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Part I Conference Schedule

Time: December 1- 3, 2017

Location: International Asia-Pacific Convention Center Sanya
 三亚亚太国际会议中心暨三亚海航度假酒店

Date	Time	Lobby	
Dec. 1	14:00-17:00	Registration	
Date	Time	Macao Room(澳门厅)	Tokyo Room(东京厅)
Dec. 2	08:30-12:00	Biomedical & Life Sciences Invited Speech Session 1: Prof. Limin Chen, Prof. Fang Zhou, Prof. Lbachir BenMohamed, Dr. Sanjay Singh Negi Chair: Dr. Dong Yu, GSK Vaccines, USA Group photo & Coffee Break: 10:00-10:15	Energy Engineering & Application Invited Speech Session 1: Prof. Liang AN, Prof. Meilin Liu, Dr. Tao Ma, Prof. John Hu Chair: Prof. John Hu & Prof. Liang AN Group photo & Coffee Break: 10:00-10:15
	12:00-13:30	Lunch Pacific Cafe (太平洋咖啡厅)	
Date	Time	Macao Room(澳门厅)	Tokyo Room(东京厅)
Dec. 2	14:00-18:00	Biomedical & Life Sciences Invited Session 2: Prof. Xiang Chen, Prof. Sofia SIEST, Dr. Lu-Yuan Lee, Dr. D.K.Das, Prof. Chunfu Zheng Chair: Group photo & Coffee Break: 16:15-16:30	Energy Engineering & Application Invited Speech Session 2 & Technical Session : Prof. Hossein Ganjidoust, Prof. Li Zhou Chair: Prof. Li Zhou, Tianjin University, China Group photo & Coffee Break: 15:30-15:45
	18:00-19:30	Dinner Pacific Cafe (太平洋咖啡厅)	
Date	Time	Macao Room(澳门厅)	
Dec. 3	08:30-12:00	Biomedical & Life Sciences Technical Session: Chair: Dr. D.K.Das & Prof. Xiang Chen Group photo & Coffee Break: 10:00-10:15	
	12:00-13:30	Lunch Pacific Cafe (太平洋咖啡厅)	

Part II Invited Speech

Biomedical & Life Sciences: Invited Speech Session 1

Invited Speech 1: Type I IFN signaling-a “double-edged sword” that contributes to HCV and HBV persistent infections

Speaker: Prof. Limin Chen, Chinese Academy of Medical Sciences, China

Time: 08:30-09:15, Saturday Morning, December 2, 2017

Location: Macao Room(澳门厅), 3rd Floor, Conference Building, International Asia-Pacific Convention Center Sanya



Abstract

Activation of the type-I interferon (IFN) signaling pathway poses the first line of defense against many virus infections, including HCV and HBV. With the activation of the Jak/STAT signaling leading to the increased expression of several hundred interferon-stimulated genes (ISGs) in the liver microenvironment, an anti-viral state was established and the virus replication was suppressed. However, over-activation of the type-I IFN signaling may actually benefit virus leading to its persistent infection. High throughput gene expression profiling identified 18 differentially-expressed hepatic genes between treatment responders (Rs) and non-responders (NRs) to IFN treatment of patients chronically infected with HCV. Many of these genes are ISGs and they all showed higher expression levels in the pretreatment liver tissues of NRs, indicating that over-activation of type I IFN signaling contributes to treatment non-response leading to persistent infection. Similar findings were observed in chronic HBV infection. Mechanistically, some of these ISGs, such as ISG15 and ISG16 stimulated HCV replication and blunted IFN anti-HCV activity. In line with our observations, studies from other labs demonstrated that blocking IFN signaling facilitated viral clearance in chronic infections, such as in LCMV. All these data point out that type-I IFN signaling is a “double-edged” sword: while activation of this pathway is indeed necessary to control viral spread, over-activation actually benefits virus to facilitate its persistent infection. Detailed molecular mechanisms warrant further investigation.

Invited Speech 2: Human papilloma virus (HPV) 16-encoded E7 onco-protein inhibits IFN- γ -mediated CTL lysis via blocking IRF-1 expression in keratinocytes

Speaker: Dr. Fang Zhou, University of Queensland, Australia
Time: 09:15-10:00, Saturday Morning, December 2, 2017
Location: Macao Room(澳门厅), 3rd Floor, Conference Building,
International Asia-Pacific Convention Center Sanya



Abstract

Infection of HPV16 leads to induction of human cervical cancer. However, immunopathogenesis of HPV 16 is still obscure. The results of experiments aimed at determining whether or not cytotoxic T lymphocytes (CTLs) can kill endogenous antigens presented by keratinocytes (KCs) indicated that specific cytotoxic T lymphocytes could recognize and kill keratinocytes expressing ovalbumin (OVA) or SIINFEKL peptide. Interferon-gamma (IFN- γ) enhanced this CTL-mediated KC lysis via up-regulation of CTL epitope presentation on the surface of target cells. HPV 16 E7 protein as a tumour antigen affected CTL-mediated KC lysis through inhibition of IFN- γ -mediated up-regulation of SIINFEKL/H-2Kb complexes on the surface of keratinocytes. Moreover, HPV 16 E7 could inhibit IFN- γ -mediated up-regulation of IRF-1 expression, and consequent up-regulation of TAP1 transcription, so that the efficiency of SIINFEKL peptide loading on MHC class I molecules was lower than that of wild type keratinocytes. Thus, CTLs failed to efficiently recognize and kill target cells expressing E7. Effect of HPV16E7 on MHC class I antigen presentation and CTL-mediated lysis can be overcome after IRF-1 expression is restored. It can be concluded that HPV 16 E7 inhibits CD8+ T cell-mediated immune responses through blocking IRF-1 expression in host cells. These findings may help explain why HPV-infected epithelial cells can escape from immune surveillance mediated by CTLs in vivo and in vitro.

Invited Speech 3: Diagnostic potential of multiplex Real Time PCR versus GeneXpert MTB/RIF, conventional culture and microscopy for the detection of extrapulmonary tuberculosis

Speaker: Prof. SANJAY SINGH NEGI, Ministry of Health & Family Welfare, Govt of India, India
Time: 10:15-11:00, Saturday Morning, December 2, 2017
Location: Macao Room(澳门厅), 3rd Floor, Conference Building,
International Asia-Pacific Convention Center Sanya



Abstract

Background: The emergence of the more worrisome forms of multidrug resistant, extensive drug resistant and total drug resistant tuberculosis (MDR, XDR & TDR-TB) has posed a serious threat to its management and requires a rapid detection of Mycobacterium tuberculosis for effective early disease management to reduce the chances of all possible transmission. GeneXpert, although approved by WHO for rapid diagnosis of pulmonary tuberculosis, has not been extensively and exclusively evaluated for diagnostic sensitivity in detecting various forms of extra-pulmonary TB with very few published studies. Accordingly, the diagnostic potential

of GeneXpert MTB/RIF and Real Time PCR have been evaluated vis a vis conventional microscopy and culture. A total of 110 multivari ed extrapulmonary samples from equal number of clinically suspected cases of tuberculosis were included in the study. Additionally, 10 samples (5 synovial tissue and 5 synovial fluid) from 10 patients with joint damage of nontuberculous origin and 15 skin biopsy samples from lesion of patients with cutaneous carcinoma were included as negative control. All the samples were subjected to conventional microscopy, liquid culture MGIT 960 system, GeneXpert and multiplex Real Time PCR. The Multiplex Real Time PCR showed the highest diagnostic positivity of 88.8% versus GeneXpert (52.72%), Liquid culture MGIT 960 system (44.54%) and microscopy (4.5%) respectively and found to be statistically significant ($p < 0.01$). Considering culture as gold standard, the positivity, specificity, PPV and NPV for GeneXpert were found to be 87.25%, 100%, 100% and 80.64% respectively while the same parameters for multiplex real time PCR was calculated 100%. 5 cases of rifampicin drug resistance by GeneXpert and 17 NTM by multiplex Real Time PCR were also detected. The diagnostic sensitivity obtained in the present study clearly concludes that GeneXpert should not be used as a sole molecular parameter for diagnosis of extrapulmonary TB. Instead, Multiplex Real Time PCR based on Taqman probe chemistry amplifying the target specific region of both Mycobacterium tuberculosis complex and Non Tuberculous Mycobacteria (NTM) should be employed in addition to GeneXpert in Government and policy makers strategy to identify more rapidly and effectively all cases of extrapulmonary tuberculosis for their early antitubercular intervention. However, further research may also be required to enhance the sensitivity of both GeneXpert and multiplex Real Time PCR to exclude all possibility of false negative extrapulmonary tubercular cases.

Keywords: M.tuberculosis, NTM, Multiplex Real Time PCR, GeneXpert.

Invited Speech 4: Human HSV-Specific Memory CD8+TEM Cells with Unique JAK/STAT, Chemokine and Anti-Inflammatory Gene Signatures Are Associated with Asymptomatic Herpes Infection

Speaker: Prof. Lbachir BenMohamed, University of California, Irvine, USA

Time: 11:00-11:45, Saturday Morning, December 2, 2017

Location: Macao Room (澳门厅), 3rd Floor, Conference Building, International Asia-Pacific Convention Center Sanya



Abstract

A large proportion of the world population harbors herpes simplex virus type 1 (HSV-1) which causes potentially blinding recurrent herpetic disease. HSV-specific CD8+ T cells provide immunosurveillance of the virus that periodically reactivates from latency to cause recurrent herpetic disease. However, the molecular signatures of CD8+ T cells that protect asymptomatic (ASYMP) individuals who, despite being infected with HSV-1, never experienced any recurrent herpetic disease, remain to be elucidated. In this study, we used Flow cytometry and NanoString assays to compare the phenotype, the function, and the expression of a

comprehensive panel of 579 immune genes in memory CD8⁺T cells, that shared the same epitope-specificity, but were freshly sorted from the peripheral blood of well-characterized cohorts of ASYMP and symptomatic (SYMP) individuals, with a history of numerous episodes of recurrent herpetic disease. Regardless of the epitope specificity we: (i) detected frequent multifunctional HSV-specific CD62L^{low}CD44^{high}CD8⁺ TEM cells in ASYMP individuals compared to more CD62L^{high}CD44^{high}CD8⁺ TCM cells in SYMP individuals; (ii) found memory CD8⁺ T cells from ASYMP individuals to express high level of JAK/STAT, chemokine and anti-inflammatory genes. The finding indicated that a unique molecular signature of HSV-specific memory CD8⁺TEM cells, that is associated with activation, migration and anti-inflammatory function, might play an important role in asymptomatic herpes infection in humans.

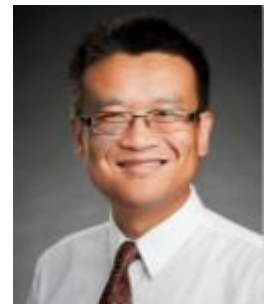
Biomedical & Life Sciences: Invited Speech Session 2

Invited Speech 5: LCA: a robust and scalable algorithm to reveal subtle diversity in large-scale single-cell RNA sequencing data

Speaker: Prof. Xiang Chen, St. Jude Children's Research Hospital, USA

Time: 14:00-14:45, Saturday Afternoon, December 2, 2017

Location: Macao Room(澳门厅), 3rd Floor, Conference Building, International Asia-Pacific Convention Center Sanya



Abstract

Single-cell RNA sequencing (scRNA-seq) is a powerful emerging tool for characterizing cell-to-cell variation and dynamics in a seemingly homogenous population. Efficient and affordable, scRNA-seq is gaining in popularity in both basic and translational biological research areas. However, significant challenges arise in the analysis of scRNA-seq data, from the ability to distinguish signals from a highly noisy background to scalability challenges when attempting to analyze hundreds of thousands of cells. Due to inherent complexities in scRNA-seq data, the performance of currently available algorithms may not always be optimal even for fundamental tasks such as identifying heterogeneous subpopulations in the data. In this study, we developed Latent Cellular Analysis (LCA), a machine learning based scRNA-seq analytical pipeline that combines similarity measurement by latent cellular states and a graph based clustering algorithm featuring dual-space model search for both the optimal number of subpopulations and the informative cellular states distinguishing them. LCA provides heuristic solutions for population number inference, dimension reduction, feature selection and confounding factor removal without explicit gene filtering. LCA has proved to be robust, accurate and powerful by comparison to multiple state-of-the-art computational methods on large-scale real and simulated scRNA-seq data. Importantly, LCA's ability to learn from representative subsets of the data provides scalability, thereby addressing a significant challenge for large-scale scRNA-seq data analysis.

Invited Speech 6: VEGF-A, a potential biomarker for systems medicine

Speaker: Prof. Sofia Siest, INSERM/University of Lorraine, Nancy, France

Time: 14:45-15:30, Saturday Afternoon, December 2, 2017

Location: Macao Room(澳门厅), 3rd Floor, Conference Building,
International Asia-Pacific Convention Center Sanya



Abstract

Vascular endothelial growth factor-A (VEGF-A) is implicated in angiogenesis, lymphangiogenesis, vascular permeability, and haematopoiesis. It is associated with numerous pathologies including cardio-vascular diseases and several types of cancer. We specifically developed an integrative systems biology strategy for clinical improvement of this biomarker. A high heritability of this trait, 60%, was estimated in the STANISLAS cohort giving us the needed arguments to continue for a deep characterization of the genetic component of VEGF-A levels. Therefore, we searched, by a Genome Wide Association Study (GWAS), the VEGF-A genetic variants and the inter-connexions of these biomarkers with other disease-associated molecules in healthy populations. The GWAS was performed in 3,527 healthy participants (Framingham Heart Study) and the most significant results ($P < 5 \times 10^{-8}$) were replicated in 1,727 individuals (STANISLAS Family Study, PIVUS study). Functional transcriptomic analyses were performed in peripheral blood mononuclear cells (PBMCs). Furthermore, in 403 healthy adults the associations between VEGF-A and adhesion/inflammation molecules were tested. Also, associations between VEGF-A and blood lipids were assessed in a discovery ($n=1,006$) and in a replication population ($n=1,145$) of healthy individuals. Four polymorphisms (rs6921438, rs4416670, rs6993770, rs10738760) explaining ~50% of VEGF-A heritability were identified. These variants, directly or via gene x gene x environment interactions had significant effects on HDL, LDL, TNF- α , IL-6, E selectin and ICAM-1 plasma levels. SNP rs6993770 was shown to increase VEGF121 mRNA levels and rs4416670 was associated with L-selectin expression. Recently, thanks to a meta-GWAS we identified 6 additional rsfurther explaining VEGF-A levels variability and ongoing investigations focus on clinical implementation of the ‘-omics’ determinants of this biomarker. Our integrative strategy resulted to significant results indicating molecular links between VEGF-A and cardio-vascular disease biology and the importance of epistatic and gene x environment interactions. This example illustrates an improved strategy to be applied for every biomarker with high heritability levels, consequently with potential interest in Personalised Medicine, using familial design and the existing biobanks.

Invited Speech 7: Role of TRPV1 as a trigger of acute bronchoconstriction in asthma: from ion channel to patient

Speaker: Prof. Lu-Yuan Lee, University of Kentucky, USA

Time: 15:45-16:30, Saturday Afternoon, December 2, 2017

Location: Macao Room(澳门厅), 3rd Floor, Conference Building, International Asia-Pacific Convention Center Sanya



Abstract

Transient receptor potential vanilloid type 1 receptor (TRPV1) is a nonselective cation channel and a polymodal transducer. In the respiratory tract, it is expressed predominantly in non-myelinated (C-fiber) sensory nerves. Stimulation of these TRPV1-expressing sensory endings is known to elicit reflex responses such as cough and reflex bronchoconstriction. Increasing evidence suggests that activation of TRPV1 plays an important part in the manifestation of various symptoms of airway hypersensitivity associated with airway inflammatory diseases. Indeed, allergen sensitization-induced airway inflammation markedly enhanced the expression of TRPV1 and the sensitivity of pulmonary C-fiber afferents in an animal model of asthma. Recent studies in our laboratory have shown a considerably lower temperature threshold for activating TRPV1 expressed in pulmonary sensory nerves. Increasing temperature to ~39 °C significantly elevated the baseline activity and sensitivity of isolated rat vagal pulmonary sensory neurons, and an involvement of TRPV1 was primarily responsible. Furthermore, a brief isocapnic hyperventilation (at ~40% of maximum voluntary ventilation) of humidified warm air triggered an immediate increase in airway resistance (Raw) and coughs in patients with mild and stable asthma. In sharp contrast, the same challenge failed to evoke any significant change in Raw or cough in healthy individuals. Pretreatment with ipratropium bromide completely prevented the bronchoconstriction in the asthmatic patients, but did not abolish the cough response, indicating an involvement of airway sensory nerves and cholinergic reflex. Hyperventilation of humidified air at room temperature did not cause bronchoconstriction or cough in the same patients. In conclusion, increasing airway temperature stimulated airway sensory nerves, presumably via an activation of TRPV1, and elicited both cough and cholinergic reflex bronchoconstriction in patients with mild asthma. These results further suggest that the sensitivity of TRPV1-expressing sensory nerves is upregulated in asthmatic airways.

(Supported in part by National Institute of Health grants AI123832, HL96914 and UL1TR001998)

Invited Speech 8: Expression of a bacterial chitinase (ChiB) gene enhances resistance against *E. polygona* induced powdery mildew disease in the transgenic Black gram (*Vigna mungo* L.) (cv. T9)

Speaker: Prof. D.K. Das, T.M.Bhagalpur University, India

Time: 16:30-17:15, Saturday Afternoon, December 2, 2017

Location: Macao Room(澳门厅), 3rd Floor, Conference Building, International Asia-Pacific Convention Center Sanya



Abstract

To enhance the antifungal response of blackgram (*Vigna mungo* L.), transgenic plants were generated by transferring bacterial chitinase gene with a CaMV 35S promoter. The chopped multiple shoot cells developed on the cotyledonary node were transformed by Particle gun method. The calli were raised on the Murashige and Skoog (MS) modified media supplemented with 50mg/l-1 kanamycin. The transformation efficiency was 13%. The resultant shoot buds were selected and the antibiotic resistant transgenic plantlets were regenerated. The development of the transgenic plants from the shoot buds took about four to six months. The transgenic status was confirmed by PCR, RT-PCR, Southern and western blot analyses. The transgenic plants exhibited higher chitinase activity than the non-transformed plants. The chitinase activity was examined using the native polyacrylamide in-gel assay. The transgenic plants showed enhanced resistance as evidenced by the delayed onset of the disease and smaller lesions following an in vitro inoculation of the powdery mildew pathogen (*E. polygona* DC). The transgenic plants adapted well to the greenhouse and did not show any phenotypic alterations.

Key words *Vigna mungo* L., Bacterial chitinase, transgenic plants, Fungal resistance, *E. polygona*

Invited Speech 9: Evasion of Cytosolic DNA-Stimulated Innate Immune

Responses by HSV-1

Speaker: Prof. Chunfu Zheng, Fujian Medical University, China

Time: 17:15-18:00, Saturday Afternoon, December 2, 2017

Location: Macao Room(澳门厅), 3rd Floor, Conference Building, International Asia-Pacific Convention Center Sanya



Abstract

Recognition of virus-derived nucleic acids by host pattern recognition receptors (PRRs) is crucial for early defense against viral infections. Recent studies revealed that PRRs also include several newly identified DNA sensors, most of which could activate the downstream adaptor stimulator of interferon genes and lead to the production of host

antiviral factors. Herpes simplex virus type 1 (HSV-1) is extremely successful to establish an effective infection due to its capacity to counteract host innate antiviral responses. In the present review, I summarized the most recent findings on the molecular mechanisms utilized by HSV-1 to target different steps of the cellular DNA sensor-mediated antiviral signal pathway.

KEYWORDS

HSV-1, immune evasion, DNA sensing, innate immunity, interferon

Energy Engineering & Application: Invited Speech Session 1

Invited Speech 1: Recent Advances in Direct Ethanol Fuel Cells for Sustainable Energy Production

Speaker: Dr. Liang AN, The Hong Kong Polytechnic University (HKPU), Hong Kong (China)

Time: 08:30-09:15, Saturday Morning, December 2, 2017

Location: Tokyo Room(东京厅), 3rd Floor, Conference Building, International Asia-Pacific Convention Center Sanya



Abstract

Direct ethanol fuel cells (DEFC), which convert the chemical energy stored in ethanol directly into electricity, are one of the most promising energy-conversion devices for portable, mobile and stationary power applications, primarily because ethanol is a carbon-neutral, sustainable fuel and possesses many unique physicochemical properties including high energy density and ease of transportation, storage as well as handling. However, conventional DEFCs that use acid proton exchange membranes and precious metal catalysts result in rather low performance. In our research, we use alkaline anion exchange membranes as the ion conductor in DEFCs. The change from the acid membrane to an alkaline one leads to a significant performance boost. In addition, we propose a novel hybrid DEFC system, which consists of an alkaline anode and an acid cathode. The power density now is as high as 360 mW cm⁻², which represents the highest power density for this type of fuel cell.

Invited Speech 2: Surface Modification and In Situ Characterization of Electrodes for Energy Storage and Conversion

Speaker: Prof. Meilin Liu, Center for Innovative Fuel Cell and Battery Technologies, USA

Time: 09:15-10:00, Saturday Morning, December 2, 2017

Location: Tokyo Room(东京厅), 3rd Floor, Conference Building, International Asia-Pacific Convention Center Sanya



Abstract

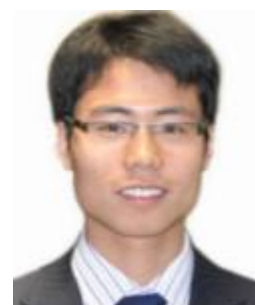
The performances of electrochemical systems are often limited by the charge and mass transfer along surfaces and across interfaces - the most active sites for chemical and electrochemical reactions. Fundamental understanding of the rate-limiting steps is vital to achieving rational design of novel electrode materials or structures with enhanced energy and power density. This presentation will highlight some recent advances in surface modifications and characterization of electrodes in energy storage and conversion systems. Surface enhanced Raman spectroscopy (SERS) has been used for probing and mapping new phases and reaction intermediates on electrode surfaces under or near operating conditions. In particular, it is demonstrated that SiO₂ shell isolated Ag nanoparticles have excellent chemical and thermal robustness and stability for in situ SERS study of electrode materials under in situ or operando conditions, providing valuable information on reaction intermediates or structural changes that critically influence the performance and stability of the electrodes. Further, synchrotron-based X-ray absorption spectroscopy (XAS) and XPS has been used to characterize the local atomistic structure variation and oxidation state changes of electrode surfaces and interfaces, which may critically affect the activation or degradation processes of electrodes. These experimental studies, together with modeling and simulation, have helped us to gain important insights into the mechanisms of chemical and energy transformation, electro-catalytic reactions, and degradation processes, providing valuable guidelines for rational design of new electrode materials, surfaces, and interfaces with desired functionalities.

Invited Speech 3: Energy storage for built environment: enhancing energy flexibility and renewable energy self-consumption

Speaker: Prof. Tao Ma, Shanghai Jiao Tong University, China

Time: 10:15-11:00, Saturday Morning, December 2, 2017

Location: Tokyo Room(东京厅), 3rd Floor, Conference Building, International Asia-Pacific Convention Center Sanya



Abstract

TBD

Invited Speech 4: Process Intensified Conversion of Stranded Gas to Value-Added Chemicals

Speaker: Prof. JOHN (JIANLI) HU, West Virginia University, USA

Time: 11:00-11:45, Saturday Morning, December 2, 2017

Location: Tokyo Room(东京厅), 3rd Floor, Conference Building, International Asia-Pacific Convention Center Sanya



Abstract

In the United States and rest of the world, there are abundant gas resources which are either physically or economically stranded. These gases include flaring gas in shale oil field, refinery off-gas, coal-bed methane, shale gas in disadvantaged locations, etc. Upgrading of these gases to value-added liquid products could reduce the demand on crude oil by about 20% in the United States.

On-site modular production of value-added products from stranded gases become attractive. Due to economy of scale, modular production typically doesn't compete well with conventional large scale production. As a result, process intensified modularity becomes important because it will enhance productivity, energy efficiency and flexibility that allows on-site production to be economically viable. What is process intensified modular production? It consists of novel apparatuses and techniques that, compared to those conventionally practiced today, are expected to bring dramatic improvements in manufacturing and processing, substantially decreasing the ratio of equipment size to production capacity. Most importantly, the process intensification should reduce energy consumption, waste production, and ultimately resulting in cheaper and sustainable technologies. Illustrated in this presentation are synergistic integration of the following unit operations: reactor design, heat management and separation. Process intensification sets the foundation for small modular production to achieve both energy efficiency economic production.

Indirect conversion of natural gas to liquid products (GTL) via syngas has been commercialized but it requires huge capital investment, varying from \$15 to 20 billion for a 100-140 bbl/d plant. Direct conversion of natural gas without going through syngas route has been explored in the past 5 decades, but no commercial processes are practiced to date. A large number of studies have been published on the subject over the past 50 years.

This presentation emphasizes the direct conversion of natural gas constituents (C1-C3) into aromatics and olefins using transition metal promoted ZSM-5 zeolite catalysts. Catalyst activity, selectivity, deactivation and regeneration of metal-promoted ZSM-5 zeolite catalysts will be discussed. We will introduce a new approach that employs low temperature plasma to intensify catalytic reaction for natural gas conversion. Under low reaction severity, this approach synergistically integrates plasma reaction chemistry with novel heterogeneous catalysis that decouples methane activation from

catalytic surface reaction, shifting rate-determining step from methane activation (cracking C-H bond) to surface C-C formation.

In summary, this presentation illustrates experimental research on direct non-oxidative conversion of natural gas. The challenge in advance the fundamental science aspects presented in direct natural gas conversion is discussed. By comparing with commercial hydrocarbon conversion processes, the industrial perspective on direct methane conversion is illustrated. Specifically, the strategies on the selection of reactor configuration, heat management and catalyst regeneration are highlighted. These commercialization strategies along with techno-economic analysis are critical for direct natural gas conversion to value-added chemicals.

Energy Engineering & Application: Invited Speech Session 2

Invited Speech 5: Impact of Biodiesel Fuels on Air Quality and Human Health

Speaker: Prof. Hossein Ganjidoust, Tarbiat Modares Univ., Iran

Time: 14:00-14:45, Saturday Morning, December 2, 2017

Location: Tokyo Room(东京厅), 3rd Floor, Conference Building, International Asia-Pacific Convention Center Sanya



Abstract

Type of vehicles and the consuming fuels, number of ignition engine and the health effects are considered as the most significant factors regarding the producing of pollutants statistics in cities. Changing the human life-style over time attracts the society to live in mega cities.

Reduction of fossil-base fuels resources and harmful effect of using them in environment, are the two most considerable motives for researchers to focus on finding alternative ways of providing energy instead of oil and the fractions.

Among the renewable fuels, the one that is produced from oil seeds and food waste as the sources is considered by majority of researchers, because of decreasing air pollution and greenhouse gases and also reduction of fuel import dependency which results in declining total energy cost. Vegetable-base fuels are the main alternative sources for fossil-base fuels. Since these bio resources are used mostly in ordinary diesel engines, it is known as biodiesel. There is a variety of vegetable species from different climate region have been used for this purpose including soybean, Canola, sunflower, coconut, castor, palm, corn, cottonseed etc. which each one can carry special amount of oil with its own specific characters. Biodiesel is diesel fuel made from vegetable oils, animal fats, or recycled restaurant greases. It's safe, biodegradable, and produces less air pollutants than petroleum-based diesel.

Some significant chemical and physical properties of the product, such as kinematic viscosity, flash point, pour point etc. were calculated to approve conformity to ASTM D6751 standards. Eventually,

the polluted emissions were measured by an orsat gas analyzer. The outcomes completely confirm the assumption which claims that adding biodiesel to conventional diesel fuels has a strong influence on lowering CO₂, CO, HC and smoke.

One of the great advantages of biodiesel is that it can be used in existing engines, vehicles and infrastructure with practically no changes. Biodiesel can be pumped, stored and burned just like petroleum diesel fuel, and can be used pure, or in blends with petroleum diesel fuel in any proportion. Power and fuel economy using biodiesel is practically identical to petroleum diesel fuel, and year round operation can be achieved by blending with diesel fuel.

Invited Speech 6: Energy, Environment and Living Crisis

Speaker: Prof. Li Zhou, School of Chemical Engineering, Tianjin University, China

Time: 14:45-15:30, Saturday Afternoon, December 2, 2017

Location: Tokyo Room(东京厅), 3rd Floor, Conference Building, International Asia-Pacific Convention Center Sanya



Abstract

People are searching for clean and sustainable energy, and great efforts have been dedicated to utilization of hydrogen energy, nuclear energy, shale gas, flammable ice and all kinds of natural energy to avoid of burning coal. To the author's opinion, these ideas may not be correct. Hydrogen energy is still far away from reality due to existence of two barriers. First, hydrogen energy must base on reproducible hydrogen, i.e., the hydrogen comes from water, but not from any fossil fuels; second, the hydrogen must be densely and safely stored on moving objects. However, these barriers have not been taken away even theoretically. Nuclear energy includes fission and fusion energy. The former has been widely applied in practice, but how to deal with the long term (hundred thousand years) radioactivity of reactor residue is still a serious challenge; the latter is believed to be an endless energy source, although the resources of lithium, an inevitable material for fusion reaction, is quite limited. Exploitation of shale gas depressed the price of crude oil, however, a lot of fresh water expends, not mention the possible damage on environment. The resource of flammable ice is shown much more abundant than other fossil fuels, but ecological disaster might happen on exploiting not mention the shortage of sophisticated exploitation technology. All kinds of natural energy have a common problem: storage of the energy produced unevenly. This problem is a serious challenge for extensive utilization of them. Besides, it has been indicated that natural energy alone cannot satisfy all human requirements for energy. To the author's opinion, coal is the most reliable clean energy because zero emission is guaranteed when "carbon reduction" is applied to the flue gas of power plants. Methanol as by-product of such power plants will be widely used in fuel cells to provide power for miscellaneous moving objects. Deterioration of environment is usually attributed to the expenditure of fossil fuels. This is very superficial comprehension of nature. Although CO₂ is released on burning fuels, the global emission

of CO₂ is linearly correlated to the world population, and zero emission is recorded when the population is less than 1.3 Billion. The ecological crisis is caused by over large population of the world. The present world population is 7.5 billion and it increases exponentially. The world must consider which will sustain longer, the energy source or human kind itself.

Part III Technical Sessions

Energy Engineering & Application: Invited Speech Session 2 & Technical Session

Session Chair: Prof. Li Zhou, School of Chemical Engineering, Tianjin University, China

Tokyo Room(东京厅), 3rd Floor, Conference Building

14:00-18:00, Saturday Afternoon, December 2, 2017

ID	Paper Title	Author	Affiliation
Invited Speech	Impact of Biodiesel Fuels on Air Quality and Human Health	Prof. Hossein Ganjidoust	Tarbiat Modares Univ., Iran
Invited Speech	Energy, Environment and Living Crisis	Prof. Li Zhou	School of Chemical Engineering, Tianjin University, China
15:30-15:45	Coffee Break		
15:45-16:00	Solar Thermal Application for the Dairy Industry in Taiwan	Wei-Min Lin	Tainan University of Technology
16:00-16:15	Micro/nano Carbon Electrodes for Novel Efficient Energy Conversion and Storage Devices	XIN Cai	South China Agricultural University
16:15-16:30	Improving the electrochemical stability of Pt/C catalysts in alkaline media by high surface area carbon support modification	Evgenii Gribov	Boreskov Institute of Catalysis, Novosibirsk, Russia
16:30-16:45	Desulphurization of transportation fuels by per-formic acid oxidant using MoO _x loaded on ZSM-5 catalyst	Waqas Ahmad	University of Peshawar, Pakistan

Biomedical & Life Sciences: Technical Session

Session Chair: Dr. D.K.Das & Prof. Xiang Chen

Macao Room(澳门厅), 3rd Floor, Conference Building

8:30-12:00, Sunday Morning, December 3, 2017

ID	Paper Title	Author	Affiliation
11:45-12:00 December 2	Function and clinical significance of microRNA-377 in stemness and	Bin Li	Jinan University, Guangzhou, China

progression of esophageal cancer

12:00-12:15 December 2	Id1-induced IGF2 instigates tumor micro- and macro-environment in esophageal cancer	Wen Wen Xu	Jinan University, Guangzhou, China
12:15-12:30 December 2	Plasma cfRNA – phantasm or future?	Fei Yao	Genome Institute of Singapore
08:30-08:45	Effect of Spin Magnetic Momentthe spinor field on the Exclusion Zone	Quansheng Ren	Peking University
08:45-09:00	Three forms of autophagy in colon cancer	Martyna Bednarczyk	Medical University of Silesia, Katowice, Poland
09:00-09:15	Genome-wide Transcriptome analysis of Paecilomyces hepialid on Different Stages and additives to reveal putative genes in cordycepin biosynthesis	JIN YU	Beijing Normal University
09:15-09:30	Royal jelly peptides: potential inhibitors of β -secretase in N2a/APP695swe cells	Fan Zhen	BEIJING NORMAL UNIVERSITY
09:30-09:45	Identification of hepatic thyroid hormone-responsive genes in neonatal rats	Nariaki FUJIMOTO	Hiroshima University
09:45-10:00	Transcriptome analysis of <i>Bergenia purpurascens</i> discovers putative genes involved in bergenin biosynthesis	Fenggen Guo	Yunnan Agricultural University
10:00-10:15	Coffee Break		
10:15-10:30	The Role of Epigenetics on The Process of Drug resistance Development in The Mycobacterium tuberculosis	Haicheng li	the center control for tuberculosis of guangdong province
10:30-10:45	The correlation between hepatitis B virus precore/core mutations and the progression of severe liver disease	Ahmed Al-Qahtani	A. King Faisal Specialist Hospital & Research Center
10:45-11:00	Hypothetical Protein BPSL3393 of Burkholderia pseudomallei is Involved in	Hokchai Yam	Faculty of Applied Sciences,

	Ethanolamine Catabolism		Department of Biotechnology, UCSI University, Malaysia
11:00-11:15	Molecular typing of Legionella pneumophila from air-conditioning cooling waters using mip gene, SBT, and FAFLP methods	Shouyi Chen	Guangzhou Center for Disease Congtrol and Prevention
11:15-11:30			

Part IV Abstract

Biomedical & Life Sciences

ID: CABMB2017_10000

Title: Effect of Spin Magnetic Moment on the Exclusion Zone

Author: Quansheng Ren

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Abstract:

Colloidal and molecular solutes in suspension are excluded from the vicinity of various hydrophilic surfaces, leaving an exclusion zone (EZ) of hundreds of micrometers. Such exclusion zones were observed in the vicinity of many types of surface including artificial and natural hydrogels, biological tissues as well as hydrophilic polymers. Old studies have shown that the near-surface exclusion zone expands extensively in the presence of incident radiant energy, especially the infrared light. Developments of electromagnetic biology and quantum biology indicate that spin magnetic moment may have a direct impact on the biological process. Inspired by these researches, the effects of magnetic field and spin magnetic moment on EZ were studied. It is shown that spin magnetic moment profoundly expands these zones in an irreversible manner.

ID: CABMB2017_10007

Title: Biomaterial Surface can Modify HUVEC Morphology and Inflammatory Response by Regulating microRNA Expression

Author: Shuangying Gu

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Abstract:

Abstract: Vascular inflammation is an important process which contributes to the pathogenesis of many

cardiovascular diseases, such as atherosclerosis. microRNAs (miRNAs) have been revealed as novel regulators of vascular inflammation. Prior researches had shown that alterations in gene expression of human umbilical vein endothelial cells (HUVECs) associated with topographic cues. Here, we showed that poly (dimethyl siloxane) (PDMS) substrate of 10 μ m width and 3 μ m depth parallel microgrooves on the surface could significantly upregulate the expression of anti-inflammatory microRNAs, miR-146a and miR-181b. In addition, the results also showed that TRAF6 and importin- α 3, target of miR-146a and miR-181b, respectively, were both down-regulated (P<0.05 and P<0.001, respectively). The expression levels of the inflammation related proteins were all significantly decreased, including VCAM-1 (P<0.05), ICAM-1 (P<0.001), E-selectin (P<0.001), and MCP-1 (P<0.05). The adhesion of the mononuclear cell line, THP-1, was significantly decreased (P<0.05). The results revealed that morphology modified HUVEC can modulate miR-146a and miR-181b and their downstream biological functions such as decreasing inflammation, suggesting that surface microtopology may affect vascular inflammation in the setting of cardiovascular disease. These interesting findings will facilitate the optimal design of microstructured materials in tissue engineering.

ID: CABMB2017_10015

Title: Three forms of autophagy in colon cancer

Author: Martyna Bednarczyk

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Abstract:

Autophagy plays two basic roles in a cell: on the one hand, it removes the damaged cell components or organelles in result of autodigestion, on the other, being a catabolic process, it enables generation of substrates necessary to maintain cell energetic homeostasis during restricted access to nutrients. Also, it is considered to promote programmed cell death type II.

There are three forms of autophagy depending on the way the substrate is delivered to lysosome: macrophagy, chaperone-mediated autophagy and specific autophagy, the latter causing removal of specific structures (e.g. mitophagy in mitochondria).

The study material consisted of biopsy specimens from colon cancer in four clinical stages, confirmed by histopathology as adenocarcinoma, and biopsy specimens from normal colon operative margin as controls.

The purpose of the study was to assess changes in transcriptive activity of genes involved in the process of autophagy in four clinical stages of colon cancer compared to the controls, and to find out which of the transcripts could differentiate normal colon from that affected by cancer, thus having a diagnostic or prognostic or predictive value.

The analysis included 435 mRNA engaged in regulation of the autophagy process and found on HG-U133A micromatrix (Affymetrix, Santa Clara, CA). Differentiating genes were determined using PL-Grid infrastructure (<http://www.plgrid.pl/>).

Statistical analysis ANOVA revealed that among the group of 435 mRNA of the genes connected with autophagy, 50 mRNA could differentiate cancerous specimens from the control K. Among the 50 differentiating mRNA, 1 gene was selected as typical for macrophagy (BECN1), chaperone-mediated autophagy (LAMP2) and mitophagy (PINK1), and their transcriptive activity was determined in four stages of the cancer and compared to the controls.

The results show that transcriptive activities PINK1 and BECN1 are lower in all stages of the cancer in comparison with the controls. This may suggest that both mitophagy and macrophagy become suppressed in case adenocarcinoma has been diagnosed.

The parameter FC - showing log₂ of the fluorescence

signals between study groups - was for PINK1: CSI vs K = -2.475, CSII vs K = -2.032, CSIII vs K = -1.753 and CSIV vs K = -2.703 whereas for BECN1: CSI vs K = -1.324, CSII vs K = -1.417, CSIII vs K = -1.631 and CSIV vs K = -1.772. On the other hand, LAMP2 showed lower expression in CSI and overexpression in the remaining stages, FC being as follows: CSI vs K = -1.075, CSII vs K = 1.729, CSIII vs K = 1.445 and CSIV vs K = 1.416.

The differences in mRNA concentration profiles of the genes connected with autophagy as shown in adenocarcinoma specimens may suggest that autophagy plays a role in pathogenesis of adenocarcinoma. mRNA concentration profile of the genes connected with autophagy may be considered a supplementary marker in differentiating adenocarcinoma from controls depending on a clinical stage of the cancer.

ID: CABMB2017_10016

Title: Genome-wide Transcriptome analysis of *Paecilomyces hepialid* on Different Stages and additives to reveal putative genes in cordycepin biosynthesis

Author: JIN YU

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Abstract:

Paecilomyces hepialid (PH) is one of the primary fungus of *Cordyceps sinensis*(CS) and has become the substitute of CS due to the similar pharmacological activities and institutes. Because of the special living environment of CS and people's over-harvest, CS is hard to satisfy the commanding of market, and cordycepin, as an effective compound of CS, is hard to realize industrial production. In order to alleviate this situation, we produced 5 samples of PH by culturing for different time and adding distinct additives in the broth of PH and detected their content of cordycepin with UPLC ESI MS/MS. Then we grouped them into five transcriptome comparisons which contain 3 time variable groups and 2 additive variable groups. And we used next-generation (NG) sequencing methods to get

the transcriptome information of them and understand their response to the induction of additives and the influence of different growth stages to the gene expression. It revealed that there are 1347, 1467, 1523, 284, and 766 differentially expressed genes(DEGs) in these comparisons of P_C vs P_9, P_9 vs P_15, P_C vs P_15, P_A vs P_C and P_P vs P_C respectively. After performing GO annotation and KEGG pathway analysis, we analyzed the gene expression situation in purine pathway and found some key enzymes in cordycepin biosynthesis pathway and adenosine metabolic pathway. This work will contribute to a better understanding of the biosynthetic pathway of cordycepin in PH, and possibly in other Cordyceps species. It will provide a vital resource to further advance transcriptomics studies in Cordyceps species.

ID: CABMB2017_10017

Title: Royal jelly peptides: potential inhibitors of β -secretase in N2a/APP695swe cells

Author: Fan Zhen

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Abstract:

Royal jelly (RJ) is a type of natural health product with a long history of use. Royal jelly peptides (RJPs) obtained from RJ have numerous bioactivities. To study the neuroprotective effect of RJPs, major royal jelly proteins were digested into crude RJPs and subsequently purified by RP-HPLC. Purified RJP fractions were evaluated in an AD cell model, N2a/app695swe cells. Our results indicated that purified RJPs (1-9 μ g/ml) could inhibit external A β 1-40 and A β 1-42 accumulation through the down-regulation of β -secretase (BACE1) in the AD model. The modulation of BACE1 may be related to histone acetylation modification. Our results demonstrated a neuroprotective function of RJPs, which indicates that RJPs may serve as a promising agent in ameliorating A β -related pathology in Alzheimer's disease.

ID: CABMB2017_10004

Title: Identification of hepatic thyroid hormone-responsive genes in neonatal rats

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Abstract:

There have been great concerns about the possible adverse effects of environmental chemicals on the thyroid system. Disruption of thyroid hormones (T3 and T4) during the neonatal period could be deleterious, since these hormones are essential for the development. We postulated that there are target genes that are sensitive to thyroid hormones particularly during the neonatal period and that would thus be susceptible to environmental chemicals. A cDNA microarray analysis was employed to find these genes in the liver of F344 rats on postnatal day 3; thirteen upregulated and four downregulated genes were identified. Among these, Pdp2 and Slc25a25 were found to be upregulated being more sensitive to T3 than the others, whereas Cyp7b1 and Hdc were found to be downregulated even at the lower dose. Interestingly, one-third of them did not respond to T3 in adults rats (8 weeks old). When some hydroxylated polybrominated diphenyl ethers, environmental chemicals with weak thyroid hormone-like activity, were given to neonatal rats, they were indeed capable of changing the expression of Slc25a25 and Hdc. Our results demonstrated a series of hepatic T3-responsive genes that are more sensitive to hormones during the neonatal period than during adulthood. These genes are the potential targets of thyroid hormone-disrupting chemicals in newborns. Investigating these genes is also important to understand the molecular mechanisms underlying neonatal specific gene regulations by thyroid hormones.

ID: GC2017_10000

Title: Transcriptome analysis of *Bergenia purpurascens* discovers putative genes involved in bergenin biosynthesis

Author: Fenggen Guo

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Abstract:

Background: *Bergenia purpurascens* is an important medicinal plant belonging to the Saxifragaceae and its main active compounds are bergenin and arbutin. Bergenin has multiple pharmacological values of anti-tussive, anti-inflammatory, anticancer, anti-HIV, anti-arrhythmia, antiurolithic, α -glucosidase and α -amylase inhibitory, immunomodulatory, hepatoprotective and neuroprotective activities. It is mainly extracted from the rhizomes of *B. purpurascens* and has been applied in clinic. However, the mechanisms of biosynthesis and regulation for bergenin in *B. purpurascens* are considerably unknown. In addition, genomic information of this herb is also unavailable.

Results: The transcriptome dataset of leaves and rhizomes of *B. purpurascens* cultivated in Qiaojia and Xianggerila counties were constructed on the Illumina HiSeq™2000 platform. A total of 423,028,226 raw sequencing reads were generated and de novo assembled to 94,755 unigenes. Among them 44,372 and 31,447 unigenes were annotated by non-redundant protein database (Nr) and swiss-protein database (Swissprot) respectively. 15,687 unigenes were divided into 25 categories based on cluster of orthologous groups of proteins (COG), while 22,600 unigenes were classified into 45 functional groups at 3 functional levels according to the gene ontology (GO) functional classification. 14,162 unigenes were annotated in Kyoto Encyclopedia of Genes and Genome database (KEGG) and 124 metabolic pathways were found in *B. purpurascens*. 101 candidate genes involved in the last 5 steps in bergenin biosynthesis were discovered according to the bioinformatics analysis results. The temporal and spatial expressions of 14 candidate genes in various sites, stages and organs of *B. purpurascens* were analyzed by real-time quantitative PCR (qRT-PCR), while the bergenin and gallic acid contents in various sites, stages and organs of *B. purpurascens* were determined by high performance liquid chromatography (HPLC). Based on the results of

correlation analysis between gene expression amounts and bergenin or gallic acid contents, 5 putative genes encoding key enzymes for bergenin biosynthesis in *B. purpurascens* (BpDAHPS for DAHP synthase, BpDHQS for 3-dehydroquinate synthase, BpDHQD/SD for bifunctional 3-dehydroquinate dehydratase / shikimate dehydrogenase, BpUGT for UDPG glucosyltransferase, BpMT for methyltransferase) were preliminary confirmed.

Conclusion: Using next generation sequencing technology, this study firstly provides abundant genomic data for *B. purpurascens*. The putative genes involved in bergenin biosynthesis were also firstly obtained. They will provide a scientific basis for breeding new varieties of *B. purpurascens* with high bergenin contents and directly producing bergenin via biotechnology means.

ID: GC2017_10003

Title: The Role of Epigenetics on The Process of Drug resistance Development in The Mycobacterium tuberculosis

Author: Haicheng Li

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Abstract:

Drug resistance is the most important challenge for the globally control of tuberculosis. However, the mechanism involved in the process of resistance development is unclear now. The effect loss of old drugs and deficient of new drugs make the condition more serious. Here, in order to elucidate the mechanism of drug resistance and describe the evolution history of drug resistance for mycobacterium tuberculosis we construct 10 drugs resistance mycobacterium tuberculosis strains out of the standard H37RV strain by the selection of growth pressure with sub-optimized concentration of anti-tuberculosis drugs in the Lowenstein-Jensen medium through a long period culture. Then we investigated the change of epigenetics, transcriptomics between the drug resistance strains and

the control strain. Show the profile change of epigenetics underlying the process of drug resistance development through bioinformation analysis and offer clues for subsequent molecular mechanism research about drug resistance. The results of comparisons of the genes methylated in the mutant strains and the control strain show that if a gene reveals a strong methylation (coverage 10 and above) in one strain, it is most likely (98%, 331/337) also weakly methylated (coverage below 10) in another strain and for the genes methylated in every mutant strains, but not in the control strain, only about 55% (99/181) highly methylated genes are found to be weakly methylated in other strains, while for the genes, whose methylation is not shared across all the mutant strains, a strong methylation level in one strain co-occurs with a weak methylation levels in other strains at a medium frequency (83%, 129/156). These results may indicate that strongly methylated genes are epigenetically inherited from the primary strain while low methylation maybe the causes for drug resistance. Therefore, our next step was the functional analysis, using GOs. Overall, the results of GO cluster analysis indicated that genes with high methylation are characterized with more functions associated with host-microbe interactions, while low-methylated genes demonstrated enrichment of various metabolic pathways, largely of nutritional functions. Our research work supports the hypothesis that genes with strong methylation signals (detected by sequencing coverage 10x and higher), are likely to be epigenetically inherited from multiple previous generations. At the same time, the the genes with low methylation signals likely represent de novo methylation in response to the changed environment, i.e. transfer of bacteria from the hosts to the artificial medium and adaptation of the bacterial metabolism to antibiotics.

ID: CMVI2017_10010

Title: The correlation between hepatitis B virus precore/core mutations and the progression of severe liver disease

Author: Ahmed A. Al-Qahtani

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Center

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Abstract:

Viral mutations acquired during the course of chronic hepatitis B virus (HBV) infection are known to be associated with the progression and severity of HBV-related liver disease. This study of HBV-infected Saudi Arabian patients aimed to identify amino acid substitutions within the precore/core (preC/C) region of HBV, and investigate their impact on disease progression towards hepatocellular carcinoma (HCC). Patients were categorized according to the severity of their disease, and were divided into the following groups: inactive HBV carriers, active HBV carriers, liver cirrhosis patients, and HCC patients. Two precore mutations, W28* and G29D, and six core mutations, F24Y, E64D, E77Q, A80I/T/V, L116I, and E180A were significantly associated with the development of liver cirrhosis and HCC. Six of the seven significant core mutations that were identified in this study were located within immuno-active epitopes; E77Q, A80I/T/V, and L116I were located within B-cell epitopes, and F24Y, E64D, and V91S/T were located within T-cell epitopes. Multivariate risk analysis confirmed that the core mutations A80V and L116I were both independent predictors of HBV-associated liver disease progression. In conclusion, our data show that mutations within the preC/C region, particularly within the immuno-active epitopes, may contribute to the severity of liver disease in patients with chronic hepatitis. Furthermore, we have identified several distinct preC/C mutations within the study population that affect the clinical manifestation and progression of HBV-related disease. The specific identity of HBV mutations that are associated with severe disease varies between different ethnic populations, and so the specific preC/C mutations identified here will be useful for predicting clinical outcomes and identifying the HBV-infected patients within the Saudi population that are at high risk of developing HCC.

ACKNOWLEDGMENTS

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Science and Technology (KACST), National plan for Science, Biotechnology, and Innovation (NSTIP) (Project number 11-MED1430-20). This study was approved by Research Advisory Council (RAC) of King Faisal Specialist Hospital and Research Centre (KFSHRC), project number 2150008.

ID: CMVI2017_10006

Title: Hypothetical Protein BPSL3393 of Burkholderia pseudomallei is Involved in Ethanolamine Catabolism

Author: Hokchai Yam

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Abstract:

Burkholderia pseudomallei is a highly pathogenic Gram-negative bacterium that causes a lethal disease called melioidosis. This globally emerging disease is overlooked for decades due to its diverse clinical appearances and the lack of standardized identification methods. Its genome comprises approximately 30% hypothetical genes that are difficult to be functionally characterized. It is partly due to their respective mutants have no discernible. Manual securitization on hypothetical genes revealed an interesting gene designated as BPSL3393, it presumptively encodes a small protein of 10 kDa with a CoA binding domain. BPSL3393 is conserved in *B. pseudomallei* and tentatively found in other species of *Burkholderia* Genus. Taking into consideration that CoA plays a ubiquitous metabolic role in all life forms, characterization of BPSL3393 may uncover a previously over-looked metabolic feature of *B. pseudomallei*. The BPSL3393 was deleted from the genome using a double homologous recombination approach that yielded a null mutant strain without insertion of antibiotic resistance gene. The BPSL3393 mutant showed no different in growth rate with wild-type strain under growth conditions of rich and minimal media. This indicated that BPSL3393 may not be involved in the central metabolism pathway. Thus, a

largescale metabolic phenotyping was performed using Phenotype MicroArrays (Biolog). For 95 metabolic substrates tested, deletion of BPSL3393 severely impaired metabolism of ethanolamine. Concomitantly, the growth rate of the mutant was attenuated when ethanolamine was used as the sole carbon source. Further examination on transcription level of ethanolamine metabolism genes indicated that they were down-regulated upon deprivation of BPSL3393 in the genome. It is obvious that BPSL3393 functions as a positive regulator for ethanolamine metabolism. This study provides preliminary experimental evidence to prove that a hypothetical gene BPSL3393 is not remnant of evolution but it has a regulatory role in ethanolamine metabolism.

ID: CMVI2017_10000

Title: Molecular typing of Legionella pneumophila from air-conditioning cooling waters using mip gene, SBT, and FAFLP methods

Author: Shouyi Chen

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Abstract:

Legionella spp. are important waterborne pathogens. Molecular typing has become an important method for outbreaks investigations and source tracking of Legionnaires. In a survey program conducted by the Guangzhou Center for Disease Control and Prevention, multiple serotypes *Legionella pneumophila* (*L. pneumophila*) were isolated from waters in air-conditioning cooling towers in urban Guangzhou region, China between 2008 and 2011. Three genotyping methods, mip (macrophage infectivity potentiator) genotyping, SBT (sequence-based typing), and FAFLP (fluorescent amplified fragment length polymorphism analysis) were used to type these waterborne *L. pneumophila* isolates. The three methods were capable of typing all the 134 isolates and a reference strain of *L. pneumophila* (ATCC33153), with discriminatory indices of 0.7034, 0.9218, and 0.9376,

for the mip, SBT, and FAFLP methods respectively. Among the 9 serotypes of the 134 isolates, 10, 50, and 34 molecular types were detected by the mip, SBT, and FAFLP methods respectively. The mip genotyping and SBT typing were more feasible for comparison of different types of *L. pneumophila*. The SBT and

FAFLP typing methods were rapid with higher discriminatory abilities. Combinations of two or more of the typing methods enables more accurate typing of *Legionella* isolates for outbreak investigations and source tracking of Legionnaires.

Energy Engineering & Application

ID: NESD2017_10003

Title: Discussion on Energy Internet and Its Key Technology

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Abstract:

Energy and environmental problems are among the important factors restricting economic development. The development of green energy is an important measure to deal with energy and environmental problems, such as wind energy and photovoltaic. Energy Internet is an important mean to promote the transformation of the energy structure, improve energy efficiency and reduce pollution. In introduction, the energy Internet is put forward. Then the architecture and characteristics of energy Internet, such as integration, openness, intelligence and marketization of energy Internet are analyzed. Next, key technologies such as energy router, virtual power plant and network security technology are discussed. Finally, a few suggestions for the development of energy Internet is proposed, and hoped to promote the development of energy Internet.

ID: NESD2017_10004

Title: Solar Thermal Application for the Dairy Industry in Taiwan

Author: Wei-Min Lin

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Abstract:

Taiwan has been developing clean energy and solar heating for hot water production is a mature technology. The subsidy program (2000-2016) for solar water heaters means that the cumulative area of solar collectors installed was approximately 2.52 million square meters at the end of 2016, in which more than 93% have been installed in the domestic sector. Industrial heat processes represent an area for solar thermal application. This study presents field measurements for solar water heaters installed for sterilization in dairy industry. Global solar radiation can be correlated with the system's thermal efficiency reasonably well. As a pre-heating system, financial viability is validated.

ID: CEES2017_10002

Title: Effects of substituting Ni with Mn on electrochemical hydrogen storage characteristics of melt spun Mg₂Ni-type alloys

Author: Yanghuan Zhang

Affiliation: Inner Mongolia University of Science and Technology

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Abstract:

A partial substitution of Ni by Mn has been implemented in order to improve the hydriding and dehydriding kinetics of Mg₂Ni-type alloys. The nanocrystalline and amorphous Mg₂Ni-type Mg₂₀Ni_{10-x}Mn_x (x = 0, 1, 2, 3, 4) alloys were synthesized by melt-spinning technique. The structures

of the as-cast and spun alloys were studied by X-ray diffraction (XRD), scanning electron microscope (SEM) and high resolution transmission electron microscope (HRTEM). The results show that the as-spun Mn-free alloy holds a typical nanocrystalline structure, whereas the as-spun alloys containing Mn displays a nanocrystalline and amorphous structure, confirming that the substitution of Mn for Ni can enhance the glass forming ability of Mg₂Ni-type alloys. The substitution of Mn for Ni significantly improves the electrochemical hydrogen storage performances of alloys, involving both the discharge capacity and electrochemical cycle stability.

ID: PECER2017_10004

Title: Desulphurization of transportation fuels by per-formic acid oxidant using MoO_x loaded on ZSM-5 catalyst

Author: Waqas Ahmad

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Abstract:

Desulphurization of model and real oil samples was investigated using performic acid as oxidant assisted by air as co-oxidant. The catalysts used was Mo-oxide supported on ZSM-5 zeolite, which was synthesized in the laboratory and characterized by FT-IR, XRD, SEM and SSA analysis. In case of model oil, the optimum condition de-termined for complete oxidation of all the model compounds including thiophene, DBT and 4,6-DMDBT were; 60 °C, 60 min, ambient pressure and air flow rate of 100 mL/min. The oxidation reactivity decreased from 4,6-DMDBT to DBT and thiophene, which was found to follow pseudo first order kinetics. The real oil sample used in the study included untreated naphtha (NP), light gas oil (LGO), heavy gas oil (HGO) and Athabasca bitumen (Bit.). In case of NP and LGO the sulfur removal of above 78 % was attained whereas in case of HGO and Bit. samples about 60 % of desulfurization was achieved.

ID: CEES2017_10008

Title: Micro/nano Carbon Electrodes for Novel Efficient Energy Conversion and Storage Devices

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Abstract:

Flexible electronics/optoelectronics have attracted widespread attention for their light-weight, application convenience and adaptability to roll-to-roll printing process, which are significantly promising for advancing cheap, light-weight, implantable and efficient portable electronic products. Recently, fiber-shaped electronic devices are emerging as one type of flexible electronics, offering a novel strategy for developing flexible/wearable electronic devices. In this regard, fiber solar cells have advantages such as TCO-free, flexibility/weavability, outstanding 3-D light harvesting capacity and various application forms, etc., show broad application prospects. To achieve more efficient, lower cost and more durable fiber solar cells, further development of highly cost-performance electrode materials is still the key. In virtue of the excellent mechanical performance, high conductivity, low cost, light-weight, thermal/chemical stability and easy modifications, carbon fibers are utilized as electrode materials to prepare fiber solar cells. In order to acquire efficient carbon fiber-based catalytic electrode and functional photoanode, designed nano-structured catalytic film or metal oxide semiconductor nano-structured functional layer are prepared onto non-planar, microscaled and multiple carbon fiber substrates. Finally, low cost and environmental-friendly carbon fiber-based solar cells with considerable photoelectrical conversion performance were realized. Moreover, novel inexpensive flexible fiber electrochemical capacitors and rechargeable lithium-ion batteries were fabricated based on micro/nano carbon electrodes, which exhibited high electrochemical capacitance, considerable charge/discharge and stable cycling performance.

ID: CEES2017_10004

Title: Cobalt and Nitrogen Co-doped Nano-porous Carbon: Synthesis and Application for Lithium-sulfur Battery

Author: Shiqiang Luo

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Abstract:

S@C-Co-N nanoporous carbon co-doped with cobalt and nitrogen as the cathode of lithium-sulfur battery are prepared. The synthetic route is carried out via the carbonization of metal organic frameworks polyhedron ZIF-67, followed by the heat treatment with sulfur. The SEM images suggest that C-Co-N composite maintains almost the same size and polyhedron shape of ZIF-67. The XRD pattern confirms the existence of cobalt element. As cathode for lithium-sulfur battery, the S@C-Co-N composite delivers a reversible capacity of 916.6 mAh g⁻¹ at the initial cycle and 460.5 mAhg⁻¹ after 500 cycles at 0.5C, with a capacity fading of 0.09% per cycle.

ID: CEES2017_10005

Title: Synthesis of LiCoPO₄ Powders as a High-Voltage Cathode Material via Solvothermal Method

Author: Jianhuang Ke

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Abstract:

Lithium cobalt phosphate (LiCoPO₄, LCP), having a high operating potential (4.8 V vs. Li/Li⁺), a flat voltage profile and a good theoretical capacity (167 mAh/g), is considered a promising cathode material for improving the energy density of lithium-ion batteries (LIBs)[1,2]. Here we report a category of method for synthesizing LCP, the solvothermal (ST) method with

a binary solvent (deionized water: ethyl alcohol=1:1), controlling the concentration of cobalt ion in 0.05 mol/L (ST-0.05) and 0.25mol/L (ST-0.25). The material phase was apparently identified via X-ray diffraction (XRD). Observed by scanning electron microscopy (SEM), the grain size of LCP powders synthesizing by solvothermal method with two kinds of the concentration of cobalt ion were 400*400*1000 nm cuboids (ST-0.05) and 150*150*250 nm hexagonal prisms with nanoparticles (ST-0.25), respectively. Discharge capacities of LCP were 76.0 mAh/g (ST-0.05) and 94.5 mAh/g (ST-0.25), in the first cycle at 0.1 C, respectively.

ID: CEES2017_10006

Title: Improvement of the cycle performance of LiNi_{0.5}Mn_{1.5}O₄ Cathode active material through in-situ coating with poly(3,4-ethylenedioxythiophene)

Author: Jinfeng Liu

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Abstract:

LiNi_{0.5}Mn_{1.5}O₄ (LNMO)/poly(3,4-ethylenedioxythiophene) (PEDOT) composite cathode material was prepared via in-situ polymerization of thiophene monomer (EDOT), with ammonium persulphate(APS) as oxidizing agent, p-toluenesulfonic acid(PTSA) as dopant. The morphology, amount of PEDOT coating, electrochemical properties of LNMO/PEDOT were characterized by scanning electron microscopy (SEM), thermogravimetric analysis (TGA) and galvanostatic charge and discharge tests. The result shows that the composite material shows better cycle performance than uncoated.

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Title: Improving the electrochemical stability of

Pt/C catalysts in alkaline media by high surface area carbon support modification

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Abstract:

Polymer electrolyte fuel cells (PEMFC) are promising devices for converting the energy of chemical bonds into electrical power. The main problem of PEMFC is the degradation of cathode platinum-containing oxygen reduction reaction (ORR) catalysts, which includes several mechanisms. This leads to a decrease in the electrochemical surface area of the active component and its mass activity. Another problem is the high content of platinum, which is required to increase the rate of the ORR on platinum in an acidic medium. A promising approach to reducing the content of platinum is to carry out the reaction in an alkaline medium, which is now possible with the use of anion-exchange membrane fuel cells. In this case, non-platinum transition metal catalysts show activities in the cathodic ORR comparable to those of platinum, which allows a significant reduction in the content of platinum. Despite the great progress in the field of non-platinum catalysts in anodic electrooxidation of hydrogen, platinum-based electrocatalysts remain the most optimal in the ORR. For the commercialization of such devices, research is needed on the stability of such catalysts. It should be noted that while the stability of platinum based catalysts in acidic medium has been extensively studied, little work has been devoted to studies of the stability of Pt/C catalysts in an alkaline medium. For a high degree of use of platinum, the size of its particles should not exceed 3-5 nm. The specific surface of the most common used support Vulcan XC-72 is rather low (230 m²/g), which

does not allow obtaining highly dispersed active component in Pt/C catalysts with high (up to 40 wt.%) platinum content. The solution to this problem is to use carbon supports with a specific surface area of at least 400 m²/g.

The main goal of this work is to increase the specific surface area of carbon support to produce highly dispersed platinum nanoparticles that are stable to electrochemical oxidation in an alkaline medium. In this work, a series of 40 wt. % Pt/C catalysts based on commercial and modified carbon supports, and their stability, as well as the stability of carbon supports were studied in an alkaline (0.1 M NaOH) medium using accelerated stress test protocol (potential scanning in the 1-1.5 V RHE range up to 1000 cycles). The obtained materials were studied by a set of physicochemical (Raman spectroscopy, XPS, TEM) and electrochemical methods. It is shown that the modification with methane (at 900 °C for 15 minutes) of the Ketjen black DJ-600 carbon support results in the deposition of highly-structured carbon on the support surface, showing the specific surface area decreases from 1420 to 620 m²/g. A 40 wt. % Pt/C catalyst based on this support is characterized by low size of Pt nanoparticles (dPt ~ 3 nm), and showed the electrochemical stability closed to that of the 40 wt. % Pt/Vulcan XC-72 catalyst, having a specific surface 2.7 times lower (SBET = 230 m²/g). The TEM method was used to study catalysts before and after electrochemical oxidation. It is shown that surface diffusion and coalescence of platinum nanoparticles are the main mechanisms of degradation of the active component.

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Part V Instructions for Presentations

Oral Presentation

Devices Provided by the Conference Organizing Committee:

- Laptops (with MS-office & Adobe Reader)
- Projectors & Screen
- Laser Sticks

Materials Provided by the Presenters:

- PowerPoint or PDF files

Duration of each Presentation:

- Regular Oral Session: 15-20 Minutes of Presentation
- Invited Speech: 45 Minutes of Presentation

Part VI Hotel Information

About Hotel

International Asia-Pacific Convention Center Sanya is a five star standard luxury hotel, which locates beside the seashore, and is the ideal place for vacation and conference. The hotel has 254 luxury and comfortable rooms, and 16 conference rooms in different sizes. The conference rooms can accommodate people from 20-1000 and totally square 5400m2. Housing, dining, recreation facilities... everything needed is ready, Even National initiative seawater swimming pool, sea recreational centre and so on, which make you a pleasant vacation. High-speed net connectors are equipped in the houses and service of renting laptops is provided, all these give you a convenient office atmosphere while you are on vacation.

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Tel: (86 898) 88332666

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How to Get to the Hotel

Downtown of Sanya: 30 minutes ride

Sanya Phoenix Airport: 15 minutes ride

Sanya International Golf Club: 20 minutes ride

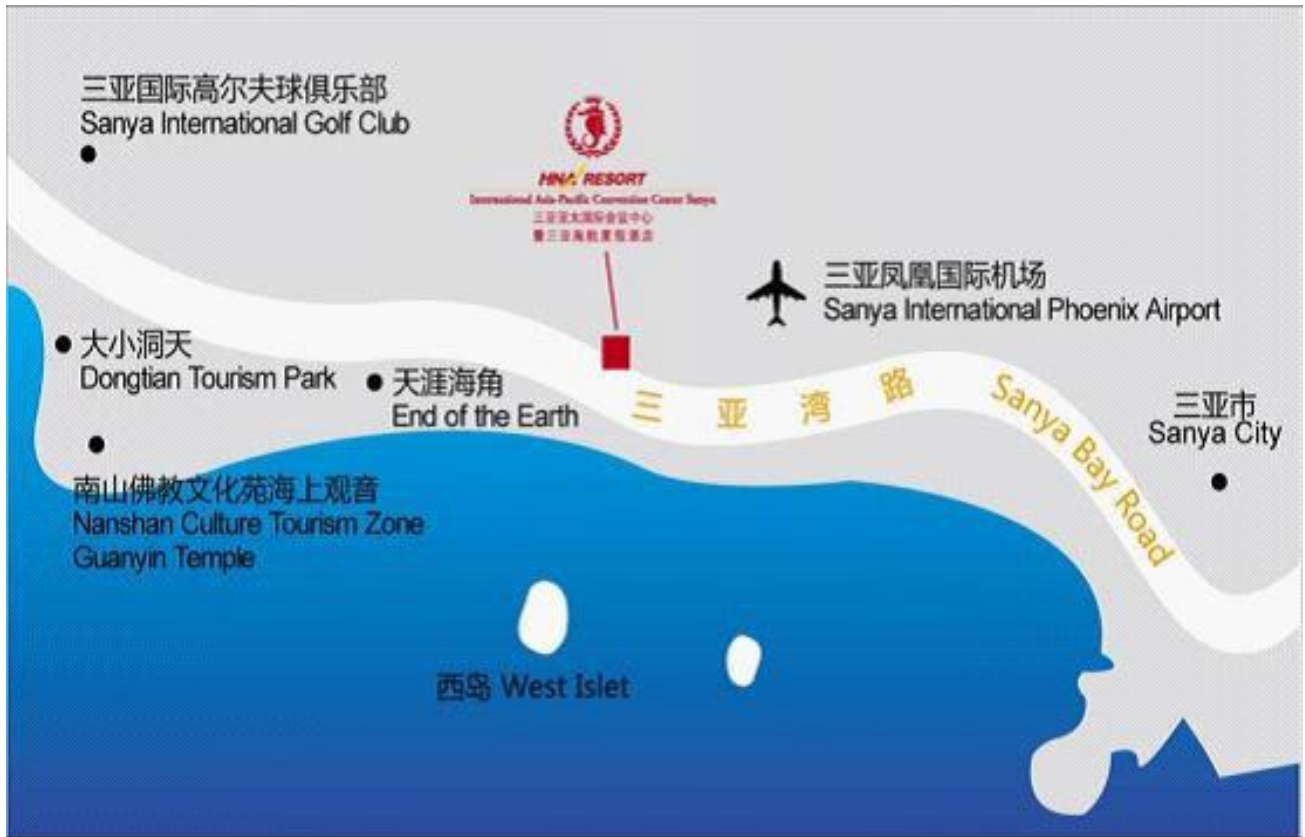
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