JOINT EVENT ON

9th WORLD BIOMARKERS CONGRESS

&

20th International Conference on

PHARMACEUTICAL BIOTECHNOLOGY

December 07-09, 2017 | Madrid, Spain

Scientific Tracks & Abstracts

Day 1

Sessions 1

Biomarkers | Cancer Biomarkers | Pathology Diagnosis

Session Chair
Wancai Yang
University of Illinois at Chicago, USA

Session Introduction

Title: **Genetic and epigenetic alterations in chronic colitis malignant transformation**
Wancai Yang, University of Illinois at Chicago, USA

Title: **Genetic deficiency of PRSS8 causes mouse intestinal inflammation and tumors**
Yonghua Bao, Jining Medical University, China

Title: **Gastric Endoscopic Submucosal Dissection (ESD) as a treatment for early neoplasia and for accurate staging of early cancers in a UK Caucasian population**
M Davenport, Salford Royal NHS Foundation Trust, UK

Title: **The ERK MAP kinase-PEA3/ETV4-MMP-1 axis is operative in oesophageal adenocarcinoma**
Yeng S Ang, Salford Royal University Hospital, UK

Wancai Yang et al., J Proteomics Bioinform 2017, 10:12(Suppl)
DOI: 10.4172/0974-276X-C1-109

Genetic and epigenetic alterations in chronic colitis malignant transformation

Wancai Yang[1,2] and **Yonghua Bao**[1]
[1]University of Illinois at Chicago, USA
[2]Jining Medical University, China

Chronic colitis malignant transformation is one of major causes to colorectal cancer, but the mechanisms of colitis develops and how the chronic colitis progress to malignance is largely unknown. Using a unique mouse model, we have demonstrated that the mice with targeted disruption of the intestinal mucin gene Muc2 spontaneously develop chronic inflammation at colon and rectum at early age, whose histopathology was similar to ulcerative colitis in human. In the aged mice, Muc2-/- mice develop colonic and rectal adenocarcinoma accompanying severe inflammation. To determine the mechanisms of the malignant transformation, we conducted miRNA array on the colonic epithelial cells from Muc2-/- and +/+ mice. MicroRNA profiling showed differential expression of miRNAs (i.e. lower or higher expression enrichments) in Muc2-/- mice. Based on relevance to cytokines and cancer, the miRNAs were validate and were found significantly downregulated or upregulated in human colitis and colorectal cancer tissues, respectively. The targets of the miRNAs were further characterized and their functions were investigated. More studies from the Muc2-/- mice showed disorder of gut microbiota. Moreover, a novel tumor suppressor PRSS8 also plays a critical role in colorectal carcinogenesis and progression, for instance, tissue-specific deletion of the PRSS8 gene resulted in intestinal inflammation and tumor formation in mice. Gene set enrichment analysis showed that the colitis and tumorigenesis were linked to the activation of Wnt/beta-catenin, PI3K/AKT and EMT (epithelial-mesenchymal transition) signaling pathways. Taken above, the disorder of gut microbiota could result in genetic mutations, epigenetic alterations, leading to the activation of oncogenic signaling, in colorectal epithelial cells, and finally, to colitis development, promoting malignant transformation and mediating colorectal cancer metastasis.

Biography

Wancai Yang is the Dean of the Institute of Precision Medicine and School of Basic Medical Sciences, Jining Medical University, China, and a Professor of Pathology, University of Illinois at Chicago, USA. He is also an Adjunct Professor of Biological Sciences, University of Texas, El Paso, USA. He obtained his MD degree and was trained as a Pathologist from China and received Post-doctoral training on Cancer Biology from Rockefeller University and Albert Einstein Cancer Center, US, and was promoted as Assistant Professor. In 2006, he moved to the Department of Pathology, UIC and serving as a Grant Reviewer for the National Institutes of Health (USA) and the National Nature Science Foundation of China. His research focuses on: (1) the determination of mechanisms of gastrointestinal carcinogenesis, (2) identification of biomarkers for cancer detection and patient selection for chemotherapy, (3) implication of precision medicine in cancers. He has published more than 80 peer-reviewed articles and has brought important impact in clinical significance.

wyang06@uic.edu

Notes:

Yonghua Bao et al., J Proteomics Bioinform 2017, 10:12(Suppl)
DOI: 10.4172/0974-276X-C1-109

Genetic deficiency of PRSS8 causes mouse intestinal inflammation and tumors

Yonghua Bao[1] and **Wancai Yang**[1,2]
[1]Jining Medical University, China
[2]University of Illinois at Chicago, USA

PRSS8 is a glycosylphosphatidylinositol anchored serine protease, has physiological and pathophysiological functions and shows important roles in the epidermal barrier function and in the regulation of glucose homeostasis. However, the biological functions of PRSS8 in cancer initiation and progression is unknown. We have found that PRSS8 was significantly reduced in esophageal and colorectal cancers and acted as a tumor suppressor in colitis-associated colorectal cancer through targeting Sphk1/Stat3/Akt signaling pathway. To determine the roles of PRSS8 in colorectal cancer *in vivo*, we developed a conditional knockout mouse model - intestine-specific deletion of Prss8 in mice (Prss8 fl/fl-Cre+, Prss8 CKO), and found that PRSS8 deletion caused spontaneous formation of intestinal inflammation and tumors. At the age of 3 months, about 20% of the Prss8 CKO mice exhibited inflamed rectum and then exerted rectal prolapse. Histopathologic analysis showed that 65% Prss8 CKO mice had developed chronic inflammation in large intestine at 3 months. Interestingly, 45% Prss8 CKO mice had developed hyperplasia in small intestine at 3 months. At the age of 6 months, 53 % of the Prss8 CKO mice developed adenomas, and at the age of 9 months, 75% of the Prss8 CKO mice developed adenomas. Further studies showed that gastrointestinal tumorigenesis was linked to the disruption of intestinal epithelial cell maturation: more proliferative cells and moved faster in the Prss 8 CKO mouse, assayed by BrdU staining and migration assay. Moreover, Prss 8 CKO mouse intestine exhibited less mature mucin drops and goblet cells at the crypts of small and large intestine in comparison with the WT mice. Gene profile using mouse intestinal epithelial cells and gene set enrichment analysis showed that the tumorigenesis was associated with oncogenic signaling pathways, including Wnt/beta-catenin and inflammatory signaling. The underlying mechanisms are under further investigation.

Biography

Yonghua Bao graduated from Jiamusi Medical University (China) with a Clinical Medicine background, received PhD on Biochemistry and Molecular Biology from Jilin University and Post-doctoral training on Biochemistry and Molecular Biology in the State Key Laboratory of China Agricultural University. She was promoted as Associate Professor and worked in cancer and cell signal transduction lab since 2012. She was recruited by Jining Medical University as a Professor of Pathology in 2015, and was appointed as Vice Dean of Institute of Precision Medicine. Her study focuses on cancer biology and cell signaling pathways in gastrointestinal carcinogenesis, progression and metastasis. As PI, she was funded by the National Natural Science Foundation of China. She has published 22 papers and was awarded 3 patents.

baoyonghua2005@126.com

Notes:

M Davenport et al., J Proteomics Bioinform 2017, 10:12(Suppl)
DOI: 10.4172/0974-276X-C1-109

Gastric Endoscopic Submucosal Dissection (ESD) as a treatment for early neoplasia and for accurate staging of early cancers in UK Caucasian population

M Davenport[1], Aisha Sooltangos[1], S McGrath[3], J Vickers[3], S Senapati[3], K Akhtar[3], R George[2] and **Yeng Ang[1]**
[1]Salford Royal NHS Foundation Trust, UK
[2]Pennine Acute NHS Trust - Salford Royal NHS foundation Trust, UK
[3]Salford Royal NHS Foundation Trust, UK

Aim: To investigate the efficacy of Endoscopic Submucosal Dissection (ESD) at diagnosing and treating superficial neoplastic lesions of the stomach in a Caucasian population.

Methods: Data of Caucasian patients treated with or considered for ESD at a tertiary referral center were retrieved for a 3-year period. Primary outcomes were curative resection (CR), which was defined as ESD resections with clear margins and an absence of lymphovascular invasion, poor differentiation and submucosal involvement on histology. Secondary outcomes were reversal of dysplasia at 12 months follow-up and/or at the latest follow up. Change in histological diagnosis pre and post ESD was recorded.

Results: Twenty four patients were identified with intention to treat. Nineteen patients were considered eligible, and ESD was attempted on 25 lesions, 4 of which failed and were aborted. Out of 21 ESD performed, en-bloc resection was achieved in 71.4% of cases. Resection was considered complete on endoscopy in 90.5% of cases compared to only 38.1% on histology. Six resections were considered curative (28%), 5 non-curative (48%) and 10 indefinite (24%). ESD changed the histological diagnosis in 66.6% of cases post ESD. Endoscopic follow-up in the indefinite group and CR group showed that 50% and 80% of patients were clear of dysplasia at the latest follow-up respectively; 2 cases of recurrence were observed in the indefinite group and survival rate for the entire cohort was 91.7%.

Conclusion: This study provides evidence for the efficacy of ESD as a therapeutic and diagnostic intervention in Caucasian populations and supports its application in the UK.

Biography

M Davenport is a Foundation Year 2 Doctor at Salford Royal Hospital, Manchester, UK. He is presenting on behalf of a team headed by Dr. Yeng S Ang, MD, FRCP, Consultant Gastroenterologist, Salford Royal University Hospital, UK. Honorary Reader, University of Manchester, Manchester, UK.

Matthew.Davenport3@srft.nhs.uk

Notes:

Yeng S Ang, J Proteomics Bioinform 2017, 10:12(Suppl)
DOI: 10.4172/0974-276X-C1-109

The ERK MAP kinase-PEA3/ETV4-MMP-1 axis is operative in oesophageal adenocarcinoma

Yeng S Ang[1,2]
[1]Salford Royal University Hospital, UK
[2]University of Manchester, UK

Many members of the ETS-domain transcription factor family are important drivers of tumorigenesis. Their activation by Ras-ERK pathway signaling is particularly relevant to the tumorigenic properties of many ETS-domain transcription factors. The PEA3 subfamily of ETS-domain transcription factors have been implicated in tumor metastasis in several solid tumors. We have studied the expression of the PEA3 subfamily members PEA3/ETV4 and ER81/ETV1 in oesophageal adenocarcinomas and determined their role in oesophageal adenocarcinoma cell function. PEA3 plays an important role in controlling both the proliferation and invasive properties of OE33 oesophageal adenocarcinoma cells and a key target gene is *MMP-1*. The ERK MAP kinase pathway activates PEA3 subfamily members and also plays a role in these PEA3 controlled events, establishing the ERK-PEA3-MMP-1 axis as important in OE33 cells. PEA3 subfamily members are upregulated in human adenocarcinomas and expression correlates with MMP-1 expression and late stage metastatic disease. Enhanced ERK signaling is also more prevalent in late stage oesophageal adenocarcinomas. This study shows that the ERK-PEA3-MMP-1 axis is upregulated in oesophageal adenocarcinoma cells and is a potentially important driver of the metastatic progression of oesophageal adenocarcinomas.

Biography

Yeng S Ang has an international professional standing and research expertise to enhance clinical interventions in Barrett's oesophagus and oesophageal cancer. He is a Member of the BSG/National Clinical Research Institute Upper GI early cancer prevention research subgroup. He is a peer reviewer for the NIHR RFPB programme and a member of the Research Steering Board of Manchester Cancer Research Centre (Cancer Research UK Manchester Institute). These research initiatives have shaped his contribution for the management of GORD, Barrett's oesophagus and oesophageal cancer. He has published over 45 articles and he is a Supervisor for PhD and MD students in the molecular cancer group of the University of Manchester.

Yeng.Ang@srft.nhs.uk

Notes:

Sessions 2

Day 1 December 07, 2017

Biopharmaceuticals | Computer Aided Drug Design (CADD) | Medicinal Chemistry in Modern Drug Discovery | Drug Metabolism and Drug Designing

Session Chair
Vladimir A Baulin
Universitat Rovira I Virgili, Spain

Session Introduction

Title: **Targeting viral membrane proteins *in silico***
Wolfgang B Fischer, National Yang-Ming University, Taiwan

Title: **Crocin, a carotenoid pigment of saffron inhibits the replication of HSV and HIV *in vitro***
Sepehr Soleymani, Pasteur Institute of Iran, Iran

Title: **RNAi-based tailored therapeutic strategies: Are we there yet?.**
Sukru Tuzmen, Translational Genomics Research Institute, USA

Title: **Anticancer efficacy of self-nanoemulsifying drug delivery system of sunitinib malate**
Saad M Alshahrani, Prince Sattam Bin Abdulaziz University, Saudi Arabia

Title: **Cucurbitacin B mitigates experimental autoimmune encephalomyelitis by inhibition of IL-17/IL-23 immune axis**
Nima Sanadgol, University of Zabol, Iran

Title: **Design strategies for nanoparticles translocating through lipid bilayers**
Vladimir A Baulin, Universitat Rovira I Virgili, Spain

Wolfgang B Fischer, J Proteomics Bioinform 2017, 10:12(Suppl)
DOI: 10.4172/0974-276X-C1-109

Targeting viral membrane proteins *in silico*

Wolfgang B Fischer
National Yang-Ming University, Taiwan

Many viral membrane proteins interact with membrane proteins of the host to steer the cell for a successful mass production of novel virions. The viral proteins rely on selective interactions of their transmembrane domains (TMDs) with those of the host protein. An understanding of the modalities of recognizing the proper host target, on the revers, can be turned against the virus. Getting insights into the specificity of binding, the interaction of oncoprotein E5 of *Human papillomavirus*-16 (HPV-16), an 83-amino acid membrane protein containing 3 TMDS, with a peptide corresponding to the fourth TMD (TMD4) of the 16 kDa subunit of the ATP6V0C is investigated as an example. HPV-16 is the major cause of cervical cancer diagnosed today. E5 is a membrane protein which is expressed at an early (hence the letter E) stage of the infectivity cycle when the virus turns the cell malignant. The protein interacts with a series of host factors, but has also been identified experimentally to allow channel activity when most likely in a hexameric assembled form. Computational modeling suggests a weak selectivity of the channel. Docking approaches as well as coarse grained molecular dynamics (CGMD) simulations of the peptides within a hydrated lipid membrane specify the mode of binding of TMD4 with either E5 protein or its individual TMDs. From potential of mean force calculations (PMF) and statistical analysis enthalpy and entropy contributions are attributed of TMD4 binding to TMD3 and TMD2 of E5, respectively.

Recent Publications:

1. Fischer W B, Li L-H, Mahato D R, Wang Y T and Chen C P (2014) Viral channel proteins in intracellular protein - protein communication: Vpu of HIV-1, E5 of HPV16 and p7 of HCV. Biochim. Biophys. Acta. 1838:1113-1121.
2. Mahato D R and Fischer W B (2016) Weak selectivity predicted for modeled bundles of the viral channel forming protein E5 of human papillomavirus-16. J. Phys. Chem. B. 120: 13076-13085.
3. Fischer W B, Kalita M M and Heermann D (2016) Viral Channel forming proteins - how to assemble and depolarize lipid membranes in silico. Biochim. Biophys. Acta. 1858: 1710-1721.

Biography

Wolfgang B Fischer is Professor at the Institute of Biophotonics, School of Biomedical Science and Engineering, National Yang-Ming University, Taipei, Taiwan. He has obtained his PhD in Chemistry at Heidelberg University, Germany, working in the field of vibrational spectroscopy in 1991. After years in the US, he has completed his Postdoctoral, working on bacteriorhodopsin using vibrational spectroscopy in Boston University, Germany. Then he has worked in Analytical Chemistry, working on ion channels as potential biosensors, UK (Oxford University as EU Marie Curie Research Fellow and later as Lecturer, working on viral ion channels using bilayer recordings and molecular dynamics simulations. He has moved to Taiwan. The field of research is on biophysical aspects describing dynamics and energetic of protein-protein interactions (PPIs) of membrane proteins. The focus is on the development of computational platform technologies to support drug discovery and design as well as materials sciences.

wfischer@ym.edu.tw

Notes:

Sepehr Soleymani et al., J Proteomics Bioinform 2017, 10:12(Suppl)
DOI: 10.4172/0974-276X-C1-109

Crocin, a carotenoid pigment of saffron inhibits the replication of HSV and HIV *in vitro*

Sepehr Soleymani[1,2], **Rezvan Zabihollahi**[1], **Sepideh Shahbazi**[1] and **Azam Bolhassani**[1]
[1]Pasteur Institute of Iran, Iran
[2]High Institute for Research and Education in Transfusion Medicine, Iran

Human immunodeficiency virus type 1 (HIV-1) belonging to the retrovirus family is the major agent of acquired immunodeficiency syndrome as a public health problem in the world. There are more than 253 types of approved anti-HIV drugs, but further development of novel anti-HIV agents would be needed especially in low-income countries without anti-retroviral treatment. Some limitations of the recent viral therapies include high risk of resistant viruses, and adverse side effects in long-term therapy. Therefore, it is necessary for improvement of novel potent and safe anti-HIV drugs with decreased side effects especially tolerability and toxicity. Furthermore, other problem in treatment of HIV-infected patients is their susceptibility to *Herpes simplex virus* (HSV) infection; thus, both anti-HSV and anti-HIV drugs with novel modes of action are required. Recently, saffron components have been proposed to treat various pathological conditions. In this study, crocin, a major carotenoid of saffron, was extracted from the ethanolic saffron extract by adsorption chromatography using neutral aluminum oxide 90 active. Then, the anti-HSV-1 and anti-HIV-1 activities of crocin were assessed as well as its cytotoxicity in vitro. The data indicated that crocin was active against HIV-1 and HSV-1 virions at certain doses. Crocin inhibited the HSV replication at before and after entry of virions into Vero cells. Indeed, crocin carotenoid suppressed HSV penetration in the target cells as well as disturbed virus replication after entry to the cells. This sugar-containing compound extracted from saffron showed to be an effective anti-herpetic drug candidate. In general, crocin would be a promising anti-HSV and anti-HIV agent for herbal therapy against viral infections.

Recent Publications:

1. Bolhassani A, Khavari A and Bathaie S Z (2014) Saffron and natural carotenoids: Biochemical activities and anti-tumor effects. Biochimica et Biophysica Acta. 1845: 20-30.
2. Bolhasani A, Bathaie S Z, Yavari I, Moosavi-Movahedi A A and Ghaffari M (2005) Separation and purification of some components of Iranian saffron. Asian Journal of Chemistry. 17: 725-729.
3. Zabihollahi R, Namazi R, Aghasadeghi M R, et al (2012). The in vitro anti-viral potential of Setarud (IMOD™), a commercial herbal medicine with protective activity against acquired immune deficiency syndrome in clinical trials. Indian Journal of Pharmacology. 44: 448-453.
4. D'Alessandro A M, Mancini A, Lizzi A R, et al. (2013) Crocus sativus stigma extract and its major constituent crocin possess significant anti-proliferative properties against human prostate cancer. Nutrition and Cancer. 65: 930-942.

Biography

Sepehr Soleymani has graduated from Tehran University of Medical Science in Clinical Laboratory Science. Currently, he is a Master student of Medical Biotechnology in Blood Transfusion Organization and also as a Research Assistant in Pasteur Institute of Iran for 3 years. His activity focuses on natural and synthetic antiviral agents, drug delivery system and vaccine research.

dss.soleymani@gmail.com

Notes:

Şükrü Tüzmen, J Proteomics Bioinform 2017, 10:12(Suppl)
DOI: 10.4172/0974-276X-C1-109

RNAi-based tailored therapeutic strategies: Are we there yet?

Şükrü Tüzmen[1,2]
[1]Eastern Mediterranean University, Turkey
[2]Translational Genomics Research Institute, USA

A classical technique to determine the function of a gene is to experimentally inhibit its gene expression in order to examine the resulting phenotype or effect on molecular endpoints and signaling pathways. RNA interference (RNAi) is one of the recent discoveries of a naturally occurring mechanism of gene regulation facilitated by the induction of double stranded RNA into a cell. This event can be utilized to silence the expression of specific genes by transfecting mammalian cells with synthetic short interfering RNAs (siRNAs). siRNAs can be designed to silence the expression of specific genes bearing a particular target sequence and may potentially be presented as a therapeutic strategy for inhibiting transcriptional regulation of genes, which in such instances constitute a more attractive strategy than small molecule drugs. Low dose drug and siRNA combination studies are promising strategies for the purpose of identifying synergistic targets that facilitate reduction of undesired gene expression and/or cell growth depending on the research of interest. Commercially available RNAi libraries have made high-throughput genome-scale screening a feasible methodology for studying complex mammalian cell systems. However, it is crucial that any observed phenotypic change be confirmed at either the mRNA and/or protein level to determine the validity of the targeted genes. Currently, qPCR is widely utilized for accurate evaluation and validation of gene expression profiling. In this study, we describe a high-throughput screening of RNAi based gene knock-down approach and qPCR validation of specific transcript levels. Considering such advantageous applications, siRNA technology has become an ideal research tool for studying gene function in research fields including Pharmaceutical Biotechnology, and holds the promise that the utilization of siRNA-based therapeutic agents will accelerate drug discovery in clinical trials.

Recent Publications:

1. Son A Y, Tüzmen Ş and Hizel C (2013) Omics for Personalized Medicine, "Designing and Implementing Pharmacogenomics Study: Appropriateness and Validation of Pharmacogenomics" Chapter 6. Springer. 97-122.
2. Tuzmen S, Tuzmen P, Arora S, Mousses S., Azorsa D (2011) "RNAi-Based Functional Pharmacogenomics", Methods and Protocols, In: Methods in Molecular Biology, Disease Gene Identification, Part 4, Johanna K. DiStefano Ed., Springer, New York, USA. 700: 271-290.
3. Sevtap Savas, David O Azorsa, Hamdi Jarjanazi, Irada Ibrahim-Zada, Irma M. Gonzales, Shilpi Arora, Meredith C. Henderson, Yun Hee Choi, Laurent Briollais, Hilmi Ozcelik, and Sukru Tuzmen (2011) "NCI60 cancer cell line panel data and RNAi analysis help identify EAF as a modulator of simvastatin and lovastatin response in HCT-116 Cells, PLoS ONE (SCIE). 6 (4): 18306.
4. Sukru Tuzmen, Jeff Kiefer, and Spyro Mousses (2007) Validation of siRNA knockdowns by quantitative real-time PCR", Methods in Molecular Biology, In: Methods in Molecular Biology, Protocols for Nucleic Acid Analysis by Non-Radioactive Probes, Second Edition, E. Hilario and J. Mackay Eds., Humana Press, Totowa, USA. 535: 177-203.

Biography

Şükrü Tüzmen is a Molecular Biologist and Geneticist. He has more than 28 years of multi-disciplinary research experience integrating studies of the molecular basis of human diseases, including cancer genetics. He has a passion for advancing the molecular genetics of diseases by studying the associations between drugs, genes, pathways, and diseases. His mission is to discover and validate links between gene states and disease phenotypes, and further use these links to identify druggable targets to be utilized as biomarkers in the early diagnostic stages of genetic diseases. He has focused his career on developing and applying cutting edge methods and technologies to ensure excellence in translation of his basic scientific research including cancer genetics, from bench to bedside. He has been invited to deliver talks in many national and international settings, and he has served on many expert panels including The Research Grant Council, Hong Kong, China.

sukru.tuzmen@emu.edu.tr

Saad M Alshahrani, J Proteomics Bioinform 2017, 10:12(Suppl)
DOI: 10.4172/0974-276X-C1-109

Anticancer efficacy of self-nanoemulsifying drug delivery system of sunitinib malate

Saad M Alshahrani
Prince Sattam Bin Abdulaziz University, Saudi Arabia

Sunitinib malate (SM) is reported as a weakly soluble drug in water due to its poor dissolution rate and oral bioavailability. Hence, in the current study, various "self-nanoemulsifying drug delivery systems (SNEDDS)" of SM were prepared, characterized and evaluated for the enhancement of its *in vitro* dissolution rate and anticancer efficacy. On the basis of solubilization potential of SM in various excipients, "Lauroglycol-90 (oil), Triton-X100 (surfactant) and Transcutol-P (cosurfactant)" were selected for the preparation of SM SNEDDS. SM-loaded SNEDDS were developed by spontaneous emulsification method, characterized and evaluated for "thermodynamic stability, self-nanoemulsification efficiency, droplet size, polydispersity index (PDI), zeta potential (ZP), surface morphology, refractive index (RI), the percent of transmittance (% T) and drug release profile." *In vitro* dissolution rate of SM was significantly enhanced from an optimized SNEDDS in comparison with SM suspension. The optimized SNEDDS of SM with droplet size of 42.3 nm, PDI value of 0.174, ZP value of −36.4 mV, RI value of 1.339% T value of 97.3%, and drug release profile of 95.4% (after 24 h via dialysis membrane) was selected for *in vitro* anticancer efficacy in human colon cancer cells (HT-29) by MTT assay. MTT assay indicated significant anticancer efficacy of optimized SM SNEDDS against HT-29 cells in comparison with free SM. The results of this study showed the great potential of SNEDDS in the enhancement of *in vitro* dissolution rate and anticancer efficacy of poorly soluble drug such as SM.

sms85@live.com

Notes:

Nima Sanadgol, J Proteomics Bioinform 2017, 10:12(Suppl)
DOI: 10.4172/0974-276X-C1-109

Cucurbitacin B mitigates experimental autoimmune encephalomyelitis by inhibition of IL-17/IL-23 immune axis

Nima Sanadgol
University of Zabol, Iran

Pharmacological approaches to inhibit brain acute inflammation may represent important strategies for the control of autoimmune diseases. Multiple sclerosis (MS) is a chronic, inflammatory, demyelinating and autoimmune disease of the central nervous system (CNS). Cucurbitacin B (CuB), an oxygenated tetracyclic triterpenoid compound extracted from Cucurbitaceae plant species, is a bioactive agent by disruption of microtubule polymerization and inhibition of JAK/STAT signaling. However, there has been little information about impact of CuB on MS treatment. In this research, for the first time we examine effects of CuB (specific STAT3 blocker), in experimental autoimmune encephalomyelitis (EAE) mouse model of MS. EAE was induced by subcutaneous immunization of MOG35-55 in 8-week-old C57BL/6 mice. CuB was administered at different doses (0.25, 0.5 and 1 mg/kg body weight/day/i.p) from the first day of the experiment. Inflammatory responses were examined using qRT-PCR, western blot and immunohistochemistry (IHC) analysis of specific markers such as p-STAT3, IL-17A, IL-23A, CD11b and CD45. CuB reduced STAT3 activation, leukocyte trafficking, and also IL-17/IL-23 immune axis in this model. Treated mice with lower doses of CuB exhibited a considerable depletion in the EAE clinical score which correlated with decreased expression of IL-17, IL-23 and infiltration of CD11b+ and CD45+ cells into the CNS. Our *in vivo* results suggest that STAT3 inhibition by CuB will be an effective and new approach for the treatment of neuro-inflammatory disease such as MS.

Recent Publications:

1. Doan V, Kleindienst A M, McMahon E J, Long B R, Matsushima G K and Taylor L C (2013) Abbreviated exposure to cuprizone is sufficient to induce demyelination and oligodendrocyte loss. J Neurosci Res. 91: 363-73.
2. Kastelein R A, Hunter C A and Cua D J (2007) Discovery and biology of IL-23 and IL-27: related but functionally distinct regulators of inflammation. Annu. Rev. Immunol. 25: 221-242.
3. Haines C J et al (2013) Autoimmune memory T helper 17 cell function and expansion are dependent on interleukin-23. Cell Rep. 3: 1378-1388.
4. Ramroodi N, Khani M, Ganjali Z, Javan M R, Sanadgol N, Khalseh R and Abdollahi M (2015) Prophylactic effect of BIO-1211 small-molecule antagonist of VLA-4 in the EAE mouse model of MS. Immunological Investigations. 44: 694-712.

Biography

Nima Sanadgol is expert in field of Cell and Molecular Neurobiology. His recent research emphasis is in treatment of neurodegenerative disease with use of new natural compounds. He has particular interest in evaluation of mechanisms of neuron-glia interactions, in order to fascinating myelin repair and control of neuro-inflammatory and neuro-degenerative diseases (Multiple sclerosis, Alzheimer, Parkinson, etc.). He has already gained so much experience in neuro-immune and circuit-specific signaling in glial-neuron networks (T cell biology, NF-κB, Nrf2, MAP kinase, AMP kinase, apoptosis and autophagy).

Sanadgol.n@gmail.com

Notes:

Vladimir A Baulin et al., J Proteomics Bioinform 2017, 10:12(Suppl)
DOI: 10.4172/0974-276X-C1-109

Design strategies for nanoparticles translocating through lipid bilayers

Vladimir A Baulin[1], Marco Werner[1], Yachong Guo[1], Emmanuel Terrazi[2], Ralf Seeman[3] and **Jean Baptiste Fleury[3]**
[1]Universitat Rovira I Virgili, Spain
[2]University of Geneva, Switzerland
[3]Universitat des Saarlandes, Germany

Design of nanomaterials able to cross lipid bilayers is a challenging task in nanotechnology. Large variety of shapes, sizes and surface coatings are used for the design of nanomaterials to overcome this barrier. However, the potential barrier is quite high for carbon nanotubes and nanoparticles to cross the lipid bilayer to translocate by thermal motion. It is generally accepted that small hydrophobic nanoparticles are blocked by lipid bilayers and accumulate in the bilayer core, while nanoparticles with sizes larger than 5 nm can only penetrate cells through a slow energy-dependent processes such as endocytosis, lasting minutes. In one example, we show how variation of hydrophobicity of the nanoparticles can lead to passive translocation of nanoparticles through lipid bilayer. This adsorption transition through reversible destabilization of the structure of the bilayer induces enhanced permeability for water and small solutes. In another example, we demonstrate that lipid-covered hydrophobic nanoparticles may translocate through lipid membranes by direct penetration within milliseconds. We identified the threshold size for translocation: nanoparticles with diameters smaller than 5 nm stay trapped in the bilayer, while nanoparticles larger than 5 nm insert into bilayer, open transient pore in the bilayer. Using the Single Chain Mean Field (SCMF) theory a mechanism of passive translocation through lipid bilayers is proposed. Observing individual translocation events of gold nanoparticles with 1-dodecanethiol chains through DMPC bilayers, we confirm the particle translocation and characterize the kinetic pathway in agreement with our numerical predictions. Mechanism relies on spontaneous pore formation in the lipid bilayer. The observed universal interaction behavior of neutral and chemically inert nanoparticles with bilayer can be classified according to size and surface properties.

Recent Publications:

1. S Pogodin and V A Baulin (2010) Can a Carbon Nanotube Pierce through a Phospholipid Bilayer? ACS Nano, 4: 5293–5300.
2. S Pogodin and V A Baulin (2011) Equilibrium Insertion of Nanoscale Objects into Phospholipid Bilayers. Curr. Nanosci. 7 (5): 721–726.
3. S Pogodin, M Werner, J U Sommer and V A Baulin (2012) Nanoparticle-Induced Permeability of Lipid Membranes, ACS Nano, p. 10555–10561.
4. Y Guo, E Terazzi, R Seemann, J B Fleury, and V A Baulin (2016) Direct proof of spontaneous translocation of lipid-covered hydrophobic nanoparticles through a phospholipid bilayer. Sci. Adv. 2 (11): 1600261.
5. S Pogodin and V A Baulin (2010) Coarse-Grained Models of Phospholipid Membranes within the Single Chain Mean Field Theory," Soft Matter. 6: 2216–2226.

Biography

Vladimir A Baulin has completed his graduation with honors from the Physics Department at Moscow State University in 2000. He spent three years in the Commissariat à l'Energie Atomique, Grenoble, France, pursuing his PhD in theory of polymer physics and received a PhD in Physics in 2003. In 2004-2006 he was a Postdoctoral Researcher at the Institut Charles Sadron, Strasbourg, France. Since 2008, he leads a group of Soft mater theory at the University Rovira i Virgili, Tarragona, Spain. He is a Coordinator of EU funded initial training network SNAL: smart nano-objects for alteration of lipid bilayers.

Vladimir.baulin@urv.cat

Sessions 3

Day 1 December 07, 2017

Advance in Biomarkers Discovery | Biomarkers and Non Cancerous Diseases | Cell Free Biomarkers

Session Chair
Bodour Salhia
University of Southern California, USA

Session Introduction

Title: Clinical utility of cell-free DNA methylation in managing breast cancer recurrence
Bodour Salhia, University of Southern California, USA

Title: Antiae a novel biomarker for cytodiagnostics
Elena V Pikuta, Athens State University, USA

Title: Prognostic biomarkers of Amyotrophic Lateral Sclerosis (ALS): A step forward in the understanding of the disease
Ana Cristina Calvo, University of Zaragoza, Spain

Title: Advances on flow cytometry and new immunophenotypic markers on AML diagnosis, prognosis determination and overall survival
Amanda Costa, Federal University of Sergipe, Brazil

Bodour Salhia, J Proteomics Bioinform 2017, 10:12(Suppl)
DOI: 10.4172/0974-276X-C1-109

Clinical utility of cell-free DNA methylation in managing breast cancer recurrence

Bodour Salhia
University of Southern California, USA

A number of clinico-pathological criteria and molecular profiles have been used to stratify breast cancer (BC) patients into high and low risk groups. Currently, there are still no effective methods to determine which patients harbor micrometastatic disease after standard BC therapy and who will eventually develop local or distant recurrence. Cell-free (cf) DNA has attracted attention for clinical use in the context of risk prediction, prognostication and prediction of response to chemotherapy in human cancer. Several groups including ours have reported the detection of tumor-associated methylation changes in cfDNA extracted from plasma or serum. We are specifically interested in the use of cfDNA methylation biomarkers for the prediction of cancer metastasis in the early stage setting. Accordingly, we are validating a DNA methylation signature, referred to as CpG4C, which discriminates metastatic BC from healthy individuals or disease free survivors using a targeted bisulfite amplicon sequencing approach. In addition, we have been investigating whether a surge of cfDNA levels after cytotoxic chemotherapy affects the sensitivity and specificity of the CpG4C assay. Lastly, we are also working on determining the technical and biological limits of detection of CpG4C in plasma. CpG4C is a potential blood-based biomarker that could be advantageous at the time of surgery and/or after the completion of chemotherapy to indicate patients with micrometastatic disease who are at high-risk of recurrence, and who could benefit from additional therapy.

Biography

Bodour Salhia is an Assistant Professor at the University of Southern California and is a Translational Genomics Scientist with extensive knowledge and expertise in mechanisms that underlie tumorigenesis and tumor biology. She received her Honors Bachelor of Science Degree (1998), Master of Health Science (2001) and PhD (2006) degrees in Human Molecular and Cellular Biology from the University of Toronto. She completed a Post-doctoral fellowship (2006-2011) at the Translational Genomics Research Institute (Phoenix, Arizona) in cancer genetics and epigenetics. She has published more than 30 papers in peer-reviewed and reputed journals.

salhia@usc.edu

Notes:

Elena V Pikuta et al., J Proteomics Bioinform 2017, 10:12(Suppl)
DOI: 10.4172/0974-276X-C1-109

Antiae a novel biomarker for cytodiagnostics

Elena V Pikuta[1] and **Richard B Hoover**[2]
[1]Athens State University, USA
[2]University of Buckingham, UK

Antiae is a recently discovered novel external organelle responsible for the gliding motility in bacteria. The antiae composed of plural thin fibers entangled in plexa that may be 10-20 folds of the cellular size, and spin in a coherent, unison rotation around the cell cylinder causing a high-sequence trembling that results a smooth slow gliding.

DAPI stain of strain A7P-90mT demonstrated the absorbance of the stain by the antiae that indicates on possible RNA or DNA molecules involvement in cellular constitution. UV absorbency pick of the living culture was at 300 nm as well as a filtrated through 0.2 μm filter liquid containing antiae. Here we discuss the results of the proton, sodium pumps and ATPase inhibition effects on the cellular motion. We also present the results of RNase and DNase treatment along with the thiamine bromide stain with UV imaging.

We also discuss the chemical composition of the antiae with increased amounts of fluorine and silicon according to X-ray spectrophotometry. Presence of the antiae was shown in other bacterial species and Archaea, as well as in viruses. Histopathology of sarcoma and other malignant cancers demonstrated presence of antiae in cell-free areas affected by cancer tissues that makes them an important biomarker in cytodiagnostics.

Key words: bacterial gliding, external organelle antiae, cytodiagnostics, pathohistology, X-ray spectroscopy.

Biography

Elena V Pikuta received her MS in 1995 at Perm State University in Russia, on Biology faculty. She was a practicing nurse in Surgery Department of the Regional Hospital in Perm for one year.She received her BS degree received in 1984 from Perm Medical College. In University she also defended Diploma in Biophysics "The Dielectric Parameters of Tissues at Hypoxia". She was employed by the Institute of Ecology and Genetics of Microorganisms, The Ural Branch of Russian Academy of Sciences, as a research assistant. She had finished her PhD in 1997 at the Institute of icrobiology of RAS in Moscow, the thesis was "Alkaliphilic Sulfate-Reducing Bacteria.

epikuta@my.athens.edu

Notes:

Ana Cristina Calvo, J Proteomics Bioinform 2017, 10:12(Suppl)
DOI: 10.4172/0974-276X-C1-109

Prognostic biomarkers of Amyotrophic Lateral Sclerosis (ALS): A step forward in the understanding of the disease

Ana Cristina Calvo
University of Zaragoza, Spain

Amyotrophic lateral sclerosis (ALS) is a neurodegenerative disease of unknown origin that causes progressive muscle paralysis and motor neuron death. The need of reliable biomarkers of ALS that can be accurately monitoring along disease progression is an increasing field of research. In this sense, our main objective is to identify molecular biomarkers as key elements of the induced neurodegeneration in ALS. Previous studies in our research workgroup analysed the transcriptional expression of a group of genes, whose expression was found up and down-regulated significantly in a preliminary microarray study and in muscle biopsy samples from transgenic SOD1G93A mice, the best characterized murine model for the disease. In this study we identified five genes, *Mef2c, Gsr, Col19a1, Calm1* and Snx10 as potential genetic biomarkers of longevity in this animal model. Next, we translated this study to ALS patient's samples to validate the potential nature of these biomarkers. Skeletal muscle biopsies and blood samples from sporadic and familial ALS patients were analyzed by real time PCR and Western blot to test the expression levels of fifteen genes and fourteen proteins. ROC curves, multinomial regression and time-dependent Cox regression analysis were performed. *COL19A1* gene and protein levels were identified as potential prognostic candidates in skeletal muscle samples from ALS patients. In addition, the same gene improved prognosis in blood samples from sporadic ALS patients. These findings provide an important first step towards the accurate prediction of potential biomarkers in ALS be the initial springboard to new clinical trials and promising therapeutic strategies.

Biography

Ana Cristina Calvo has completed her PhD in 2003 from the Anatomy and Human Histology Department in the University of Zaragoza in Spain and Post-doctoral studies from the ALS Unit in the Hospital 12 October in Madrid (Spain) and from Faculty of Medicine in the Universidad Autónoma in Barcelona (Spain). She is an Associate Professor in Genetics and member of the Laboratory of Genetics and Biochemistry (LAGENBIO, IA2-IIS) in the Faculty of Veterinary Sciences in the University of Zaragoza (Spain). She has published 30 papers in reputed journals and participated as a coauthor in three licensed patents.

accalvo@unizar.es

Notes:

Amanda Costa, J Proteomics Bioinform 2017, 10:12(Suppl)
DOI: 10.4172/0974-276X-C1-109

Advances on flow cytometry and new immunophenotypic markers on AML diagnosis, prognosis determination and overall survival

Amanda Costa
Federal University of Sergipe, Brazil

Even though there has been improvements in the understanding and treatment of acute myeloid leukemia (AML), not much advances are noted when it comes to outcome and survival. It is still substantial the association of AML to a poor prognosis followed by low remission and survival rates, where 60–70% of adult patients reach complete remission, but only about 25% survive with chances of being cured. Although younger patients show a 5-year survival rate of 62.8%, there is a decrease for people older than 65 years that hits 4%. AML diagnosis remains challenging, being cytogenetics and molecular biology primary tools for risk stratification and prognostic determination. Moreover, flow cytometry has recently stood out as a useful tool in AML diagnosis, classification and treatment evaluation, for being able to characterize heterogeneous populations of blast cells and analyze multiple parameters simultaneously. Important improvements in flow cytometry instrumentation and new analytical strategies were obtained, nevertheless, there are still limitations regarding new immunophenotypic markers for AML diagnosis, highlighting the need of new markers in clinical routines, what would increase its diagnosis and prognosis value, and also be useful for monitoring minimal residual disease (MRD) and improvement of new targeted therapy. Some research has been developed around the world to evaluate the efficiency of incorporation of new markers on AML immunophenotypic panels, which has demonstrated a relevant association with the development of the disease, either for its association to a decreased survival and poor prognosis, for being a possible therapeutic target or because its effectiveness as marker for MRD.

Biography

Amanda Costa is a Pharmacist, graduated from the Pharmacy School of Federal University of Rio Grande do Norte, Brazil. She has completed her Master's degree in Pharmaceutical Sciences from Federal University of Sergipe, Brazil, and is currently pursuing PhD from the same University, in which she teaches Hematology in the Pharmacy School. She has been serving as an Editorial Board Member of the *Journal of Hematology and Serology.*

amandafernandes@hotmail.com

Notes:

JOINT EVENT ON

9th WORLD BIOMARKERS CONGRESS

&

20th International Conference on

PHARMACEUTICAL BIOTECHNOLOGY

December 07-09, 2017 | Madrid, Spain

Scientific Tracks & Abstracts

Day 2

Sessions 4

Day 2 December 08, 2017

Cancer Biomarkers | Biomarkers & Immuno-Oncology | Biomarkers Detection & Discovery | Clinical Biomarkers | Advances in Biomarkers Discovery

Session Chair
Topolcan Ondrej
Charles University, Czech Republic

Session Introduction

Title: Usage of metabolomics profile as biomarkers itself for diagnostic diseases
P G Lokhov, Institute of Biomedical Chemistry, Russia

Title: RhoGDI3, is this small molecular regulator key orchestring the movement and tumor mass in PDAC?
Mercedes Piedad de León-Bautista, Central adn, Mexico

Title: PHI and prostate cancer - optimal management
Topolcan Ondrej, Charles University, Czech Republic

Title: PEA3/ETV4-related transcription factors coupled with active ERK signalling are associated with poor prognosis in gastric adenocarcinoma
Yeng S Ang, Salford Royal University Hospital, UK

Title: Novel biomarker proteins for cancer: Impact on diagnosis, prognosis and treatment
Varda Shoshan-Barmatz, Ben-Gurion University of the Negev, Israel

Title: Soarfenib effect on human colon cancer cells HCT116 and HCT116 p53-/-
M Al Hassan, Beirut Arab University, Lebanon

Title: Diagnostic and prognostic microRNAs in the serum of breast cancer patients measured by droplet digital PCR
Sayda Omer Ebnaof, University of Khartoum, Sudan

Title: Association of human papilloma virus with head and neck cancer patients from Khyber Pakhtunkhwa, Pakistan
Maimoona Sabir, University of Haripur, Pakistan

PG Lokhov et al., J Proteomics Bioinform 2017, 10:12(Suppl)
DOI: 10.4172/0974-276X-C1-109

Usage of metabolomics profile as biomarkers itself for diagnostic diseases

P G Lokhov and **A I Archakov**
Institute of Biomedical Chemistry, Russia

Recently, the researches to find proteins as biomarkers of various diseases have become widespread. Especially these studies are popular in oncology. However, until now proteins specific for cancer cells are not detected. In spite of it, to diagnose cancer diseases biomarkers which are specific for a neoplastic process generally are widely used (such as CA-125, CA 19-9, CA 15-3, PSA, α-fetoprotein etc.). However, they can't discharge the main task: to diagnose the initial stages of disease, because their opportunity is limited by low sensitivity of existing laboratory technologies. The situation is much better in the case of using RNA's as biomarkers, because PCR takes off such restrictions. In the case of metabolomic diagnostics there are the same concentration limits as in proteomics. Therefore, it was decided not to use separate low molecular weight compounds as biomarkers but the whole metabolomic profile of the sick person as a biomarker itself of a disease. With this purpose, at the first stage that profile was clusterized using the method of principle component analysis to detect clusters of metabolites which are different from the clusters of healthy person. At the second stage, the specificity and sensitivity of the proposed technology was evaluated using the SVM and ROC analyses, for diagnostics of lung, prostate and other cancers.

Biography

P G Lokhov is the Head of Laboratory for Mass Spectrometry-based Medical Metabolomics in the Department of Proteomic Research and Mass Spectrometry of IBMC, a position he has held since 2012. He is mainly interested in mass spectrometry-based metabolomics and proteomics, and their application for diagnostics. He graduated from the 2nd Moscow Medical Institute, took the post-graduate course and thereafter received a PhD degree in Biochemistry in 2002. During his career Dr. Lokhov has received several awards, including the State Prize of the Government of Russia.

lokhovpg@rambler.ru

Mercedes Piedad de León Bautista et al., J Proteomics Bioinform 2017, 10:12(Suppl)
DOI: 10.4172/0974-276X-C1-109

RhoGDI3, is this small molecular regulator key orchestring the movement and tumor mass in PDAC?

Mercedes Piedad de León Bautista[1,2,3], María del Carmen Cárdenas Aguayo[4], Daniel Marrero[3,5], Mauricio Salcedo[5], Lorena Gorgonio Eusebio[3], Emma Vélez Uriza[3], Miguel Vargas[3] and **Rocío Thompson Bonilla[2]**
[1]Central ADN, Mexico
[2]ISSSTE, Mexico
[3]CINVESTAV-IPN, Mexico
[4]Facultad de Medicina, UNAM, Mexico
[5]XXI Century National Medical Center, Mexico

Pancreatic ductal adenocarcinoma (PDAC) is a complex pathology with poor prognosis. Efforts have been focused on understanding the role of RhoGDI's in PDAC, in particular, RhoGDI1 and RhoGDI2. However, the role of RhoGDI3 has neither been studied in relation to cancer nor to PDAC. Our group have characterized the expression and functionality of RhoGDI3 and its target GTPases, RhoG and RhoB, in pancreatic cell lines and compared it to human tissue. Through immunofluorescences, pull down assays, subcellular fractionation and immunohistochemistry, we found a reduction in RhoGDI3 expression in PDAC late stages, and this reduction correlates with tumor progression and aggressiveness. Despite the reduction in the expression of RhoGDI3 in PDAC, we found that RhoB was under expressed while RhoG was over expressed, suggesting that cancerous cells keep their capacity to activate this pathway, thus these cells may be eager to the stimuli needed to proliferate and become invasive. Surprisingly, we found nuclear localization of RhoGDI3 in non-cancerous pancreatic cell line and normal pancreatic tissue biopsies, which could open the possibility of novel nuclear functions for this protein, impacting gene expression regulation and cellular homeostasis. To elucidate the possible functions of RhoGDI3 in cancer maintenance, the overexpression assays have demonstrated that increased RhoGDI3 protein increases proliferation rate; besides, the xenograft tumor was smaller compared to the mock, suggesting and predicting that overexpression of RhoGDI3 is an important molecule to constrain the tumoral volume. In conclusion, RhoGDI3 protein decreases the malignant behavior in PDAC.

Biography

Mercedes Piedad de León Bautista has completed her Bachelor's Degree from UPAEP University School of Medicine, and an MSc and PhD from CINVESTAV-IPN in the Dept. of Molecular Biomedicine. She is the Medical Director and Laboratory Chief of Central ADN, a molecular laboratory focusing on human health and translational medicine. She has been working with PDAC and, nowadays, her biomedical efforts are based on molecular platforms to find new markers in cancer and hereditary diseases.

mercedespiedad@hotmail.com

Notes:

Topolcan Ondrej et al., J Proteomics Bioinform 2017, 10:12(Suppl)
DOI: 10.4172/0974-276X-C1-109

PHI and prostate cancer - optimal management

Topolcan Ondrej, Kucera R, Dolejsova O, Hora M, Fuchsova R, Svobodova S and **Kinkorova J**
Charles University, Czech Republic

Background: Prostate cancer is the fifth leading cause of cancer death among men. More than one million cases are worldwide diagnosed every year, and the mortality is over 300,000 deaths per year. Prostatic specific antigen (PSA) is a serine protease composed of 240 amino acids in a single polypeptide chain. In serum, PSA is primarily bound to alpha1-anti-chymotrypsin (95% of total PSA), to a lesser extent to alpha2-macroglobulin. 10-30% serum PSA occurs in the free form (fPSA). Since the 80s of the last century, total level of prostatic specific antigen (tPSA) is used as a tumor marker in the prostate cancer diagnostics. Most of the prostate tumors are diagnosed using biopsy based on the elevated levels of PSA. It is also useful to determine the part of PSA called proPSA. This part of PSA is more produced by tumor cells. Based on the levels of PSA, proPSA, and free PSA, the prostate health index PHI can be calculated.

Aim: Demonstration of the usefulness of PHI in the management of prostate cancer patients.

Materials & Methods: Cohort of 1865 patients was evaluated. The total of 5800 biopsies, 1448 MRI and 150 PET/MRI were performed in this cohort of patients. 4900 samples with the results of PSA, fPSA, -2proPSA, fPSA/tPSA calculated results and PHI during the follow-up period. Gleason score was established in all patients.

Results: By comparison of AUC sensitivity for each laboratory parameter, PHI achieved the highest value (0.8118). PHI achieved also the best correlation with the Gleason score (G6-G9) which allows PHI to be a reliable marker of aggressiveness of the prostate cancer. An optimal PHI cut-off value was 31 with specificity 20.4%, sensitivity 97.6%, PV+ 18%, PV- 97%, RR 8.7.

Conclusions: Determining PHI allows proposing the optimal diagnostic algorithm for prostate cancer, improvement of differential diagnosis of carcinoma vs. prostate hypertrophy, reducing biopsies and imaging techniques, more accurate prognosis estimation, optimizing the type of surgery, optimizing of the postoperative treatment and optimizing of follow-up.

Biography

Topolcan Ondrej has graduated from the Medical Faculty, Charles University in Pilsen. He is working in the Dep. of Nuclear Medicine Faculty Hospital in Pilsen and he was the Head of Imunoanalytic Laboratory in 2000. He is a Member of Scientific Committee Endocrinology Institute Prague and he was awarded the Carl R Jolliff award for lifetime achievement in Clinical and Diagnostic Immunology by the American Association for Clinical Chemistry (AACC) in 2011.

topolcan@fnplzen.cz

Notes:

Yeng S Ang, J Proteomics Bioinform 2017, 10:12(Suppl)
DOI: 10.4172/0974-276X-C1-109

PEA3/ETV4-related transcription factors coupled with active ERK signalling are associated with poor prognosis in gastric adenocarcinoma

Yeng S Ang[1,2]
[1]Salford Royal University Hospital, UK
[2]University of Manchester, UK

Background: Transcription factors often play important roles in tumorigenesis. Members of the PEA3 subfamily of ETS-domain transcription factors fulfill such a role and have been associated with tumor metastasis in several different cancers. Moreover, the activity of the PEA3 subfamily transcription factors is potentiated by Ras-ERK pathway signalling, which is itself often deregulated in tumor cells.

Methods: Immunohistochemical patterns of PEA3 expression and active ERK signalling were analyzed and mRNA expression levels of PEA3, ER81, MMP-1 and MMP-7 were determined in gastric adenocarcinoma samples.

Results: Here, we have studied the expression of the PEA3 subfamily members PEA3/ETV4 and ER81/ETV1 in gastric adenocarcinomas. PEA3 is upregulated at the protein level in gastric adenocarcinomas and both PEA3/ETV4 and ER81/ETV1 are upregulated at the mRNA level in gastric adenocarcinoma tissues. This increased expression correlates with the expression of a target gene associated with metastasis, MMP-1. Enhanced ERK signalling is also more prevalent in late-stage gastric adenocarcinomas and the co-association of ERK signalling and PEA3 expression also occurs in late-stage gastric adenocarcinomas. Furthermore, the co-association of ERK signalling and PEA3 expression correlates with decreased survival rates.

Conclusions: This study shows that members of the PEA3 subfamily of transcription factors are upregulated in gastric adenocarcinomas and that the simultaneous upregulation of PEA3 expression and ERK pathway signalling is indicative of late-stage disease and a poor survival prognosis.

Biography

Yeng S Ang has an international professional standing and research expertise to enhance clinical interventions in Barrett's oesophagus and oesophageal cancer. He is a Member of the BSG/National Clinical Research Institute Upper GI early cancer prevention research subgroup. He is a peer Reviewer for the NIHR RFPB programme and a member of the Research Steering Board of Manchester Cancer Research Centre (Cancer Research UK Manchester Institute). These research initiatives have shaped his contribution for the management of GORD, Barrett's oesophagus and oesophageal cancer. He has published over 45 articles and he is a Supervisor for PhD and MD students in the molecular cancer group of the University of Manchester.

Yeng.Ang@srft.nhs.uk

Notes:

Varda Shoshan Barmatz, J Proteomics Bioinform 2017, 10:12(Suppl)
DOI: 10.4172/0974-276X-C1-109

Novel biomarker proteins for cancer: Impact on diagnosis, prognosis and treatment

Varda Shoshan Barmatz
NIBN- Ben-Gurion University of the Negev, Israel

Cancer cells undergo re-programing of metabolism, cell survival and anti-apoptotic defenses, with the proteins mediating these re-programing representing potential biomarkers. Here, using specific antibodies, mass spectrometry and bioinformatics tools; we searched for novel biomarker proteins in chronic lymphocytic leukemia (CLL) and in non-small cell lung cancer (NSCLC) patient samples that can impact diagnosis, treatment and prognosis. By comparing protein expression profiles of CLL- and healthy donor-derived lymphocytes, we identified 1,360 differentially expressed proteins, some shown for the first time to be associated CLL. Down-regulated expression of two proteins resulted in cell growth inhibition, pointing to their essential functions. Based on changes in the levels of several proteins in CLL patients, we could distinguish between patients in a stable disease state and those who would be later subjected to anti-cancer treatments, 2-3 years before the physician's decision. In NSCLC, the adenocarcinoma (AC) and squamous cell carcinoma (SCC), sub-types present unique genomes, transcriptomes, and proteomes, and share clinical and histopathological characteristics, yet differ in treatment. We identified novel biomarker proteins in NSCLC, with 378 proteins showing a ≥|100|-fold change in level. Several, identified for the first time, allow for distinguishing between AC and SCC. These, together with markers previously proposed and confirmed here, lead us to propose a list of proteins for discriminating SCC and AC, with four being secreted. Precise diagnosis of AC and SCC is essential for selecting appropriate treatment. Finally, some of these biomarkers can serve as new targets and lead to new treatments for lung and CLL cancers.

Biography

Varda Shoshan Barmatz is the Hyman-Kreitman Chair in Bioenergetics at Ben-Gurion University (BGU). Her PhD is from the Weizmann Institute; Post-doctoral training was from the University of Wisconsin-Madison and the University of Toronto. In 1982, she joined the Department of Life Sciences, BGU, and served as Chair (2000-2004). Her awards include the Hestrin Prize of the Israel Biochemistry Society, Teva Award for Young Scientists (1993) and Teva Founders Award (2016). *Lady Globes* magazine selected her as one of the 50 most influential women in Israel (2009) and one of five who made breakthroughs in science (2016). She was the Founder and Director (2006-2015) of the National Institute for Biotechnology in the Negev.

vardasb@bgu.ac.il

Notes:

M Al Hassan et al., J Proteomics Bioinform 2017, 10:12(Suppl)
DOI: 10.4172/0974-276X-C1-109

Soarfenib effect on human colon cancer cells HCT116 and HCT116 p53-/-

M Al Hassan[1], **A Baltaji**[1], **J Borjac**[1], **R Fakhouri**[1] and **J Usta**[2]
[1]Beirut Arab University, Lebanon
[2]American University of Beirut, Lebanon

Sorafenib, a kinase inhibitor, has been approved among the drugs for the treatment of radioactive iodine resistant thyroid carcinoma, primary kidney and liver cancer. Reported targets of sorafenib include VEGFR, Raf family, and PDGFR belonging to the general class of tyrosine kinases. Blocking growth signals in kidney and breast cancers underlie one of the mechanisms of sorafenib anti-tumor effects' leading to cell death. We hereby examine the effect of sorafenib on human colon carcinoma cell-line HCT116. We also investigate the possible role of p53 in mediating this effect using mutant HCT116 p53-/- cells. Cultured wild and mutant cells are treated with sorafenib (0-75μM) for 24 hr. This is followed by assessing the viability of cells using MTT and trypan blue exclusion assays. We also examined if sorafenib mode of action is mediated by ROS. Levels of ROS were determined in the presence and absence of antioxidants using the colorimetric NBT assay. Our preliminary results show a concentration dependent decrease in viability (trypan blue) with an estimated EC50 of 10 and 25 μM for HCT116 and HCT116 p53-/- respectively. Compared to trypan blue, MTT results were similar in case of HCT116 p53-/- but were significantly different with HCT116. Furthermore we obtained a significant increase in level of ROS of: 37.11% and 31.30% for HCT116 and HCT116p53-/- respectively. However, 2 hr. pre-incubation of cells with antioxidants, Trolox, N-acetylcysteine (NAC), and catalase, prior to sorafenib treatment, exerted no different effect. No restoration of viability or decrease in generated ROS level was noted. Our preliminary findings show that sorafenib action is independent of ROS level and p53 expression and further investigations on the mechanism(s) of sorafenib action are ongoing.

Biography

M Al Hassan is a current PhD candidate at the Beirut Arab University, working in collaboration with the American University of Beirut on Sorafenib and its *in-vitro* and *in-vivo* effects on colorectal cancer. She has graduated from the Lebanese American University with a Master's degree in Cells and Molecular Biology. Her MS thesis was about the effect of metformin on the metastasis and the 3D motility of glioblastoma cancer cells.

ma422@aub.edu.lb

Notes:

Sayda Omer Ebnaof, J Proteomics Bioinform 2017, 10:12(Suppl)
DOI: 10.4172/0974-276X-C1-109

Diagnostic and prognostic microRNAs in the serum of breast cancer patients measured by droplet digital PCR

Sayda Omer Ebnaof
University of Khartoum, Sudan

Background: Breast cancer circulating biomarkers include carcinoembryonic antigen and carbohydrate antigen 15–3, which are used for patient follow-up. Since sensitivity and specificity are low, novel and more useful biomarkers are needed. The presence of stable circulating microRNAs (miRNAs) in serum or plasma suggested a promising role for these tiny RNAs as cancer biomarkers. To acquire an absolute concentration of circulating miRNAs and reduce the impact of preanalytical and analytical variables, we used the droplet digital PCR (ddPCR) technique.

Results: We investigated a panel of five miRNAs in the sera of two independent cohorts of breast cancer patients and disease-free controls. The study showed that miR-148b-3p and miR-652-3p levels were significantly lower in the serum of breast cancer patients than that in controls in both cohorts. For these two miRNAs, the stratification of breast cancer patients versus controls was confirmed by receiver operating characteristic curve analyses. In addition, we showed that higher levels of serum miR-10b-5p were associated with clinicobiological markers of poor prognosis.

Conclusions: The study revealed the usefulness of the ddPCR approach for the quantification of circulating miRNAs. The use of the ddPCR quantitative approach revealed very good agreement between two independent cohorts in terms of comparable absolute miRNA concentrations and consistent trends of dysregulation in breast cancer patients versus controls. Overall, this study supports the use of the quantitative ddPCR approach for monitoring the absolute levels of diagnostic and prognostic tumor-specific circulating miRNAs.

Biography

Sayda Omer Ebnaof has completed her PhD in Molecular Biology from University of Ferrara, Italy in 2016 and MSc in Molecular Medicine from Institute of Endemic Diseases, University of Khartoum-Sudan. She is a Lecturer of Histopathology and Cytology at University of Khartoum. She has published four papers in reputed journals.

saydaomer1@hotmail.com

Notes:

Maimoona Sabir, J Proteomics Bioinform 2017, 10:12(Suppl)
DOI: 10.4172/0974-276X-C1-109

Association of human papilloma virus with head and neck cancer patients from Khyber Pakhtunkhwa, Pakistan

Maimoona Sabir
University of Haripur, Pakistan

Head and neck cancer (HNC) is the sixth most common cancer causing a high mortality rate worldwide. There are number of risk factors involved in head and neck cancer such as tobacco, alcohol, radiations, inhaling asbestos, wood dust, paint fumes and viruses. Most common virus involved in the subset of head and neck cancer is human Papilloma virus (HPV). Human papilloma virus is double stranded DNA virus which is about 8Kb surrounded by protein coat consisting of two proteins L1 and L2. Out of 100 different types of HPV 15 are considered as highly pathogenic. HPV is divided into two major types; High risk HPV and Low risk HPV. In current study 150 HNC patients were screened for HPV genotyping and risk factors possibly associated with HNC. DNA was extrracted by standard phenol chloroform extraction method followed by HPV genotyping by polymerase chain reaction and agarose gel electrophoresis. In study, among the HNC affected individuals 81(54%) were HPV+ive and 69 (46%) HPV–ive. Statistically, no significant difference was observed between HPV+ive and HPV-ive. HNC cases in terms of gender. In terms of age group, statistically no significant difference was observed between two groups (age group >40, <40). With respect to anatomic site of head and neck cancer patients, highest number of HPV+iv was observed in oral cavity 51(63%) followed by pharynx 20(25%), larynx 7(8%) and hypopharynx 3(4%). Disease was more common among illiterate individuals with low socioeconomic status and trend of HPV+ive HNC cases have increaed from year 2011 to 2016. It can be concluded from the data that HPV infection can be the main risk factor for HNC cases in Pakistan. Further research is needed to elucidate the mechanism involved in HPV infection with head and neck carcinogenesis.

Biography

Maimoona Sabir has completed her PhD from the Department of Biosciences, COMSATS, Institute of Information Technolgy, Islamabad, Pakistan. She is currently working as Assistant Professor in the Department of Microbiology, University of Haripur, KP, Pakistan. She has published more than 15 reserach papers in reputed journals. She has won grant from Higher Education Commssion of Pakistan for research work, “role of HPV in head and neck cancer in Pakistani population”.

monasabir@uoh.edu.pk

Notes: