability to other solid tumors.

Biography

Kamran Shirbache has dedicated his medical career to pioneering research in cancer treatment, consistently seeking innovative approaches to eradicate the disease. His current model is the culmination of years of studying various metabolic strategies and developing targeted drug delivery systems to effectively treat cancer.

VIRTUAL EVENT



ORAL PRESENTATIONS

NOVEMBER

06-07, 2024

Maria Borrell

Sant Pau Research Institute
Spain

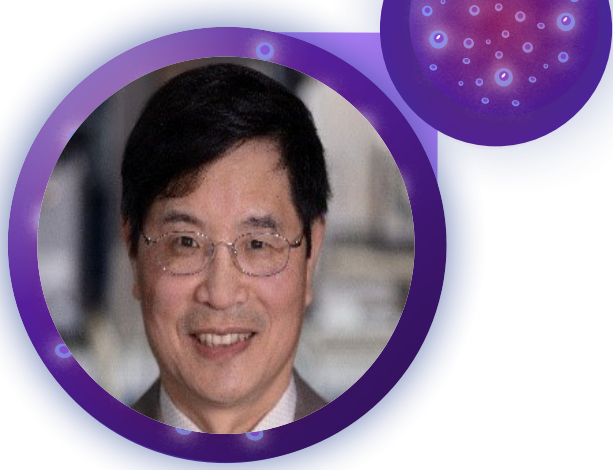
PCSK9 is a cholesterol lowering agent with a role in cancer progression

Abstract:

There are numerous evidences that Proprotein Convertase Subtilisin/Kexin 9 (PCSK9) inhibitors combat cancer. These cholesterol lowering agents, together with lipid receptors have a deep impact on the development of atherosclerosis. The role between PCSK9 inhibitors, lipid receptors and cancer progression is not fully studied. The disruption of the hepatic interaction between PCSK9 and Low-Density Lipoprotein Receptor (LDLR) downregulates blood cholesterol levels and reduces cardiovascular events. Recent data suggest that other members of the LDLR superfamily may be targets of PCSK9. In this presentation I will show that LDLR-related protein 5 (LRP5) is a PCSK9 target, and both proteins participate in foam cell formation and hence, in the mechanism of lipid accumulation and cancer progression. I will first show that LRP5 is needed for macrophage lipid uptake since LRP5-silenced macrophages have less intracellular cholesterol accumulation. Immunoprecipitation experiments will show that LRP5 forms a complex with PCSK9 in lipid-loaded macrophages opening the possibility that PCSK9 induces lysosomal LRP5 degradation in a similar manner than it does with LDLR. We have also studied the role of PCSK9 and LRP5 in the inflammatory response by TLR4/NFkB signaling pathway and show that PCSK9 gene interference decreases inflammation supporting a role for PCSK9 as an inflammatory mediator in cancer progression. We then validated our results in an in vivo mice model. We analyzed the differential expression of cholesterol and inflammation related genes in wildtype (Wt) and LRP5 knock-out (Lrp5-/-) mice fed a normocholesterolemic (NC) or a hypercholesterolemic (HC) diet. Results show that cholesterol accumulates differently in livers of Wt and Lrp5-/- mice and a that cholesterol accumulation play a role in inflammation and cancer progression

Biography

Borrell is a senior investigator at the Research Institute of the Santa Creu i Sant Pau Hospital in Barcelona. Prior appointments include a postdoctoral position in the Neurology Department of the Curie Institut, Paris, France studying Huntington's disease. She leads a project based in lipoprotein receptors role in cholesterol metabolism. In recent years she has been developing a project that analyzes the function of PCSK9 beyond its function in cholesterol lowering. These results have been published in different journals including EHJ, BRIC or CVR and lead to the concession of projects financed by both, the government and the industry.



Huawei Zeng

Grand Forks Human Nutrition Research Center
USA

Oncogenic signatures and inflammatory colon in diet-induced obese mouse models

Abstract:

Adoption of an obesogenic diet such as a high-fat diet (HFD) results in obesity, bacterial dysbiosis, chronic inflammation, and cancer. Primary bile acids (BAs) play critical roles in cholesterol metabolism, lipid digestion, and host-microbe interaction. However, HFDs increase secondary BAs (e.g., deoxycholic acid (DCA) and lithocholic acid (LCA) in the colon), are risk factors for colonic inflammation and cancer. Gut bacteria and their metabolites are recognized by interleukin-1 (IL-1R)/toll-like receptors (TLRs) which are essential to maintain intestinal homeostasis; host extracellular microRNAs (miRNAs) can alter bacterial growth in the colon. Characterization of the underlying mechanisms may lead to identifying fecal oncogenic signatures reflecting colonic health. We hypothesize that a HFD accelerates the inflammatory process, oncogenic metabolites, and disease-related gut microbiome in the colon. With diet-induced obese mouse models, we found that the concentrations of plasma interleukin 6 (IL-6), inflammatory cell infiltration, β-catenin, and cell proliferation marker (Ki67) in the colon were elevated > 60% in the HFD (45 % energy fat) group compared to the control (16 % energy fat) group. Furthermore, the content of Alistipes bacteria, the Firmicutes/Bacteroidetes ratio, microRNA-29a, and DCAs and LCAs (secondary BAs with oncogenic potential) were 50% greater in the feces of the HFD group compared to the control group. In summary, our multimodal profile data may represent a unique HFD-induced oncogenic signatures for colon health in a diet-induced mouse model. A greater understanding of these mechanistic action may open new avenues for seeking noninvasive colonic biomarkers.

Biography

Zeng was born and grew up in Xiamen, China. He obtained B.S. and M.S. degrees in Biology from Xiamen University. He attended the University of Wyoming, where he earned a Doctor of Philosophy degree in Molecular Biology in 1996. After graduation, Dr. Zeng spent three and half years as a postdoctoral researcher at the National Institutes of Health (Bethesda, MD) investigating steroid hormone-induced gene expression. Dr. Zeng joined the scientific staff of the USDA-ARS Grand Forks Human Nutrition Research Center (GFHNRC) as a Research Molecular Biologist in November 1999.

Juhyun David Oh

Korea Kent Foreign School
Korea South

Identifying chemical exposures associated with Monoclonal Gammopathy of Undetermined Significance (MGUS)

Abstract:

Monoclonal Gammopathy of Undetermined Significance (MGUS) is a condition where an abnormal protein, known as monoclonal protein or M-protein, is found in the blood. Although MGUS does not usually cause any symptoms, it is considered important because it may develop into more serious diseases like multiple myeloma or other blood disorders. Monitoring MGUS is essential to ensure early detection and intervention if it progresses. This study aimed to identify potential environmental exposures associated with MGUS. Using data from the National Health and Nutrition Examination Survey (NHANES), the goal of our study was to evaluate if exposures in a cross-sectional population including people with MGUS and matched controls were associated with increased risk of MGUS. Exposure biomarkers were downloaded from NHANES survey years 1999-2000, 2001-2002, and 2003-2004, and linked to individuals with M-protein levels measured in blood and matched controls. Since biomarker panels were measured in different individuals, the number of cases for each measure ranged from 20 to 156 and were matched to the same number of controls. To test for exposures associated with MGUS, linear regression was performed separately for each exposure, and associated biomarkers were identified using $p < 0.05$.The results showed that chemical biomarkers such as polychlorinated biphenyls, 2,3,4,7,8-pentachlorodibenzofuran, mono-benzyl phthalate, urinary cadmium, and urinary monomethylarsonic acid are all associated with increased risk of MGUS, suggesting a possible link between environmental exposures and this precursor condition that increases risk for blood cancer and other disorders.

Biography

Juhyun David Oh is a cancer researcher based in Seoul, South Korea, affiliated with Seoul National University. A graduate of Korea Kent Foreign School, David has conducted significant research on cancer, focusing on identifying environmental chemical exposures linked to Monoclonal Gammopathy of Undetermined Significance (MGUS), a precursor condition to certain blood cancers. David's work explores the intersections of environmental factors and cancer risk, contributing to the understanding of cancer etiology and prevention strategies. He will be presenting his latest findings on MGUS-associated chemical exposures at Cancer 2024

Huiling Li

Clinical Oncology School of Fujian Medical University
China

AI-assisted 3D printing transvaginal template guidance for interstitial brachytherapy in patients with gynecologic malignancy

Abstract:

Background: The three-dimensional (3D) interstitial Brachytherapy (BT) can enhance the efficacy of bulky cervical cancer treatment. BT technology guided by 3D printing templates can assist radiation oncologists in accurately inserting needles and ensuring optimal dose coverage. Artificial intelligence (AI) can enhance the accuracy, precision, efficiency, and overall quality of RT in patients with cancer objective: This is a retrospective study to show the safety and efficacy of using AI-assisted transvaginal 3D printed templates for guiding interstitial BT as a component of RT in patients with gynecologic malignancy.

Methods: Between October 2021 and December 2023,The localization data of 50 patients from computed tomography scanning were collected and imported into the software. Automated configuration of individualized 3D printing templates using AI-assisted technology according to the specific anatomical morphology and volume of the target. The accuracy of the needle insertion paths and needle depth were assessed. The target dose coverage between AI-assisted 3D printing template guidance insertion and free-hand insertion techniques was assessed and compared.

Results: The repetition of the planned needle paths was compared with that of the actual needle insertion, a mean deviation of 1.55±0.45 mm was observed. Compared with freehand BT, significant differences were observed in the DVH parameters CTV V100 ($p = 0.015$), HR-CTV D98 ($p = 0.041$), bladder D2cc ($p = 0.010$), and rectum D2cc ($p = 0.02$) of AI-assisted 3D printing.

Conclusions: This novel technique of AI-assisted 3D printing transvaginal template guidance offers high reproducibility, efficiency, and safety for the insertion BT method in patients with gynecologic malignancy.

Biography

Huiling Li is the deputy director of gynecological oncology radiotherapy department Fujian Medical University, Fujian Cancer Hospital. She has published more than 20 papers and engaged in precise radiotherapy and chemotherapy, targeted therapy, and immunotherapy for gynecological tumors.

Xiaolian Peng

Dongguan Municipal People's Hospital
China

Poly (ADP-ribose) polymerase (PARP) inhibitor regimens for platinum-sensitive ovarian cancer in phase III randomized controlled trials: A systematic review and network meta-analysis

Abstract:

Background: Poly (ADP-ribose) polymerase (PARP) inhibitors offer a new treatment option for ovarian cancer. To compare the primary efficacy and safety of different PARP inhibitors in platinum-sensitive ovarian cancer.

Methods: We searched multiple databases from 1990 to 2023. Only multicenter, randomized, double-blind, phase III-controlled trials for first-line maintenance or post-relapse treatment were included. The primary efficacy outcome was progression-free survival (PFS) and overall survival (OS), and the primary safety outcome was treatment-emergent adverse events (TEAEs). This trial was registered under PROSPERO (CRD42024511248).

Results: A total of 9 eligible trials with 5285 patients treated with 4 different PARP inhibitors were reviewed. For PFS, the median duration was significantly longer in patients who received Niraparib than placebo (hazard ratio (HR)=2.93, 95% CI 1.78–4.82). The median duration was significantly shorter in patients who received Rucaparib and Olaparib than Niraparib (HR=0.33 (0.18–0.62) and 0.32 (0.19–0.53), respectively). For TEAE, the Niraparib-based regimen tended to be associated with a lower risk compared with placebo (HR=0.13 (0.08–0.20)). Rucaparib, Olaparib, and Veliparib were associated with a higher risk compared to Niraparib. For OS, the difference was not statistically significant in patients receiving Olaparib + Bevacizumab compared to Olaparib or placebo.

Conclusions: Our study showed that Niraparib was the most effective regimen with the lowest risk of TEAE in patients with platinum-sensitive ovarian cancer. Veliparib came in second. Rucaparib was associated with the highest risk of TEAE. Our findings are useful for improving guidelines and developing clinical or national policies for platinum-sensitive ovarian cancer.

Biography

Xiaolian Peng completed a master's degree at the age of 39 years from Central South University and participated in the doctoral examination of gynecologic Oncology at Peking Union Medical College in 2015. She is the associate chief physician of gynecology and obstetrics with many years of clinical experience, a member of ESMO, ESGO, and ASGO, a reviewer of the Journal of Gynecologic Oncology and World Journal of Gastrointestinal Surgery, and the class teacher of the Little Black House Clinical Scientist College. She loves literature and music her research area is gynecological oncology.

SUPPORTING JOURNAL

Archives in Oncology Research

https://www.scitechjournals.com/archives-in-oncology-research

We wish to engage with you again in 2025...

Upcoming Conference

3RD INTERNATIONAL CONFERENCE ON

INNOVATIONS AND ADVANCES IN CANCER RESEARCH AND TREATMENT

OCTOBER 30-31, 2025 | LAS VEGAS, USA

https://www.scitechseries.com/cancer

ScitechSeries

Scitechseries Publishing Limited
71-75 Shelton street, Covent Garden,
London, WC2H 9JQ
Phone: +44-2045874848
Email: info@scitechseries.com

Questions? Contact

Phone: +44 2045874848

WhatsApp: +44 2045250803