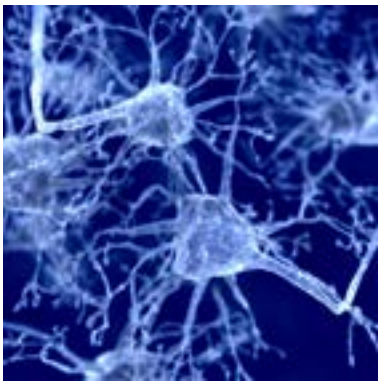
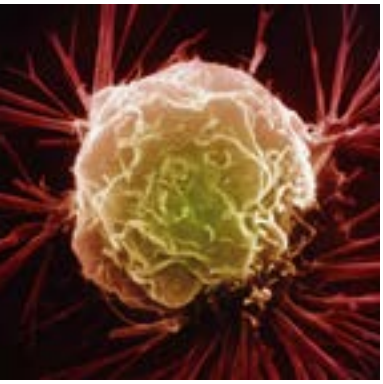
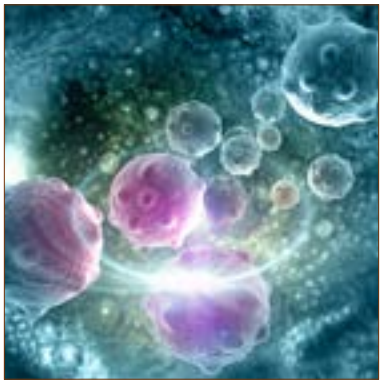
Poster Presentations

Oncology and Biomarkers Summit 2017







Annual Congress on

ONCOLOGY AND BIOMARKERS SUMMIT

November 27-28, 2017 | Atlanta, USA

Heuristic multi-objective optimization algorithm to extract biomarker based on mutation combinations in whole gene information for disease diagnosis

Yong-Joon Song
Korea Advanced Institute for Science and Technology, South Korea

There are still many efforts to diagnose diseases early. Among them, molecular diagnostics using biomarker is one of the powerful tools that can pre-diagnose diseases before symptoms appear. In critical diseases such as acute myeloid leukemia (AML), when the symptoms are present, it is already late. It is possible to bring about complete cure of cancer by performing preliminary examination and early treatment based on molecular diagnostics. However, researches related to biomarkers have been done only from a biomedical point of view, focused on specific gene sequences or protein expressions that are thought to be related to disease. To overcome this stereotype, we proposed an algorithm that uses a combination of disease-related mutation information from entire gene. We used NGS data of solid tissue normal samples from skin and primary solid tumor samples from bone marrow, which were obtained from 50 AML patients from TCGA database. In addition, we extracted mutation information by using GATK tool. In order to extract only cancer-related mutation information among the obtained mutation information, we use a following proposed algorithm. There are millions of mutations in the entire gene, and a huge number of combinations. Thus, in order to find biomarker with low complexity, we sorted all the mutations by scoring how well the disease and normal samples could be separated by each mutation. In this process, the case of genetic mutation that occurs due to the difference of skin and bone marrow was excluded. In the derived list of mutations, we obtained optimal biomarkers by heuristically solving three multi-objectives optimization problems, which includes three parameters such as disease classification ratio, the distance of inter-clusters and the distance of intra-clusters. Using proposed method, we could get a mutation combination that has 100% disease classification performance for the sample we acquired.

Speaker Biography

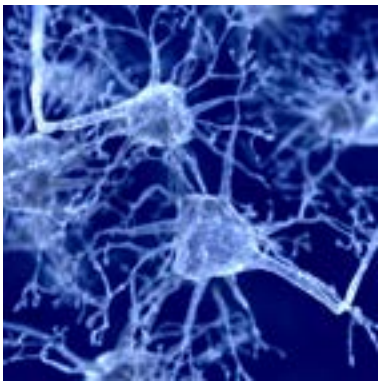
Yong-Joon Song has completed his bachelor's degree in Electrical Engineering at KAIST in 2016. Currently, he is a PhD student in school of electrical engineering at KAIST. His research interest area is Bioinformatics.

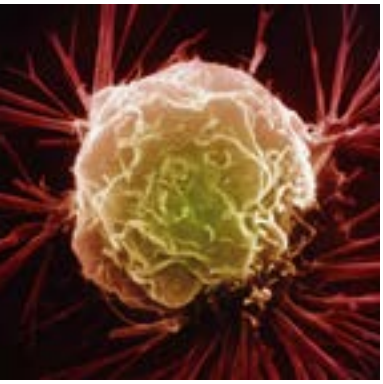
e: yjsong@comis.kaist.ac.kr

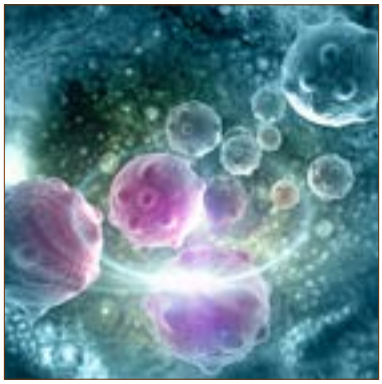
Notes:

Accepted Abstracts

Oncology and Biomarkers Summit 2017







Annual Congress on

ONCOLOGY AND BIOMARKERS SUMMIT

November 27-28, 2017 | Atlanta, USA

allied academies
Annual Congress on
ONCOLOGY AND BIOMARKERS SUMMIT
November 27-28, 2017 | Atlanta, USA

Effect of coronary artery disease risk SNPS on serum cytokine levels and cytokine imbalance in premature coronary artery disease

Wafa M Ansari
National University of Science and Technology, Pakistan

Background: Coronary Artery Disease (CAD) occurs almost a decade earlier in the South Asian population as compared to the West. Inclusion of genetic information can prove to be a robust measure to improve early risk prediction of PCAD. Aim was to estimate the genotypic distribution and risk allele frequencies of 13 Coronary Artery Disease (CAD) risk Single Nucleotide Polymorphisms in loci identified by the CARDIoGRAMplusC4D consortium namely MIA3 rs17465637;9p21 rs10757274; CXCL12 rs1746048; APOA5 rs662799; APOB rs1042031; LPA rs3798220; LPA 10455872; MRAS rs9818870; LPL rs328; SORT1 rs646776; PCSK9 rs11591147; APOE rs429358; APOE rs7412 in Pakistani PCAD patients and controls and to determine the differential serum cytokine levels (IL18,IL10,IL6, TNFalpha, IL18:IL10 & TNFalpha:IL10 ratios) with respect to the genotypic distribution of these selected SNPs.

Material & Methods: The study design was case-control and it was conducted in National University of Sciences and Technology, Islamabad in collaboration with the Cardiovascular Genetics Institute, University College London, UK. Subjects (n=340) with >70% stenosis in at least a single major coronary artery on angiography were taken as PCAD cases along with 310 angiographically verified controls. ELISA was performed for measuring the concentrations of serum IL18, TNFA, IL6 and IL10. Genotyping was done using TAQMAN and KASPar assays.

Results: The risk allele frequencies (RAF) of APOE rs7412, CXCL12 rs1746048, 9p21 rs10757274, MIA3 rs17465637 and SORT1 rs646776 were markedly higher in the PCAD cases as compared to the controls. APOE rs429358 had the greatest influence among the selected GWAS/CARDIoGRAMplusC4D consortium CAD risk SNPs by significantly altering the serum levels of TNFalpha, IL10 and TNFalpha:IL10 ratio followed by APOE rs7412 and CXCL12 rs1746048 which significantly altered the serum levels of IL18; TNFalpha and IL18; IL18:IL10 ratio respectively. The cytokine imbalance denoted by IL18:IL10 was statistically significantly greater in the risk allele carriers MIA3 rs17465637 and CXCL12 rs1746048 while TNFalpha:IL10 ratio was raised markedly in the risk allele carriers of APOE rs429358; MRAS rs9818870 and LPL rs328.

Conclusion: The association of the selected SNPs with differential serum cytokine levels especially the cytokine imbalance points towards their potential causal role in the immune inflammatory pathogenic pathway of PCAD.

e: wafamuniransari@gmail.com

allied academies

Annual Congress on

ONCOLOGY AND BIOMARKERS SUMMIT

November 27-28, 2017 | Atlanta, USA

Innovative approaches in metabolomics for understanding drug resistance in breast cancer

Umber Saeed
Dow University Of Health and Sciences, Pakistan

Breast cancer is one of the leading cause of death worldwide. In Pakistan, prevalence of this ailment is highest amongst all types of cancer i.e. 38.5%. Among various treatments available to overcome cancer, chemotherapy is the one used most widely most oftenly a combination of two or more medicines will be used as chemotherapy treatment for breast cancer. But in Chemotherapy, major clinical setback is drug resistance. Metabolomics is an emerging field that utilizes information of cellular biochemistry for the early detection, diagnosis and establishment of predictive biomarkers of breast cancer. Currently, metabolics is use to evaluate a much comprehensive picture of tumor development and growth This review highlights potential metabolomics applications towards developing a more personalized and tailored chemotherapy treatment. The methodology is based on inclusion exclusion criteria. Literature survey and questionnaire were included while clinical trials was excluded. This report provides a review of 12 articles out which few were excluded. The objective was to explore: Early breast cancer detection; Increasing life expectancy of cancer patients; Mechanisms for breast cancer drug resistance; Chemotherapy in breast cancer and its success rate and Side effects of chemotherapy in breast cancer. According to the survey the average response rate of a cancer drug is the lowest at 21%, suggesting that 79% of patients with cancer are over-dosed. While according to an international study, 40%–50% of breast tumors will display acquired resistance. When specific therapies are chosen on the basis of a patient's metabolomics profile, it will give rise to customized medicine and personalized tailored treatment. Using high throughput information using metabolomics to clinical diagnosis and treatment can help accelerate the patient safety, quality of life and survival rate by identifying pathways involved in drug resistance. Metabolomics is future of anti-cancer pharmacology, following "the right drug for the right patient at the right time" can offer safety, quality and effectiveness of anti-cancer treatment.

e: mahi.umber@gmail.com

allied academies
Annual Congress on
ONCOLOGY AND BIOMARKERS SUMMIT
November 27-28, 2017 | Atlanta, USA

CDER initiatives to encourage biomarker use in drug development

Shashi Amur
FDA, USA

Biomarkers have been used in drug development and clinical practice for many years. Despite this, there has been confusion about the definitions and inconsistent use of key terms–including biomarkers and surrogates. Recently, an FDA-NIH Biomarker Working Group developed a glossary of terms and definitions to ensure consistency and clarity, termed BEST (Biomarkers, Endpoints and other Tools), to advance scientific progress. The "BEST" glossary describes seven categories of biomarkers: diagnostic, prognostic, susceptibility/risk, predictive, pharmacodynamic/response, monitoring and safety biomarkers. Concepts important in developing biomarkers for use in drug development include: need for biomarkers in a specific disease; purpose of use; how the biomarker performs compared to current standards; development and analytical validation of a reproducible, sensitive and accurate assay to measure the biomarker of interest; and clinical validation that establishes the use of the biomarker for a specific purpose. These biomarkers can be integrated into drug development through the drug approval process and through qualification of the biomarkers through the Biomarker Qualification Program. An additional route also exists where a biomarker gains regulatory acceptance of biomarkers that have evolved through scientific community consensus. CDER, FDA, has developed efforts to encourage development of biomarkers for use in drug development; Critical Path Innovation Meeting (CPIM) Program and the Letter of Support (LOS) initiative. The CPIM can be utilized to discuss biomarkers in the early phase of development and not yet ready for the Biomarker Qualification Program (BQP) with FDA and receive advice. The goal of the LOS is to enhance the visibility of the biomarker, encourage data collection and sharing and potentially stimulate additional scientific studies.

e: shashi.amur@fda.hhs.gov

allied academies

Annual Congress on

ONCOLOGY AND BIOMARKERS SUMMIT

November 27-28, 2017 | Atlanta, USA

Personalized and precision medicine as a model of healthcare of the newest generation to get armed with innovative translational platforms, new knowledge and tools, upgraded education and mentality to secure the impact of the latter

Sergey Suchkov
I M Sechenov First Moscow State Medical University, Russia

A new systems approach to diseased states and wellness result in a new branch in the healthcare services, namely, personalized medicine (PM). To achieve the implementation of PM concept, it is necessary to create a fundamentally new strategy based upon the subclinical recognition of biopredictors of hidden abnormalities long before the disease clinically mani-fests itself. Each decision-maker values the impact of their decision to use PM on their own budget and well-being, which may not necessarily be optimal for society. It would be ex-tremely useful to integrate data harvesting from different databanks for applications such as prediction and personalization of further treatment to thus provide more tailored measures for the patients resulting in improved patient outcomes, reduced adverse events and more cost-effective use of health care resources. A lack of medical guidelines has been identified by most responders as the predominant barrier for adoption, indicating a need for the develop-ment of best practices and guidelines to support the implementation of PM. Implementation of PM requires a lot before the current model “physician-patient” could be gradually dis-placed by a new model “medical advisor-healthy person-at-risk”. This is the reason for de-veloping global scientific, clinical, social and educational projects in PM to elicit the content of the new branch.

e: ssuchkov57@gmail.com

allied academies

Annual Congress on

ONCOLOGY AND BIOMARKERS SUMMIT

November 27-28, 2017 | Atlanta, USA

Analysis of small fragment deletions of the APC gene in Chinese patients with familial adenomatous polyposis

Senqing Chen
Jiangsu Institute of Cancer Research, China

Statement of the Problem: Familial adenomatous polyposis (FAP) is an autosomal dominant inherited disease mainly caused by mutations of the adenomatous polyposis coli (APC) gene with almost complete penetrance. These colorectal polyps are precancerous lesions that will inevitable develop into colorectal cancer at the median age of 40-year old if total proctocolectomy is not performed. So, identification of APC germline mutations has great implications for genetic counseling and management of FAP patients.

Methodology & Theoretical Orientation: In this study, we screened APC germline mutations in Chinese FAP patients, to find novel mutations and the APC gene germline mutation characteristics of Chinese FAP patients. The FAP patients were diagnosed by clinical manifestations, family histories, endoscope and biopsy. Then patients peripheral blood samples were collected, afterwards, genomic DNA was extracted. The mutation analysis of the APC gene was conducted by direct DNA sequencing for micromutations and MLPA for large duplications and/or deletions.

Findings: We found 6 micromutations out of 14 FAP pedigrees, while there were no large duplications and/or deletions found. These germline mutations are c.5432C>T (p. Ser1811Leu), two c.3926_3930delAAAAG (p.Glu1309AspfsX4), c.3921_3924delAAAA (p.Ile1307MetfsX13), c.3184_3187delCAAA (p.Gln1061AspfsX59) and c.4127_4126delAT (p.Tyr1376LysfsX9), respectively and all deletion mutations resulted in a premature stop codon. At the same time, we found c.3921_3924delAAAA and two c.3926_3930delAAAAG are in AAAAG short tandem repeats, c3184_3187delCAAA is in the CAAA interrupted direct repeats and c4127_4128 del AT is in the 5'-CCTGAACA-3', 3'-ACAAGTCC-5 palindromes (inverted repeats) of the APC gene. Furthermore, deletion mutations are mostly located at codon 1309.

Conclusion & Significance: Though there were no novel mutations found as the pathogenic gene of FAP in this study, we found nucleotide sequence containing short tandem repeats and palindromes (inverted repeats), especially the 5 bp base deletion at codon 1309, are mutations in high incidence area in APC gene.

e: chensenqing2008@126.com

allied academies

Annual Congress on

ONCOLOGY AND BIOMARKERS SUMMIT

November 27-28, 2017 | Atlanta, USA

HbA1C, lipid profile and magnesium as a biomarker for early diagnosing type ii diabetes mellitus and its associated complications in the rural region of Vidarbha, Maharashtra, India

Sarmistha Sarkar
Datta Meghe Institute of Medical Sciences, India

Introduction: Diabetes mellitus (DM) is a group of metabolic diseases characterized by hyperglycemia resulting from defects in insulin secretion, insulin action, or both. We aimed to research association between serum HbA1C, lipid profile, magnesium and blood glucose levels, hypothesizing that early detection and treatment of lipid and magnesium abnormalities can minimize the risk for cardiovascular disorder and cerebrovascular accident in the type II diabetic group.

Methodology: Fasting blood glucose, HbA1C, TC, HDL, LDL, VLDL, TG and magnesium levels were evaluated. Study period from July 2016 to December 2016 among 60 patients including male and females and divided into two groups. 30 patients study group with known history of Type II DM, who attended the OPD of the Medicine Department of AVBRH Hospital and 30 ages, sex matched healthy controls. The age group between 30-40 years included in the study. Statistical analysis was done by using descriptive and inferential statistics and software used in the analysis was SPSS 17.0 version.

Results: Results of serum lipid profile showed that the mean values for TC, TG, HDL, LDL and VLDL in study group were 227.76±30.72, 152.23±40.94, 40.5±6.43, 153.30±27.70 and 33.00±9.94 mg/dl respectively and lipid profile level is significantly higher in the cases as compared to controls. Higher HbA1C level increases the risk for diabetic complications. FBS showed significant positive correlation with HBA1C ($p<0.002$). HDL has significant negative correlation with HBA1C ($p<0.008$). Serum magnesium levels were found low in study group as compared to controls.

Discussion/Conclusion: Early detection in the abnormalities of serum HbA1C, lipid profile and Mg can minimize the risk for micro and macro angiopathies in the known type II diabetic patients.

e: sarmistha0035@gmail.com

allied academies
Annual Congress on
ONCOLOGY AND BIOMARKERS SUMMIT
November 27-28, 2017 | Atlanta, USA

Research on antidote of chemical weapons and cyanides poisons known as sodasulphanecoblamin

Salako N Olatunji
Federal Institute of Industrial Research Oshodi, Nigeria

Sodasulphanecobalamin (Na4S5 CoC69N15H89O26) is an antidote for Cyanide poison, mainly high concentration of Cyanides (Sodium and hydrogen Cyanide) which displaces the Cyanides to a free toxic compound, thiocyanocobalamin. It also added the amide group of protein when used. However, recent studies show that this antidote can serve as a replacement for the antidote of Orange agent (2,3,4,7-tetra chlorobenzodioxin) which displaced millions of Vietnam Citizens during the world war II. Though Mercury (I) Oxalate is been used for this antidote for the orange agent, but we all know that Mercury is highly toxic and poisonous to the human. (Na4S5 CoC69N15H89O26) N O + H o c b l + 2 N a o H + N O 2 + 3 N a 2 S O 4 + N a 2 S 5 2Na2S2O3+2NaNO2+4NaOH +HOSCb1+SO2(g) Na4(S2O3)2 (NO2)2 C62H87 SCON13O16P Hydroxocobalamin with the decomposition of Sodium nitrite and Sodium thiosulfate will led to a faster return to baseline mean arterial pressure compared with sodium nitrite with sodium thiosulphate; however, there was no difference between the antidote combinations in mortality, serum acidosis, or serum lactate. The most efficient and reliable way to treat cyanide poison is by using Sodasulphanecobalamin. It is non-carcinogenic, non-mutagenic and non-teratogenic compound which is composition doesn't have any toxicity and health effect when administered.

e: salakoolatunji9@gmail.com

allied academies

Annual Congress on

ONCOLOGY AND BIOMARKERS SUMMIT

November 27-28, 2017 | Atlanta, USA

Next generation sequencing and immuno-histochemistry profiling identify numerous biomarkers for personalized therapy of endometrioid endometrial carcinoma

Said El Shamieh
Beirut Arab University, Lebanon

Endometrial cancer (EC) is the most common cancer of the female reproductive tract. In the current study, we were presented with a case of premenopausal woman suffering from EC and having a cancer family history from both paternal and maternal sides, an observation that suggests the presence of germline mutations. The main aim was to accurately classify our case of EC into a subtype, then, to report the associated genetic alterations and protein bio-markers. Furthermore, we aimed to develop individualized treatment strategies designed for maximum effectiveness. Multiple profiling technologies, including immunohistochemistry (IHC), next-generation sequencing (NGS) and chromogenic in situ hybridization (CISH) were used. Forty-four genes including proto-onco and tumor suppressor genes were sequenced to identify causal mutations, in total, 8 mutations in 5 genes were reported (phosphatase and tensin homolog, phosphatidylinositol-4, 5-bisphosphate 3-kinase, catalytic subunit alpha, etc.). Chromogenic in situ hybridization did not show any gene duplications or deletions. In addition, immuno-histochemistry analysis revealed altered levels of programmed death (PD-1) protein biomarker. Since the tumor was positive for PD-1, pembrolizumab (monoclonal) treatment followed Everolimus. Interestingly, the affected individual responded positively after 5 cycles of treatment (over 24 weeks) and tumor size decreased in size from 7 cm x 4.4 cm x 10.5 cm to 6.5 cm x 3 cm x 7.5 cm. Our results have deciphered genetic and protein biomarkers that might be implicated in the aetiology of endometrial cancer. Furthermore, it has established the guideline for a personalized treatment targeting the altered gene products.

e: said.elshamieh@bau.edu.lb

allied academies
Annual Congress on
ONCOLOGY AND BIOMARKERS SUMMIT
November 27-28, 2017 | Atlanta, USA

Biomarkers and psoriasis

Saed Sayad
University of Toronto, Canada

Psoriasis is a chronic inflammatory skin disease mediated by the cells and molecules of both the innate and adaptive immune systems that involves red elevated patches and flaking silvery scales. Despite intensive research, psoriasis pathogenesis remains unknown. Our purpose was to study the role of nickel in psoriasis using microarray gene expression data. The unexpected outcome from this study was the role of metronidazole in the treatment of psoriasis. Six psoriasis microarray assays were downloaded from the GEO database. Statistical tests have been done on both normalized and nonnormalized data. We used KEGG, Reactome and Biosystems for pathway analysis and RGD for gene-chemicals interactions. Nickel upregulates the top upregulated genes in psoriasis including AKR1B10, IL36G, SERPINB4, KYNU, SERPINB3, TCN1, DEFB4A, HPSE, PI3, SPRR2C, SPRR3, VNN3 and several S100 family members without downregulating any of those upregulated genes. Nickel also downregulates the top downregulated genes such as KRT77, ID4, BTC, CCL27, CHP2, IL37 and RORC without upregulating any of those downregulated genes. The strongly upregulated pathways included immune response, defense response (e.g., amebiasis), cell cycle and metabolic pathways and the top downregulated pathways included inflammatory bowel disease, keratins, ErbB, Chemokine, cytokine and TGF-beta pathways. Based on the best of our knowledge, this is the first study that highlighted the role of nickel in psoriasis pathogenesis using microarray gene expression data. The significant and unique effect of nickel in upregulating the upregulated genes and downregulating the downregulated genes in psoriasis and a strong affinity between the imidazole ring were an indication of a possible dramatic effect of metronidazole on improving psoriasis skin inflammation in our limited case study. Using microarray data, we showed that recognition of the role of abnormal nickel concentration could point the way to greater understanding of psoriasis pathogenesis.

e: saed.sayad@utoronto.ca

allied academies
Annual Congress on
ONCOLOGY AND BIOMARKERS SUMMIT
November 27-28, 2017 | Atlanta, USA

Association of Vitamin D level and SLCO1B1 gene polymorphisms; rs2306283A>G and rs4149056T>C, with the risk of statin induced myopathy in Saudi Arabia

Rajaa Fakhoury
Beirut Arab University, Lebanon

Background & Aim: Lowering cholesterol with statin therapy results in substantial reductions in cardiovascular complications. Mild to moderate muscular symptoms occur especially when the statins are administered at high doses. Vitamin D deficiency is common in Saudi Arabia but also worldwide and may cause muscle dysfunction and ache. Previous observations in European populations showed that rs2306283A>G, p.Asn130Asp and rs4149056T>C, p.Val174Ala in solute carrier organic anion transporter 1B1 (SLCO1B1) gene encoding the organic transporter protein, may be responsible for statin uptake and thus explain the majority of statin associated symptoms. The aim of the present study was first to reveal a possible effect of Vitamin D (Vit D) status, rs2306283A>G and rs4149056T>C on muscle related symptoms, most importantly muscle ache and investigate possible interactions between Vit D status and the above-mentioned variants.

Methods: 50 individuals of Arab origin diagnosed with hypercholesterolemia (half of them with statin associated muscle symptoms) were recruited from outpatient clinics in Riyadh and underwent phenotypic data assessment including serum markers (lipid profile, creatine kinase and Vit D status). In addition, genomic DNA was extracted and genotyped using hybridization probes on a LightCycler® 96 Instrument Roche.

Results: Vit D status was associated with muscle ache (O.R=3.6, P=0.03). However, for creatine kinase levels, rs2306283A>G and rs4149056T>C we did not find associations. Interesting, both rs2306283A>G and rs4149056T>C were interacting with Vit D status to influence muscle ache (P=0.05 and P=0.02 respectively). When stratified according to Vit D status, rs4149056T>C showed a significant association with muscle ache (P=0.05).

Conclusion: Our preliminary results show an involvement of Vit D and rs4149056T>C of SLCO1B1 in statin induced muscle ache. This result encourages us to increase our sample size to confirm our findings.

e: rajaa.fakhoury@gmail.com

allied academies
Annual Congress on
ONCOLOGY AND BIOMARKERS SUMMIT
November 27-28, 2017 | Atlanta, USA

Evaluation of sHLA-G levels in serum of patients with prostate cancer identify as a potential of tumor marker

Mohamadreza Mashhoudi Barez
Shahid Beheshti University, Tehran

Prostate cancer is the most common cancer type in men and is the second cause of death, due to cancer, in patients over 50, after lung cancer. Prostate specific antigen (PSA) is a widely-used tumor marker for prostate cancer. Recently, PSA is discovered in non-prostatic cancer tissues in men and women raising doubts about its specificity for prostatic tissues. PSA exists in low serum level in healthy men and in higher levels in many prostate disorders, including prostatitis and prostate cancer. Thus, a supplementary tumor marker is needed to accurately diagnose the cancer and to observe the patient after treatment. Recently, soluble human leukocyte antigen-G (sHLA-G) has been introduced as a new tumor marker for different cancer types, including colorectal, breast, lung and ovary. The present descriptive-experimental study was carried out including patients with malignant prostate tumor, patients with benign prostate tumor and a group of health men as the control group, as judged by an oncologist as well as a pathologist. After sterile blood sampling, sHLA-G was measured by enzyme-linked immunosorbent assay in each group. The data was then analyzed using one-way ANOVA. $P \leq 0.05$ was considered as statistically significant. The results showed that the mean of sHLA-G level was high in patients. Also, it was found that there was a significant difference in sHLA serum level between the three groups. The data revealed that sHLA-G can be a novel supplementary tumor marker in addition to PSA to diagnose prostate cancer.

e: barvetic@gmail.com

allied academies
Annual Congress on
ONCOLOGY AND BIOMARKERS SUMMIT
November 27-28, 2017 | Atlanta, USA

Paraneoplastic antigens as biomarkers for early detection and prediction of recurrence of ovarian cancer

Michael A Tainsky
Wayne State University School of Medicine, USA

Routine disease monitoring of ovarian cancer patients is generally recommended by gynecologic oncologists for women from high-risk families and for ovarian cancer patients during after the completion of primary surgery and first-line chemotherapeutic treatments. The recurrence is determined by measuring the level of serum CA125, one of the most extensively used tumor biomarkers in standard clinical practice for disease surveillance. Numerous studies have shown the role of tumor autoantibodies as biomarkers for ovarian cancer diagnosis and its recurrence. These autoantibodies to tumor associated antigens (TAAs) arise due to the generation of humoral immune response before evidence of clinical symptoms in cancer patients. Previously, we showed that 3 biomarker panel predicted ovarian cancer recurrence at a median lead time of 9.07 months with 94.7% sensitivity, 86.7% specificity and 93.3% accuracy, in a cohort of ovarian cancer patients where normalization of CA125 had occurred after the surgery and completion of chemotherapy. One of those biomarkers was a peptide epitope from a known paraneoplastic antigen, HARS. Paraneoplastic antigens can elicit a humoral immune response in cancer patients as these antigens are expressed in the cells of nervous system and tumor. The appearance of these onconeural antibodies in ovarian cancer patients leads to the development of various neurological disorders called paraneoplastic syndromes, particularly dermatomyositis or polymyositis but can precede the occurrence of dermatomyositis or polymyositis. Although the clinical implication of these onconeural antibodies as biomarkers for early diagnosis of ovarian cancer has been reported in many case studies, the usefulness of these antibodies has yet to be evaluated in monitoring disease status in ovarian cancer patients after cytoreductive surgery and chemotherapy treatments. In the present study we evaluated the role of a panel of 3 recombinant paraneoplastic antigens, HARS, CDR2 and Ro52 in combination with 3 of our previous biomarkers in predicting recurrence in new and independent cohort of ovarian cancer patient population in which most of the patients had no elevation in CA125 level months before their clinical recurrence. Our results indicate that autoantibodies to HARS, Ro52 and CDR2 and 5H6 antigens predicted ovarian cancer recurrence 5.03 months before the clinical or symptomatic relapse in 21 ovarian cancer patients with a sensitivity of 90.5% when CA125 levels were below the standard cutoff (35 U/ml). We have expanded the biomarker panel and test a larger sample size for the early detection of ovarian cancer using a newly developed ELISA protocol employing a large number of sera from patients and women with benign gynecological diseases.

e: tainskym@med.wayne.edu

allied academies

Annual Congress on

ONCOLOGY AND BIOMARKERS SUMMIT

November 27-28, 2017 | Atlanta, USA

Discussion on the value of combined hs-TnT and NT-proBNP with ultra-window stable of STEMI patient's risk of stratification and prognosis in direct percutaneous coronary intervention

Lao Yi
Sun Yat-sen University, China

Objective: The objective of this study was to investigate the value of hs-TNT and NT-proBNP levels in predicting the stratification and prognosis risk of patients with STEMI undergoing percutaneous coronary intervention directly.

Method: Eighty-six patients with STEMI were divided into fourgroups according to hs-TNT and NT-proBNP levels. Group A: TNT≤1 ng/L, BNP>1800 ng/L, 22 patients. Group B: TNT≤1 ng/L, BNP≤1800 ng/L, 21 patients. Group C: TNT>1 ng / L, BNP>1800 ng/L, 24 patients. Group D: TNT>1 ng/L, BNP≤1800 ng/L, 19 patients. Every group has carried out Percutaneous Coronary Intervention (PCI) immediately after admission into hospital and followed up for 30 days. The cardiac death of patients in each group was compared with hospitalization and within 30 days. The onset of MACE (Major Advance Cardiovascular Events) within 30 days, the changes of LVEF and left ventricular shortening (FS) about emergency PCI treatment immediately after surgery 7 days and 30 days should be collected.

Results: One patient (1/22, 4.5%) was died in Group A, no patient was died in Group B, 3 patients (3/24, 12.5%) was died in Group C and 1 patient (1/19, 5.3%) was died in Group D. 12 patients (12/22, 54.5%) were occurred MACE in Group A, 1 patient (1/21, 4.8%) was in Group B, 19 patients (19/22, 86.4%) were in Group C and 4 patients (4/19, 21.2%) were in Group D during hospitalization. 1 patients (1/21, 4.8%) in were occurred MACE in Group A, 1 patient (1/21, 4.8%) was in Group B, 8 patients (8/22, 36.4%) were in Group C and 3 patients (3/18, 16.7%) were in Group D and followed up for 30 days. Compared with other groups, the level of LVEF and FS were the lowest (46±0.10, 23.33±5.68, p=0 .001) after the surgery immediately and the level of LVEF (0.09±0.09 (p=0.003), 0.09±0.08 (p=0.000)) within 7 days and 30 days were significantly improved in Group A. The level of LVEF and FS were the highest (60±0.08, 32.16±5.85, p=0.001) within 30 days in Group B, which was higher than after the surgery immediately (0.05±0.06). The level of LVEF and FS were the lowest (48±0.11, 24.41±5.13) within 30 days in Group C, which were decreased significantly (-0.03±0.10, p=0.000) after the surgery immediately. In Group D, the level of LVEF and FS (55±0.07) were lower slightly within 30 days than after surgery immediately.

Conclusion: Cast aside the limit of different time when ultra-window stable STEMI patients seek treatment. Based on the level of hs-TNT and NT-proBNP risk stratification, both the patients of low level of hs-TNT and NT-proBNP and low level of hs-TNT and high level of NT-proBNP can benefit more from emergency PCI treatment. The above situation was possible to break the STEMI guidelines defined that the window time of treatment in the emergency PCI. The concept and strategies of the STEMI treatment should be optimized and improve the prognosis of patients and the overall level of STEMI treatment.

e: yilaoyilao@126.com

allied academies
Annual Congress on
ONCOLOGY AND BIOMARKERS SUMMIT
November 27-28, 2017 | Atlanta, USA

Development of SCLC immunotherapy using isoaspartylated ELAVL4

Laird-Offringa
Keck School of Medicine of USC, USA

Small cell lung cancer (SCLC) patients can develop autoimmune responses against neuronal proteins misexpressed in their tumors. Rarely, this response is severe, resulting in debilitating disease and death. One family of antigens is the neuronal embryonic lethal altered visual system-like (ELAVL) RNA-binding proteins ("Hu" proteins). All SCLC tumors misexpress neuronal ELAVL proteins, most commonly ELAVL4. Although less than 1% of SCLC patients develop high titer anti-ELAVL antibodies and exhibit paraneoplastic encephalomyelitis/sensory neuropathy (PEM/SN), lower titer antibodies are seen in about 15-20% of SCLC patients without autoimmune symptoms. Based on the sequence and presumably unstructured nature of the N-terminal region of neuronal ELAVL proteins, we hypothesized that in the context of SCLC these proteins can undergo isoaspartylation, an immunogenic post-translational modification, triggering an immune response in a subset of SCLC patients. Indeed, we recently showed that neuronal ELAVL proteins undergo isoaspartylation *in vitro* and *in vivo*, that this makes these proteins highly immunogenic and that sera from SCLC patients react specifically with the isoaspartyl-prone N-terminal region of ELAVL4. Here, we build upon these results by using a SCLC mouse model to develop and test a variety of immunization methods to determine whether mice can be protected from induced SCLC, laying the foundation for immunotherapy.

e: ilaird@usc.edu

allied academies
Annual Congress on
ONCOLOGY AND BIOMARKERS SUMMIT
November 27-28, 2017 | Atlanta, USA

Molecular cloning involving AAV-CXCL 12 gene

Kripa Raj Ahuja
University of North Carolina at Chapel Hill, USA

The American Cancer Society reports that this year there will be an estimated 600,920 deaths due to cancer in the United States. Current cancer research includes the use of biomarkers on the surface of cancer cells to distinguish the cancerous cells from normal body cells. Molecular cloning can enhance these biomarkers. Over the past thirty years, molecular cloning has progressed immensely. From digestion to plasmid insertion, the possibilities are endless. The AAV (Adeno Associated Virus) CXCL 12(C-X-C Motif Chemokine Ligand 12) is a protein coding gene that shows great promise with cloning and plasmid insertion. Our project aims to use this gene to bind tightly to biomarkers on the surface of cancer cells. However, before this optimal binding can occur, it is essential to know more about the *AAV CXCL 12* gene itself. For this reason, our project includes multiple gel electrophoresis assays, plasmid insertion/digestion assays and PCR purification. From the results of these assays, the efficacy of *AAV CXCL 12* to bind to cancer biomarkers will become clear. In particular, the cloning assay for the *AAV CXCL 12* gene holds great potential, as it is possible to clone extraneous DNA into a different host. If extraneous DNA can be cloned into a different host, then there is the possibility of that DNA binding to a biomarker on a cancer cell.

e: kripa@live.unc.edu

allied academies
Annual Congress on
ONCOLOGY AND BIOMARKERS SUMMIT
November 27-28, 2017 | Atlanta, USA

MiRNAs as potential biomarkers for human glioblastoma

Jian Shi
University of California, San Francisco, USA

Cancer is a fatal human disease capable of spreading throughout the body extremely fast. As of now, early diagnosis of cancer is the most effective method to prevent cancer development and devise the most efficient and effective treatments. Therefore, early diagnosis is critical to achieving higher survival rates for patients. Many traditional diagnostic methods for cancer are still inadequate for early, convenient, accurate and noninvasive diagnosis. Specifically, glioblastoma multiform (GBM) is the most common primary malignant brain tumor, which the five-year survival rate is only 0.05% to 4.7%. Thus, the need to find more effective biomarkers is paramount in insuring early discovery and effective treatments for patients. Recently, there have been reports that indicate the possibility of micro RNAs (miRNAs) as potential biomarkers for cancers. In this study, we attempt to answer two questions like: Could the exosomal miR-21 be used as a universal biomarker for cancer? We used the Meta-analysis method to evaluate ten studies involving 318 patients and 215 healthy controls. In all, the analysis covered ten types of cancers. In addition, we also examined and evaluated many other common issues with biomarkers, including cutoff points, internal controls and detection methods. This initial meta-analysis indicates that the exosomal miR-21 from body fluids has a strong potential to be used as a universal biomarker to identify cancers. As a continuation from the first question, we also consider; Could we find any miRNA biomarkers specifically for the diagnosis of GBM? In order to predict GBM related miRNAs and their targets, we used a bioinformatics algorism, the relative R-squared method (RRSM), to analyze the miRNA and mRNA expression profiles and motif complementary sequences. Then, real-time PCR was used to confirm the predicted miRNA candidates in human GBM tissues and cancer cell lines. Furthermore, we used bioinformatics methods and molecular techniques to analyze the related gene expression and regulatory pathways. The results of these studies indicate that variations in miRNA expression have been observed in cancer tissues and biological fluids. The fact that some highly stable miRNAs circulate in the blood and cerebrospinal fluid (CSF) of both healthy individuals and diagnosed patients has raised the possibility that miRNAs may serve as novel diagnostic markers. Also, increased understanding of the interaction between miRNAs and mRNAs involved in GBM progression may lead to the discovery of predictive biomarkers, some of which are clinically relevant for targeted therapy and predicting prognosis. However, as this field is in the beginning, some different studies have conflicting results. In order to make more progress in the field, there is still a need to combine different advanced techniques, such as bioinformatics methods and other molecular and cellular techniques.

e: jian.shi@ucsf.edu

allied academies

Annual Congress on

ONCOLOGY AND BIOMARKERS SUMMIT

November 27-28, 2017 | Atlanta, USA

Metabolic biomarker for hepatic ischemia in a rat model using ^{13}C hyperpolarized 13C MR spectroscopy

Gwang-Woo Jeong
Chonnam National University Medical School, Korea

This study investigated the metabolic alterations in a rat model of hepatic ischemia reperfusion injury (IRI) using the combined *in vivo* hyperpolarized ^{13}C MRS and intravoxel incoherent motion (IVIM)-diffusion weighted imaging (DWI). Hyperpolarized 13C MRS with IVIM-DWI was performed on the liver of nine sham-operated control rats and nine rats before and after hepatic IRI. The hepatic IRI-induced rats showed significantly higher ratios of [1-13C] alanine/pyruvate, [1-13C] alanine/total carbon, [1-13C] lactate/pyruvate and [1-13C] lactate/total carbon compared with both sham-operated controls and rats before IRI, whereas [1-13C] pyruvate/total carbon ratio was decreased in IRI-induced rats. In IVIM-DWI study, apparent diffusion coefficient (ADC), perfusion fraction (f) and D values in rats after hepatic IRI were significantly lower than those of rats before IRI and sham-operated controls. The levels of [1-13C] alanine and [1-13C] lactate was negatively correlated with ADC, f and D values, whereas the level of [1-13C] pyruvate was positively correlated with these values. The levels of [1-13C] alanine, [1-13C] lactate and [1-13C] pyruvate in conjunction with IVIM-DWI and serum enzyme levels will be helpful to evaluate the hepatic IRI.

e: gwjeong@jnu.ac.kr

allied academies

Annual Congress on

ONCOLOGY AND BIOMARKERS SUMMIT

November 27-28, 2017 | Atlanta, USA

Toxicological studies of aqueous extract of *Adenia cissampeloides* in *Clarias batrachus* fish

Emmanuel Emeji
Ebonyi State College of Education, Nigeria

The effects of aqueous stem extract of *Adenia cissampeloides* on selected liver function biomarkers of fish (*Clarias batrachus*) were investigated. The aims were to determine the lethal concentration (LC50) of the extract to the fish and the effects on Aspartate aminotransferase (AST), Alanine aminotransferase (ALT), Alkaline phosphatase (ALP) and Unconjugated Bilirubin (UB). A total of one hundred and sixty (160) fish of average weight of 122 g were used in the study and grouped into five (A, B, C, D and E). The 24 hr, 48 hr and 72 hr lethal concentration (LC50) of the stem extract were determined. Those for the assay were exposed to 00 g/l, 0.6250 g/l, 1.250 g/l, 2.50 g/l and 5.0 g/l concentrations respectively, in triplicate for a total of eight hours. Blood sample was collected from one fish picked from each group at one-hour interval and assayed. One factor completely randomized ANOVA design was adopted in the analysis. The 24 hr, 48 hr and 72 hr, LC50 were 5.00 g/l, 2.50 g/l and 2.50 g/l respectively. There were increases in the activities of all the parameters assayed for. The results of analysis showed significant ($p<0.05$) increases in AST activities and concentrations of UB. However, increases in the activities of ALT and ALP were not significant ($p>0.05$). Large effect size ($\omega 2$) of 0.42 and 0.52 for UB and AST, respectively, were obtained. AST/ALT ratio of 1:5 indicated damages to liver cells and disruption of vital processes that might have elicited unfavorable cytotoxic reactions in the fish. It is possible that the same effects may occur in man; therefore, it was recommended that fish killed with this plant should be avoided if not properly heat treated.

e: emejiemmanuelo@yahoo.com

allied academies
Annual Congress on
ONCOLOGY AND BIOMARKERS SUMMIT
November 27-28, 2017 | Atlanta, USA

Optimizing next-generation sequencing (NGS) and biomarkers in cancer clinical trials in Asia

Allen Lai
ACT Genomics, Singapore

Coupled with the availability of molecular therapeutic targeting genomically defined population, next-generation sequencing (NGS) based multiplexed genomic profiling has created a growing interest among cancer specialists and pharmaceutical companies. Among all, using the adequate technology platform to identify the right genomic biomarker and provide treatment options is pivotal in drug discovery and development, as well as clinical trial design. There is little doubt that the interest has been prompted by advances in the use of biomarkers, improvements in NGS platforms and accumulating paradigms of benefit. There is much opportunity to pioneer the development of precision oncology. In this talk, the author will walk the audience through the evolution of cancer precision medicine in the search of biomarkers, and the impact to cancer clinical trials in Asia, as well as business growth potential.

e: allenlai@actgenomics.com

allied academies
Annual Congress on
ONCOLOGY AND BIOMARKERS SUMMIT
November 27-28, 2017 | Atlanta, USA

Overcoming challenges of clinical biomarker development

Xuemei Zhao
Merck Research Laboratories, USA

The utility of various types of clinical biomarkers is to aid decision-making in drug development. After a pre-clinical candidate is approved for development in clinical studies, biomarker activities are transitioned from discovery to clinical biomarker development and implementation. Clinical biomarker development includes clinical biomarker assay development, fit-for-purpose assay validation, and clinical biomarker qualification in clinical studies. After a clinical biomarker is qualified, it will then be implemented in clinical studies to aid decision-making. Overcoming challenges of clinical biomarker development such as preanalytics, assay selectivity, and matrix effect will be discussed.

e: xuemei_zhao@merck.com