SciUn Research Journal

CONFERENCE PROCEEDING

An Inter-Disciplinary Conference

International Conference of Interdisciplinary Sciences (ICIS-2017)

July 16-17, 2017

Topic Sessions for ICIS-2017

- ✓ **Physical Sciences**
- ✓ **Agricultural Sciences**
- ✓ **Health Sciences**
- ✓ **Engineering Sciences**
- ✓ **Biological Sciences**
- ✓ **Management and Social Sciences**
- ✓ **Ethical and Law Issues**
- ✓ **Chemical Sciences**
- ✓ **Mechatronics**

VENUE: CONCEPT INSTITUTE OF TECHNOLOGY, INDIA

ORGANIZATION: PHENOME RESEARCH FOUNDATION, INDIA

ICIS
Conference
2017

1ST International Conference of Interdisciplinary Sciences

Proceedings of the
International Conference of Interdisciplinary Sciences
July 16 -17, 2017

Organized by

Phenome Research Foundation, Varanasi India

Edited by

Mr. Abhishek Mishra

Sub-Editors

Mr. Abhishek Sinha

Mr. Brajesh Pratap Singh

ICIS
Conference
2017

ABOUT ICIS

"International Conference of Interdisciplinary Science (ICIS)" is an initiative taken by Phenome Research Foundation to provide a platform that will stimulate discussion on key interdisciplinary topics in the fields of engineering, biological, physical, agricultural management and social sciences and many more.

ICIS-2017 will take place in Varanasi, India during July 16-17, 2017. ICIS-2017 will consist of 3 Sessions of many presentations:

Session 1: Breakthroughs in Basic Research via modern technologies (NGS, Cloud Computing, Big Data analysis)

Session 2: Innovations in Biomarker Research (Diagnostics, Molecular, Immunological, Medicine, Engineering)

Session 3: Human up gradation (Social reforms, Ecofriendly environment, Organic forming)

In ICIS-2017, all qualified abstracts will be published as conference proceedings in following journals-

MP Research Journal (ISSN :0974-1917)
SciUn Research Journal (ISSN : SCIUN, Open Access Journal);
http://sciunrj.org/.

About the Host:

Concept Institute of Technology is managed by Concept Educational Society (CES), Registered under the society act. Concept Institute of Technology equips today's youth with the skills, the attitude and the confidence to stride ahead and be a leader in their dream careers. The Institute also promises to make a brilliant professional with cutting edge technology strength and management skills.

Address: IVth floor, Shiva Complex, Opposite Kuber Complex, Rathyatra Crossing, Varanasi - 221 010, Uttar Pradesh (India)
E-mail: conceptvns@gmail.com, info@conceptvns.org
Land Line: (0542) - 6458474

Phenome Research Foundation, Varanasi, India
http://phenomeresearch.com

Conference
Convenor Message

It is our great pleasure and privilege to welcome you to join the ICIS-2017, which will take place in Varanasi, India during July 16-17, 2017. This year's theme is "Cutting-edge Research of Interdisciplinary Science and Technologies for Human up gradation".

ICIS-2017 features a very strong technical program, mainly focused on: breakthroughs in the basic research, new discovery, emerging areas for medicine applications, robust technology development in engineering, cutting-edge biotechnology and social reforming via modern knowledge. ICIS-2017 aims to provide a platform for all experts from academia and industry to discuss latest hot researches and achievements.

With the participation of outstanding international experts, we hope productive discussions would stimulate new creative ideas to translate new discoveries into better practice and application. ICIS-2017 will continue to build upon the success of past 2 years, offering a top-notch scientific program created by international experts in related fields.

We look forward to seeing you in Varanasi in 2017 for this influential event!

Sincerely Yours,

Anshuman Mishra

Dr. Anshuman Mishra

Conference Chairperson of ICIS-2017
Visiting Research Scientist

Phenome Research Foundation, Varanasi, India
http://phenomeresearch.com
http://sciunrj.org/announcement/
Corresponding Address:
Prasad College
Pandeypur, Varanasi, India (221002)
Mobile (India): +91-8299740184 / +91-7068119291; E Mail: conference.icis@gmail.com

Phenome Research Foundation, Varanasi, India
http://phenomeresearch.com

Conference Chairperson Message

I am extremely glad to know that, the Phenome Research Foundation (PRF) is organizing the "International Conference of "Inter-disciplinary Science" on July 16-17, 2017 in collaboration with SciUn Research Journal.

I earnestly trust that, this conference will provide an effective platform for the practicing Researchers and Information Scientists to share their experience and to discuss the issues and challenges concerning in the field of inter-disciplinary science. I have, therefore, the strong conviction that, the deliberations of the conference would be of immense help to contemporary Researchers and Scholars.

May the conference be enriching, fruitful and memorable. I wish the conference a success.

Sincerely Yours,

Dr. Raghvendra Raman Mishra
(Assistant Professor)
Medical Lab Technology
Banaras Hindu University, Varanasi
Uttar Pradesh, India

BIOGRAPHY

Dr. RAGHVENDRA RAMAN MISHRA
Ph. D. Biomedical Technology, Institute of Medical Sciences, Banaras Hindu University, VaranasiAssistant Professor, Medical Lab. Technology, DDU Kaushal Kendra, Banaras Hindu University

Dr. Raghvendra Raman Mishra, is Assistant Professor in Medical Lab. Technology Course of DDU Kaushal Kendra, RGSC, Banras Hindu University from academic session 2016. Dr. MishrarecivedhisMasters degree in Biomedical Technology (2005 fromJiwaji University Gwalior.He completed his project from Molecular Virology Laboratory, School of Life SciencesJawaharlal Nehru University, New Delhi. He earned his Ph. D. (2009) in Biomedical Technology from Molecular Oncology Laboratory, Department of Surgical oncology Institute of Medical Sciences, Banaras Hindu University, Varanasi with the Junior Research Fellowship of University Grant Commission New Delhi and Senior Research Fellowship of Indian Council of Medical Research. He then went to Thyrocare Technologies Limited, Navi Mumbai as Officer-Central Processing Lab (2010). In 2011 he did Post Doctorate in Microbiology from Bacteriophage Research Laboratory,Department of Microbiology,Institute of Medical Sciences, Banaras Hindu University, Varanasi with the funding of Council of Scientific and Industrial Research, New Delhi. In 2013 he joined Ashoka Institute of Technology & Management (Approved by AICTE, New Delhi, and Affiliated to Dr. APJ Abdul Kalam Technical University, Lucknow, Uttar Pradesh) as Assistant Professor & Department of Biotechnology andCarporate Relation Manager, CRC-AITM Varanasi.With these 11 years of research and teaching experiences, his area of specializationisMedicalLabTechnologyincludingsubjectssuch as Biotechnology, Bioinformatics, Cancer Biology, Microbiology, Molecular Biology, Biomedical Engineering & Technology. He had published more than 30 National and International Peer Reviewed Papers with 153 citations having 8 h-index with 5 i10 index among his field of scholars. He gain honor as speaker, guest speaker and presenter of paper in more than 25 National&Inter National conference/seminar/workshop.He had organized three national seminars and two workshop on Biomedical and Biotechnology topics. He had enrolled five Ph. D. students and active co-supervisor in a DST, Government of India funded project of Rapid Grant for Young Investigator (2010). He did course of Basic in Pranic Healing from All India Pranic Healing Foundation Lucknow, India (A unit of World Pranic Healing Foundation Inc, Manila) &"General Course on Intellectual Property Right" from World Intellectual Property Organization, (WIPO). He is Life Time Member of "*The Cytometry Society"* Hyderabad & "All India Medical Laboratory Technologists Association" New Delhi and Life Time Member of "International Association of Advanced Materials",Mjärdevi Science Park, Teknikringen 4A, S58330, Linköping, Sweden, Membership No. 799141911701.He appointed as Ambassador All India Medical Laboratory Technologists Association" .

Phenome Research Foundation, Varanasi, India
http://phenomeresearch.com

Conference
International Chairperson
Message

I am delighted to know that “The Phenome Research Foundation (PRF)” is putting their first step towards academia very thoroughly by organizing the first “International Conference of Inter-disciplinary Science (ICIS-2017)” on July 16-17, 2017 with alliance to SciUn Research Journal. I have been in interaction with the team PRF since its inception and quite overwhelmed by their progress with short span of time. I am optimistic that PRF team will establish itself as a worldwide reference for the dissemination of high-quality research and publication in the field of science, and for fostering interaction and exchange of ideas though conference series.

I am enchanted to listen from the conference convener that the enormous submission of abstracts from different countries and continents. The high number of submissions provided an admirable opportunity for a high-quality program, but also demanding and laborious paper evaluation process by eminent reviewers.The success of the conference would not have been conceivable without the commitment and hard team work.

Thanks to all for joining us and making the conference successful. Hope to see you all along with others fellows in next conference.

Sincerely Yours,

Dr. Manish Mishra
Associate Professor, Department of Biochemistry and Genetics
Trinity School of Medicine, Ratho Mill,
St. Vincent and the Grenadines (WI)

Phenome Research Foundation, Varanasi, India
http://phenomeresearch.com

Conference
International Chairperson
Message

The 1st International Conference of Interdisciplinary Science (ICIS-2017) supported by Phenome Research Foundation, Varanasi, India is helpful in promotion of scientific research and idea through interdisciplinary platform.

The theme of the Conference ‘Science without money” will underpin the need for collaboration and cooperation of individuals from a wide range of professional backgrounds. Varanasi is an exceptional location for the Congress. It is renowned as one of the world’s oldest cities, with the sparkling river Ganges providing a unique spiritual atmosphere.

The ICIS-2017 Conference will provide a wonderful forum to refresh knowledge and explore the innovations in science. The Conference will strive to offer plenty of networking opportunities, interaction with the leading scientists and researchers.

With best wishes,

Dr. Parmit Kumar Singh
ICIS 2017 International Conference Chair
Scientists
Dana-Farber Cancer Institute
United state of America

Conference
International Chairperson
Message

It gives me great pleasure to extend my sincere and hearty felicitation to the organizers and participants of the 1st International Conference of Interdisciplinary Science (ICIS-2017) organized by Phenome Research Foundation, Varanasi, India. I want to congratulate the organizers who have put this conference together for the purpose of dissemination of scientific knowledge based on verified information. The abstracts are rich and vividly show the ingenuity of the contributors.

I wish you all fruitful deliberations, and a great time of sharing and networking.

Enjoy the serenity of Varanasi and be safe.

Warm greetings from Nigeria!

Dr. Ebenezer Idowu O. Ajayi
Assistant Professor
Biochemistry Department
Osun State University
Osogbo, Nigeria

Conference
National Chairperson
Message

I am very much delighted to know that the Phenome Research Foundation (PRF) is going to organize their first ever “International Conference of Inter-Disciplinary Science (ICIS-2017)” during July 16-17, 2017. I am also pleased to know that the conference is supported by the SciUn Research Journal towards publishing its proceedings. This is an emerging step towards bringing various interdisciplinary scientific cum academic minds, not only to showcase their works but also to promote collaborations, exchange of ideas, initiating scientific ventures through industry-academia tie-ups etc. all-together on a common platform.

The idea of bringing multi-disciplinary researchers together is a commendable effort to work towards promoting the Next-Gen Scientific and Technological innovations, which, otherwise cannot be achieved remaining segregated in a single domain. I believe the conference will attract high attention of the research communities all over the world and receive outstanding research works to present and publish. I also believe that all the delegates (both speakers and participants) will have extremely wonderful two days of brainstorming sessions and exchange of productive ideas covering varied disciplines of science and technology.

I extend my heartfelt congratulations to the organizers of ICIS-2017 for this wonderful endeavor. I trust and earnestly wish for the conference to be a great success.

With all the best wishes,

Shri. Biswajit Roy
Scientist - C Gr-IV [2] , Information Technology Group& Bioinformatics Centre
CSIR-Centre For Cellular and Molecular Biology (Ministry of Science & Technology, Govt. of India)
Habshiguda, Uppal Road, Hyderabad, India
[Email :broy@ccmb.res.in, biswajittezu@yahoo.co.in]

Phenome Research Foundation, Varanasi, India
http://phenomeresearch.com

MESSAGE

It is a great pleasure and an honor to extend to all a warm invitation to attend the 1st International Conference of “Inter-disciplinary Science”, to be held July 16 – 17, 2017 at the Concept institute of Technology, Varanasi, India.

The 2017 Conference is jointly organized by the Phenome Research Foundation (PRF) and SciUn Research Journal .The theme of the 2017 Conference ‘Inter-disciplinary Science’ that will underpin the need for engineering in different branch of Sciences.
Varanasi is a holy city of India. It is renowned as one of the world’s oldest cities blessed by Kasi Viswanath Temple and holy river Ganga.

The ICIS 2017 Conference will provide a wonderful forum for you to refresh your knowledge base and explore the innovations in Inter-disciplinary Science. The Conference will strive to offer plenty of networking opportunities, providing you with the opportunity to meet and interact with the leading scientists and researchers, friends and colleagues as well as sponsors and exhibitors.
We hope you will join us for a symphony of outstanding science, and take a little extra time to enjoy the spectacular and unique beauty of this region.

Sincerely Yours,

Dr. PRAGYA MISHRA
CEO, *Phage-X Technologies Private Limited, Sorao Allahabad*

CONTENT

KEYNOTE SPEAKERS

Dr. Om Prakash Singh

Dr. Om Prakash is aimmunologist and epidemiology biologist whose research focuses on the immunoepidemiology of deadly diseases Kala-azar (Visceral Leishmaniasis) in endemic region of India. He is the scientist in Institute of Medical Sciences, Banaras Hindu University in Varanasi.

Dr. Paresh Kulkarni

Dr. Pareshis a biochemist whose research focuses on the prediction of macromolecular structures and functions. He is the Assistance Professor in the Institute of Medical Sciences, Banaras Hindu University in Varanasi.

Dr. Parmit Kumar Singh

Dr. Permit Kumar Singh is a molecular and computational biologist whose research focuses on the prediction of structures and functions of HIV diseases. He is the Scientist in NIH.

Mr. Guy Mollett

Mr. Guy is a clinical genetics and medical biologist whose research focuses on the infectious diseases. He is working in the London School of Tropical Medicine and Hygien, UK.

Dr. Santosh Kumar Singh

Dr. Santosh is a molecular biologist whose research focuses on the molecular structures and functions. He is independent PI and researchers in the Molecular Biology Unit of Institute of Medical Sciences, Banaras Hindu University in Varanasi.

Dr. Puja Tiwari

Dr. Puja is a molecular and entomology biologist whose research focuses on the prediction of disease based on epidemiology and entomology research analysis.She is the Scientist in Medicine department of Institute of Medical Sciences, Banaras Hindu University in Varanasi.

Mr. Biswajit Roy

Mr. Biswajit Roy is a computational biologist whose research focuses on the big data analysis. He is the scientist in the CSIR-Centre for Cellular and Molecular Biology, Hyderabad, India.

Organizing Committee ICIS-2017

Conference Convenor

Dr. Anshuman Mishra
Visiting Resesrch Scientist
Phenome Research Foundation, Varanasi, India

Conference Chairperson

Dr. Raghvendra Raman Mishra
Assistant Professor, Medical Lab Technology
Banaras Hindu University, Varanasi Uttar Pradesh, India

International Chairperson

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Professor and Head,Tribhuwan University,
Kathmandu, Nepal

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Professor ,Centro de Biociências, Universidade Federal do Rio Grande do Norte,
Natal, Brazil

Dr. Ebenezer Idowu O. Ajayi
Assistant Professor ,Osun State University,
Osogbo, Nigeria

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Scientist ,IICB (Council of Scientific and Industrial Research)
Kolkata, India

Dr.Aditya Nath Jha

Scientist , Sickle Cell Institute, Raipur
Chhattisgarh, India

Dr. Dinesh Chandra Upadhyay
Professor ,State Law College, Bhopal
Madhya Pradesh, India

HILIGHTED ABSTRACT

Dr. Shravan Kumar Singh

Biography- *Dr Shravan Kumar Singh has completed Doctorate in Biochemistry from CDRI Lucknow. Presently working as a scientist 'C' at Institute of Nuclear Medicine and Allied Sciences, Delhi. Currently working on development of radiation countermeasures using radioresistant bacteria against radiological emergency that is part of DRDO project 'RAKShAK-TD-15/313'. His area of research is development of radio protector drug, DNA Damage and mitochondrial response. He has published/presented more than 25 papers in journal/ symposium/conference.*

ABSTRACT

Bioinformatics analysis of big OMICS data using open source bioinformatics software: An approach of scientific research without money

Shravan Kumar Singh, Raj Kumar

Affiliation: Division of Radio protective Drug Development and Research (RDDR), Institute of Nuclear Medicine and Allied Sciences (INMAS-DRDO), Brig. S.K. Mazumdar Road, Delhi-110054.
*Corresponding *E-mail address*: shravanrb@gmail.com

The exponential growth of information technology and revolutnary advancement in the software development is the central key of the interdisciplinary scientific research. Bioinformatics is an interdisciplinary research field that combines biology, mathematics, statistics and computer science into a broad-based field that will have profound impacts on all fields of biology. Understanding health and disease requires a detailed analysis of molecular interaction and events that determine the human physiology and health status. Big data base generated by using genomic, transcriptomic, proteomic and metabolomic bench work technology. Analysis of these big data to identify the biological function, interaction, pathway, biological network and model formation is done by various open source bioinformatics software as well as commercially available software. This type of interdisciplinary approaches of science and big data analysis of omics profiling can be used to manage precision health and disease. This is an opportunity and possibility that biological research can be done without money through cell phone and internet.

Key words: *Bioinformatics, Open Source, Open Access, Free Software*

YOUNG SCIENTIST AWARD

Dr. Sheikh Nizammudin

Biography- *Dr. S. Nizammudin is youngest bioinformatician and clinical researcher from CSIR-Centre for Cellular and Molecular Biology, Hyderabad, India. His interest is to understand the role of DNA variations in different diseases and their implication in personalized medicine. He has obtained his PhD fromCSIR-Centre for Cellular and Molecular Biology, Telangana, India under supervision of Dr. K. Thangaraj, on Project "Pharmaco-genomics diversity of Indian populations: Clinical perspectives of Myasthenia gravis". He has completed his M.Sc. from Department of Biotechnology, University of Jammu, J&K, under supervisionof Dr. B.K. Bajaj on Project "Identification, characterization and partial purification of cellulase and cellulase producing bacteria"*

Genome-wide analysis correlates with extreme constitution type of Ayurveda

Sheikh Nizamuddin

(KumarasamyThangaraj group) Council of Scientific and Industrial Research-Centre for Cellular and Molecular Biology, Hyderabad, India

ABSTRACT

Ayurveda is based on the concept of 3 major constitutional types (Vata, Pitta and Kapha) defined as "Prakriti" and state that individuals with balanced doshaPrakriti (according to body constitution) remain healthy while unbalance results to the disease. Concept of Prakriti and its relationship with genomics was hypothesized over a decade but the association of genomic variations with Prakriti classification was lacking. In the present talk, I will discuss about our first attempt to classify the Prakritis using genome-wide SNP and to provide a scientific basis in Prakriti classification. After screening 3416, we selected 262 well-classified male subjects (>60% of one predominant Prakriti) and genotyped on Affymetrix 6.0. Of which, 17 were excluded in quality control filtering with dm.all_qc< 0.83. To increase the statistical power, we generated Indian specific haplotype reference panel for imputation of missing genotype in 245 subjects and obtained 791,186 SNPs with $0.95 \le R2 \le 1$. After excluding 40 outlier samples with principal component analysis (PCA), we observed 52 SNPs ($p \le 1\times10{-}5$) were significantly different between Prakritis, without any confounding effect of stratification. Subsequently, we found KLF6 (rs17731), PGM1 (rs2269238, rs2269239, rs2269240 and rs2269241) and rs10866665 correlates with phenotype of Kapha, Pitta and Vata as described in "Caraka Samhita". It suggests that classification of subjects in Ayurveda has a genetic basis.

Keywords: *genome-wide SNP, statistical power, component analysis (PCA)*

TRACK OF ABSTRACT

Abstract ID: ICIS A01

Interdisciplinary approaches of science and technology in current scenario of health science

Shravan Kumar Singh , Raj Kumar

Division of Radioprotective Drug Development and Research (RDDR),Institute of Nuclear Medicine and Allied Sciences (INMAS-DRDO), Brig. S.K. Mazumdar Road, Delhi-110054.

ABSTRACT

The health science research paradigm changes from generalized medicine to personalized medicine and the diagnosis of disease paradigm changes from generalized biochemical test to specific molecular test. This advancement in the health science is possible due to the exponential growth of technology and advancement in the instrumentation development that is the outcome of the interdisciplinary approaches of science and technology. Understanding health and disease requires a detailed analysis of molecular interaction and events that determine the human health. System biology is an interdisciplinary study that focuses on the holistic understanding of the complex molecular interactions including genomics, transcriptomics, proteomics and metabolomics in biological systems. This interdisciplinary system biology approach was used in the investigation of the molecular mechanisms of radioprotection offered by radioresistant bacterial metabolite RKIP006 in c57bl/6 mice. Overall, our results demonstrate a global and system wide level of molecular and cellular changes occur during radiation exposures and its modulation by bacterial metabolite RKIP006. This type of interdisciplinary approaches of science and big data of omics profiling can be used to manage precision health and disease.

Keywords: *System Biology, Precision Health, OMICS technology, Bioinformatic*

Abstract ID: ICIS A02

Morphometric analysis of Naina – Gorma river basin, Rewa district, M.P., India for watershed management

Vimala Singh*

GIS &RS Division, Department of Geography, University of Allahabad, Allahabad, India.

* current address DTRL, DRDO, New Delhi

ABSTRACT

Today's there is water crises in all over world and it will not be much more to say that there will be going to happen third world war for water in nearby future. So, watershed management is necessary to save the water for irrigation, public purpose and flood management. In the present study, morphometric analysis has been carried out to assess the drainage characteristics of Naina – Gorma river basin of India for watershed management. The basin is mostly having dendritic to sub-dendritic nature. There is gradual decrease in bifurcation ratio of successive orders from one order to next and this result shows the differences in rock types and stage of development. The highervalues for lower stream orders indicates that the lower streams are mostly found in mountainous region and highly dissected areas where as the low bifurcation ratio approaching a value of in higher order streams, indicates the flow of these streams in a flat to rolling terrain. The drainage density ranged from 1.54 to 1.86 and stream frequencies ranged from 1.67 to 2.54 in Naina- Gormariver sub-basins. The lowdrainage density and stream frequency indicates higher recharge of groundwater and a higher transmissibity of aquifers. The low drainage density ranged from 1.54 to 1.86 for sub-basins and low stream frequencies ranged from 1.67 to 2.54 in Naina – Gormariver sub-basins, indicating a higher recharge of groundwater.

Keywords:_Morphometric analysis, Bifurcation ratio, Stream frequency, Drainage density_

Abstract ID: ICIS A03

Antiapoptotic protection of *Bombacopsisbuonopogense*leaf extracts against perturbation of liver mitochondrial membrane permeability transition pore opening by cigarette butt leachate, *in vitro*

[1]Ajayi E. I. O.,[2]Sobulo O. B.[1]Okoye O. A.[1]

1Bioenergetics, Hormesis and Mitochondria Genetics Research Group, Biochemistry Department, Faculty of Basic and Applied Sciences, Osun State, University, P. M. B. 4494, Osogbo, Nigeria.

2Ebelola Bioenergetic Solutions, Km 1, Osogbo-Ilesa Express Way, Kajola, Osun State.

ABSTRACT

The antiapoptotic effects of the ethanol extract of B.bounopogense leaf on liver mitochondrial membrane permeabilization, in vivo, its protective effects against the perturbation of the pore opening by cigarette butt leachate, in vitro, and possible hepatoprotection in female Wistar rats were investigated. The leaves were collected, air-dried, powdered and extracted in 95% solvent using Soxhlet extraction. The extract was concentrated to a sticky mass using rotary evaporator. Twelve female rats were randomly assigned into control and 1000mg/kgB. bounopogense-treated groups and acclimatized for 2 weeks followed by administration of the ethanol extract for 21 days through oral gavage. The animals were sacrificed by cervical dislocation; the livers were excised for mitochondria isolation by standard protocols. Decreases in photometric absorption were recorded at 540nm over 12 minutesina UV-Vis spectrophotometer. The effects of the hexane extract of the leaf were also investigated on normal rat liver MMPT pore opening, in vitro. Results showed that the extract inhibited pore opening both in the absence and presence of exogenous Ca2+.Interestingly, MMPT pore opening by 200and 600µg/ml cigarette butt leachate was mitigated in treated rats in the presence of Ca2+, in vitro. Similarly in the presence of Ca2+, 200 and 600µg/ml hexane extract of theleaf induced pore opening, while the extent of poree opening by cigarette butt leachate at similar concentrations was significantly lower, in vitro.The ethanol extract significantlydecreasedAST, ALT and direct bilirubin, in vivo; thus indicating the possibility of not being toxic to the liver.

Keywords: *Mitochondrial Membrane Permeability Transition Pore, cigarette butt leachate, Bombacopsisbuonopogenseleaf extract, liver function*

Abstract ID: ICIS A04

Immuneregulatory mechanisms in Visceral Leishmaniasis pathogenesis

Bhawana Singh

(Prof. Shyamsundar Group)

Department of Medicine Institute of Medical Sciences, Banaras Hindu University, Varanasi, India

ABSTRACT

Immune cells have a spectrum of functions ranging from antibody production to antigen presentation and have additional vital roles in immune mechanisms. There has been need for understanding disease biology which gave rise to the concept of T and B-cell immunology in VL. We have explored the role of B-cell and T-cell immune dysfunctions in visceral leishmaniasis (VL) pathogenesis in terms of the phenotypic and functional properties of these cells during the course of VL as compared to healthy controls. Anti-leishmanial treatment was associated with gradual restoration of the functional features of immune cells. Therefore, this study indicated for impaired immune functions and pathological consequences in human VL paving the way for exploiting the immunotherapeutic strategy for disease intervention.

Keywords: *visceral leishmaniasis, immunotherapeutic, B-cell and T-cell*

Abstract ID: ICIS A05

Chemical reprogramming of Somatic cell to CiPSC (chemical induce pluripotent stem cells) for Various therapeutics

Digvijay Singh

Department of Chemical Biology, Indian Institute of Chemical Technology, Hyderabad, India

ABSTRACT

To reprogram somatic cells or progenitor cell to CiPSC (chemical induce pluripotent stem cells) using small molecules via targeting the various signaling mediators in presence of feeder free medium.Replacement of core pluripotency factor (Oct-4, Sox-2, KLF-4 and c-Myc) with small molecule lead to reprogramming. Small molecules inhibit or activate the various signaling pathway and play role in reprogramming. Recently reportd that VC6TFZ (VPA block the histone acetylation CHIR and Licl block the GSK3, 616452 block the TGF/activin /nodal signaling) tranylcypromine inhibitor of HDM,Forskolin (FSK), 2-Methyl-5-hydroxytryptamine (2-Me-5HT), and D4476 are chemical substitutes to replace oct-4,sox-2,KLF-4 and c-Myc, and reprogram the MEF (mouse embryonic fibroblast) in to CiPSCPingpingHou et al 2013. But the full chemical reprogramming of human iPSC is unknown. The human ESC self renewal supported by wnt activator BIO and the FGF2, also cooperate with Activin/SMAD2/3 for high level expression of Nanog at the same time also activate the PI3K/AKT for survival of human ESC.

Keywords: *VC6TFZ, MEF, PI3K/AKT, D4476*

Abstract ID: ICIS A06

Transposable elements responsible for genetic instability (diversity and evolution)

Anshuman Mishra

(Prof. Heui Soo-Kim group)

Genetic Engineering Institute, Pusan National University, Busan, Republic of Korea

ABSTRACT

Mobile genetic elements (MGE) are a type of DNA that can move around within the genome. They include Transposons (also called transposable elements; TEs), which have the ability to replicate and move from one point in the genome to another point .(TEs) are very abundant and ubiquitous in all living organisms and comprise over 50% of the mammalian genome. TEs participate in nonallelic recombination's that generate both germ-line and somatic mutations. These mutations produced into genes or intergenic regions, by deleting genetic material or by rearranging chromosomes by insertion mechanism.SometimeTEs can generate harmful mutations which have ability to cause dysfunction and disease in host organisms. Any exacerbating the deleterious nature of TEs, can effect on the protein production and generate genetic instability via human genetic diseases and various cancers. New research and findings suggests that TEs also participate and impart influence in genetic diversity and human evolution. Therefore, study of TEs will have possibilities of clinical usefulness and evolutionary perspective for future research.

Keywords: *Transposons, Human genome, Evolution, Clinical disease*

Abstract ID: ICIS A07

Genome-wide analysis correlates with extreme constitution type of Ayurveda

Sheikh Nizamuddin

(Kumarasamy Thangaraj group)

Council of Scientific and Industrial Research-Centre for Cellular and Molecular Biology, Hyderabad, India

ABSTRACT

Ayurveda is based on the concept of 3 major constitutional types (Vata, Pitta and Kapha) defined as "Prakriti" and state that individuals with balanced doshaPrakriti (according to body constitution) remain healthy while unbalance results to the disease. Concept of Prakriti and its relationship with genomics was hypothesized over a decade but the association of genomic variations with Prakriti classification was lacking. In the present talk, I will discuss about our first attempt to classify the Prakritis using genome-wide SNP and to provide a scientific basis in Prakriti classification. After screening 3416, we selected 262 well-classified male subjects (>60% of one predominant Prakriti) and genotyped on Affymetrix 6.0. Of which, 17 were excluded in quality control filtering with dm.all_qc< 0.83. To increase the statistical power, we generated Indian specific haplotype reference panel for imputation of missing genotype in 245 subjects and obtained 791,186 SNPs with $0.95 \leq R2 \leq 1$. After excluding 40 outlier samples with principal component analysis (PCA), we observed 52 SNPs ($p \leq 1\times10^{-5}$) were significantly different between Prakritis, without any confounding effect of stratification. Subsequently, we found KLF6 (rs17731), PGM1 (rs2269238, rs2269239, rs2269240 and rs2269241) and rs10866665 correlates with phenotype of Kapha, Pitta and Vata as described in "Caraka Samhita". It suggests that classification of subjects in Ayurveda has a genetic basis.

Keywords: *genome-wide SNP, statistical power, component analysis (PCA)*

Abstract ID: ICIS A08

Genetic influence of Vitamin-D in Indian Infectious disease

Sunil Kumar Tripathi, Sheikh Nizamuddin, KumarasamyThangaraj

Council of Scientific and Industrial Research-Centre for Cellular and Molecular Biology, Hyderabad, India.

ABSTRACT

VDR is important components of human immune system (T-lymphocytes, neutrophils and antigen-presenting cells, such as macrophages and dendritic cells). 1,25D play key role in various modification and alteration in Immune components (inhibition of dendritic cells and T-cell proliferation). Study shows that 1,25D suppressor of antigen presenting cells and further inhibit Th1 cells. Itssignaling represses the transcription of genes encoding key T-helper 1 (Th1) cytokines, such as gamma interferon and interleukin-2. Many infectious and inflammatory disease find its role in disease progression, however its unexplored in Indian Infectious Disease Visceral leishmaniasis. Visceral Leishmaniasis is endemic in central part of India and predominantly found in Bihar state region. This disease is called as neglegted tropical disease. We have analyzed 247 subjects in endemic region (116 cases and 131 control) for VDR gene. We have find 10 variations after sequencing of gene. (2 variations in 3'UTR, 6 intronic, 1 in fourth exon and 1 in 5'UTR). After extensive genetic analysis We have found rs11568820 SNP (5' UTR variant), associated with Visceral Leishmaniasis. LD analysis shows strong linkage of this marker with another SNPs (rs11168292, rs11168293).

Keywords: *VDR, Visceral Leishmaniasis, . LD analysis, human immune system*

Abstract ID: ICIS A09

On The Characteristic Genera of Connected Orientable 3-Manifolds

SheikhMohd. Ibrahim

Department Of Mathematics, Pusan National University, Busan, South Korea

ABSTRACT

A complete invariant defined for connected orientable 3-manifolds is an invariant defined for the 3-manifolds such that any two 3-manifolds with the same invariant are homeomorphic. Further, if the 3-manifold itself can be reconstructed from the data of the complete invariant, then it is called a characteristic invariant defined for the 3-manifolds. In this paper, a more general characteristic rational invariant defined for the 3-manifolds called the characteristic genus defined for the 3-manifolds is constructed by using an embedding of a set of lattice points called the PDelta set into the set of rational numbers .

Keywords: *3-manifolds, PDelta set into, lattice points*

Abstract ID: ICIS A10

In silico Evaluation of Genomics and phylogeny of φRAGS with other existing Staphylococcus aureus Bacteriophage

[1]Shruti Mishra,[2]Prashant AnkurJain ,[3]Raghvendra Raman Mishra

[1,3]Department of Computational Biology &Bioinformatics, Jacob Institute of Biotechnology &Bioengineering, Sam Higginbottom University of Agriculture, Technology& sciences (Allahabad U.P)

[2]Department of Medical Lab Technology, DDU Kaushal Kendra, Banaras Hindu University (BHU) Varanasi Uttar Pradesh, India

ABSTRACT

Staphylococcus aureus is a Gram positive bacterium that can cause skin and soft tissue infections. Methicillin resistant Staphylococcus aureus (MRSA) developed due to hospital acquired infectious disease. Its removal is a big challenge for us. We used Bacteriophages, which are most abundant life form in the biosphere for establishing its therapy. In the present work, by using Bioinformatics tools and techniques we report the Genomics and Phylogeny of S. aureus bacteriophages. We were analysed thatGH15 is a polyvalent phage that shows strong activity against awide range of S. aureus strain. In this work the complete genome sequence of GH15 is determined, with the genome size of 139804 bp GH15 is the largest staphylococcal phage sequenced to data, the complete genome encodes 216 ORFs and 4 tRNAs.The closest relatives are the class III Staphylococcal bacteriophages including K,A5W,ISP,Sb-1 and G1. Report conclude that the phylogentic relationship and maximum likehood analyzed between the φRAGS and other existing S. aureus bacteriophages by using PhyML and MEGA6 software is possible for its In silico evaluation.

Keywords: *Bacteriophages, Staphylococcusaureus, φRAGS, Bioinformatics tools and techniques, PhyML and MEGA6*

Abstract ID: ICIS A11

InSilico Genome Wide Analysis of Genes Associated With Type 2Diabetes Mellitus

[1]Shruti Mishra, [2]Raghvendra Raman Mishra

[1]Phage-X Technologies Private Limited (R&D Head)
[2]Department of Medical Lab Technology, DDU Kaushal Kendra, Banaras Hindu University, Varanasi, India

ABSTRACT

Type 2 Diabetes mellitus is a multi factorial disease caused due to gene defect as well as environmental factor.GWAS(Genome Wide Analysis System) have played a primary role in demonstrating that genetic variation in a number of loci, SNPs, affects the risk of T2DM.Our objective is to find out Disease pathway map by taking all genes of T2DM which are 35 in numbers andbut in all there are 10 mostly involve in T2Dm from all over world population and it is find out by GWAS methodthen after we analyzed the KEGG pathway by analyzing T2DM pathway,to find out the common protein and then after by bioinformaticsanalysis combined and expend these pathways toward common protein for understanding the Diseases mechenism.we do Protein- protein interaction(PPI) and find out their complete target hub protein and target prediction for network hub. We collect the total 35 genes involve in T2DM and take those gene which are common for all population and their SNPs ,chromosome location in these all genes and by using string database Report conclude that target protein hub which are found in this disease so there we have taken 5most frequent genes and doing PPI in human so there are all have there own target protein hub- KCNJ11 have target protein hub PPKACA&TCF7L2 have complete target protein hub TLEI&PPARG have a target protein hub EP300&CDKL1 have compete target protein hubUCB&HHEX complete target protein SOX2.

Keywords: *Type 2 Diabetes , KEGG , T2DM*

Abstract ID: ICIS A12

Cardiac Rhythm Analysis – A Study of Arrhythmias using ECG/EKG Signal Recordings

[1]DeepikaAkarapu, [2]AparnaKumari ,[2]Biswajit Roy

[1]Department of Biotechnology, ChaitanyaBharathi Institute of Technology (CBIT), Hyderabad, India

[2] Information Technology Groupand Bioinformatics Centre, CSIR-Centre for Cellular and Molecular Biology, Hyderabad, India

ABSTRACT

Heartisone of the most important and powerful organs in our body. This muscular organ is responsible for pumping blood through the blood vessels of the body'scirculatory system. It is the first functional organ to develop and starts to beat and pump blood at about three weeksinto embryogenesis. A sequential beating of the heart as a result of the generation of electrical impulses is termed as cardiac rhythm and the number of beats per minute is called as heat rate. Heart diseases are of many types. Some are the results of irregular heart rate/beat, few due to blockage of coronary artery, few due to irregular heart rhythm and many more.Heart disease is now the world's leading causes of death in which India has seen a rapid transition. Theprogression of heart disease burden over the past couple of decadeshas indicated serious concern of the lifestyle adopted or lived by the people in our country. Latest statistics suggest that in India, there are roughly 30 million heart patients and two lakh surgeries are being performed every year. Arrhythmia is one of the common but major cardiac problems and occurs when the electrical signals to the heart that coordinate heartbeats are not working properly. This can cause serious and sometimes even potentially fatal consequences. Hence, identifying the risky symptoms can be helpful in saving lives. Different arrhythmias are caused due tovarious reasons like fast heart rate, slow heart rate, disorganized heart beats, which can be diagnosed in many ways viz.echocardiography, electrocardiography (ECG/EKG), echo-phonography (EPG) etc.. Among them ECG/ EKG is the most common first level process of recording the electrical activity of the heart over a period of time using electrodes placed on the skin and which results into display of various waveforms for different types of arrhythmias. However, interpreting them needs expertise. With the advent of digital technology it has not only becomeeasier to generate, read, store, annotate and analyze ECG

signal recordings for different rhythmic conditions, but also helpful in visualizing and interpreting them. Using different software we can remove noise, magnify the view, catch the false signals and identify the patterns in signals to predict certain arrhythmias much faster and early. Our study analyzes 48 different ECG records (Holter Monitoring) from MIT-BIH Arrhythmia Database using some of the existing and popular software tools made available in www.physionet.org. The study has tried to understand the representation, behavior and clinical interpretation of those ECG signals for different cardiac rhythmic conditions and progressed towards doing comparative statistical analyses toexamine the efficacy of the used programs.

Keywords:EGC/EKG; Arrhythmia; Heart; Heart –beat; Rhythm; Signals.

Abstract ID: ICIS A13

Bioinformatic analysis of big OMICS data using open source bioinformatics software: An approach of scientific research without money

Shravan Kumar Singh, Raj Kumar

Division of Radioprotective Drug Development and Research (RDDR), Institute of Nuclear Medicine and Allied Sciences (INMAS-DRDO), Brig. S.K. Mazumdar Road, Delhi-110054.

ABSTRACT

The exponential growth of information technology and revolutnary advancement in the software development is the central key of the interdisciplinary scientific research. Bioinformatics is an interdisciplinary research field that combines biology, mathematics, statistics and computer science into a broad-based field that will have profound impacts on all fields of biology. Understanding health and disease requires a detailed analysis of molecular interaction and events that determine the human physiology and health status. Big data base generated by using genomic, transcriptomic, proteomic and metabolomic bench work technology. Analysis of these big data to identify the biological function, interaction, pathway, biological network and model formation is done by various open source bioinformatics software as well as commercially available software. This type of interdisciplinary approaches of science and big data analysis of omics profiling can be used to manage precision health and disease. This is an opportunity and possibility that biological research can be done without money through cell phone and internet.

Keywords: *Bioinformatic,Open Source, Open Access, Free Software*

Abstract ID: ICIS A14

Digitization and analysis of data using open access GIS and RS software: An approach of science without money for social benefit

Vimala Singh, L.K.Sinha

DTRL, DRDO, Metcalfe House, New Delhi, India

ABSTRACT

In the age of technique and digitization many researchers and scientists complain that they cannot do research because universities and institutions do not provided fund and opportunity to them to work with scientific software and laboratories.This paper aims to present a brief overview of free available GIS based free software, open source, open access data and its uses to solve scientific problems of people relevant to GIS and Remote Sensing (RS) field.Inthisdigital age, thesatellite and aerial imagery provides solution for environmental change, weather forecasting, disaster management, food security and other remote sensing applications. Remote sensing based software (s/w) processes images and provides solutions to local and global issues.In an open source platform, remote sensing analysts perform various techniques such as image classification, atmospheric correction and even radar decomposition. One can convert the analogue data in to digital data using digitization technique in GIS software. There are various toposheets and imageries are available for research purpose by Survey of India (SOI) and Indian Institute of Remote Sensing (IIRS), in case of India.In this digital environment one can work from home by having System installed with GIS s/w and RS data.We hope through this article to help these scholars & researchers and show them the possibility& opportunity that science can be done without money, but with the mind, heart and internet.

Keywords: *Open Source, Open Access, Free Software, Digitization, SOI, GIS, RS.*

Abstract ID: ICIS A15

Development of vaccine for Mycobacterium tuberculosis: Present, past and future

Gaurav Gupta

Genome Foundation, Hyderabad, India

ABSTRACT

Mycobacterium tuberculosis is an important human pathogenic bacteria. There are number of genes which are involved in pathogenesis. Tuberculosis is a major disease so various efforts are made to discover a potent DNA vaccine which will induce the immunogenicity, currently BCG being the only vaccine present for the induction of immunogenicity. Research is going on to discover a potent DNA vaccine against the tuberculosis. Various DNA vaccines have been tested alone or in combinations for the increased efficacy. Some vaccines even proved very beneficial. It was found that the vaccines when used in combination through various techniques such as micro-particle and electroporation, works best and induce a great immunogenic response. The DNA vaccines are safe; still they are not used for a reason that the long term and side effect are unknown. Various tests are performed and a variety of next generation vaccines i.e. DNA vaccines are made, yet they need some time to be approved for the use. DNA vaccines are far more effective than the conventional vaccines in terms of rate of action, efficiency and safety.

Keywords: pathogenesis, tuberculosis, immunogenicity, micro-particle, electroporation**.**

Abstract ID: ICIS A16

Genetic Affinities of Indo-European speaking linguistic population of east coast region of India and with their special reference to hypervariable region of mitochondrial DNA lineages

HemlataDewangan, Gautam K. Kshatriya

Department of Anthropology, University of Delhi, New Delhi, India

ABSTRACT

Indian populations are always known for their unique biological, cultural as well as linguistic diversity (Chaubey G. 2010). Generally, Indian populations are classified into two groups, cast and tribal. More than 530 tribal population groups having in India and speaks about 750 dialects (Kosambi, 1991). It can be categorized into four linguistic affinity families: Austro-Asiatic (AA), Indo-European (IE), Dravidian (DR) and Tibeto-Burman (TB) (Roychoudhary et. al., 2006). Tribal populations are always studying for major focus point by several Anthropologists in ancient times. We have choosen for randomly 5ml intravenous blood samples for 58 Indo-European (Bathudi) speaking linguistic tribal population of east coast region of Indian subcontinent. Hypervariable region mtDNA analysis showed predominant M2 and R7 sub-haplogroups of M and N macro-haplogroups of Indian subcontinent. We have complied of three other Indo-European speaking linguistic tribal groups namely Andh, Paradhi and Lambadi of central India (Kivisild e. al., 1999 ; R Cordaux et. al., 2003). The results are showing high gene diversity, high pairwise difference, negative Fu's statistics and Tajima D values are also significantly recorded in the population. Finally we have concluded the Bathudi tribes are closely related to genetic affinities of Lambadi tribal groups of central India and their genetic structure of common material gene pool of matrilineal lineages of the population histories of mtDNA.

Keywords: *Genetic affinities, Hypervariable region, mtDNA, tribal population, population history.*

Abstract ID: ICIS A17

Co-inheritance of beta thalassemia trait with sickle cell anemia in various populations of Chhattisgarh

Aditya NathJha, P. K.Patra, Hrishikesh Mishra, Ram Kumar Yadav, L. V. K. S. Bhaskar

[1]Sickle Cell Institute,Raipur, Chhattisgarh,India

ABSTRACT

Hemoglobinopathies evolved as a protective mechanism against malaria, which exhibit selective advantage in heterozygous state. However, in homozygous recessive condition pose serious socio-economic burden in the population. Sickle cell anemia (SCA) is an autosomal recessive hemoglobinopathy associated with erythrocytessickling,vaso-occlusive crisisas well as multi-organ failure and death. The co-inheritance of other hemoglobinopathies is known to substantially modulate the clinical manifestation of SCA. In present study, we aimed to analyze the co-inheritance of beta thalassemia in sickle cell patients. This retrospective hospital based study includes 918 SCA patients from ten ethnic populations of Chhattisgarh, India. Complete blood counts and hemoglobin fractionation data were collected from patient records and HbA2 level > 4% was considered as cut off for compound heterozygocity (Hb-SB) of beta-thalassemia. Presence of Hb-SB was noted in all the populations analyzed. Interestingly, high frequency of Hb-SB has been observed in Satnami (53.8%), Rawat (47.1%), Gond (35.1%) and Panika (30.6%) populations. Inter-population comparison of hematological parameters [HbF ($p < 0.001$), HbA2 ($p < 0.001$), Hb ($p = 0.03$) and RDW ($p < 0.001$)] revealed significant differences. We also observed that mean HbF level were significantly higher in Hb-SS compared to Hb-SB in respective populations while the hemoglobin, hematocrit and RDW did not show any differences. Our study highlights the higher prevalence of beta-thalassemia; population specific compound heterozygosity for SCA and beta-thalassemia alleles and set the stage for further studies to correlate the clinical spectrum with their genomic architecture.

Keywords: *Hemoglobinopathies, Sickle cell anemia (SCA), hematocrit and RDW*

Abstract ID: ICIS A18

MBL2 variations and malariasusceptibility in Indian populations

Aditya Nath Jha[1,2], [2]Pandarisamy Sundaravadivel,[2]Lalji Singh, [2]Kumarasamy Thangaraj

[1,2] Sickle Cell Institute Chhattisgarh, Raipur, India (Current affliation)
[2]CSIR - Centre for Cellular and Molecular Biology, Hyderabad, India

ABSTRACT

Background:The pathogenesis of malaria is and its severity depends on complex interplay of host genetic make-up, the parasite virulence, parasite transmission dynamics and the host immune responses. The innate immune system mainly relies on a diverse set of germ line encoded receptors, soluble chemokines, cytokines and ligands. MBL2 is a soluble pattern recognition receptor of the innate immunity, which, recognize and react to specific repertoire of carbohydrates on the surface of invading organisms and plays an important role in the course of infectious diseases. In this study, we aim to investigate the association of MBL2 variants with P. falciparum malaria infection in Indian populations.

Methods: We re-sequenced the 8.7kb of the entire MBL2 gene in 434 clinically classified malaria individuals from malaria endemic regions of India. The study cohort includes 176 patients with severe malaria, 101 with mild malaria and 157 ethnically matched asymptomatic individuals. Additionally, 830 individuals from 32 socially, linguistically and geographically diverse endogamous populations of India were investigated for the distribution of functional MBL2 variants.

***Key words**: parasite virulence, P. falciparum malaria infection, MBL2 variants*

Abstract ID: ICIS A19

Recent Advances in the Diagnosis and Treatment of Autism Spectrum Disorders

[1]Akshay Sharma, [2]Ria Anand

[1]Symbiosis School of Biomedical Sciences, Pune, India

[2]Gautam Buddha University, Greater Noida, India

ABSTRACT

Autism Spectrum Disorders (ASD) are a collection of neurodevelopmental disorders which are characterised by symptoms such as abnormalities in social interaction and communication, repetitive behaviours and restricted interests. Autism is genetically linked and generally begins in infancy. Present grouping of ASD comprise five forms viz. classical autism or Autistic Disorder, Asperger syndrome, Rett syndrome, childhood disintegrative disorder and pervasive developmental disorder not otherwise specified (PDD-NOS).Each form is distinguished from one another and is diagnosed by criteria like age of onset, social interaction and behavioural and communication impairment. In this review, we have explored some of the recent advances and approaches to diagnose and treat ASD. The inventors of these approaches have been granted patent rights.

Keywords:*Autism Spectrum Disorders (ASD),Neurodevelopmental disorders, Social interaction and Communication, Repetitive behaviours and Restricted interests, Genetics*

Abstract ID: ICIS A20

Role of Paxillin (PXN) gene in cancer

AtonuChakrabortty
Pusan National University, Busan, South Korea

ABSTRACT

Paxillin protein in the humans encoded by the PXN gene. Genomic location of PXN is chromosome 12 and size is55,333 bases. This gene encodes a cytoskeletal protein involved in actin-membrane attachment at sites of cell adhesion to the extracellular matrix (focal adhesion). Alternatively spliced transcript variants encoding different isoforms exhibit different expression pattern, and have different biochemical, as well as physiological properties. Diseases associated with PXN include Corneal Opacification (other Ocular Anomalies) and various Cancers (gastric, lung and prostate). Mutations in PXN as well as abnormal expression of paxillin protein has been implicated in the progression of various cancers. Study shows that during tumor transformation, paxillin protein is recruited and phosphorylated. Additionally, paxillin plays a role in the MET tyrosine kinase signaling pathway, which is upregulated in many cancers.

Cancer is the most common cause of death in men, and women in the world. The geographic incidence of various cancers has changed dramatically over the last few decades. Modern research into its pathogenesis and identification of new genetic risk factors, have led to earlier detection of various cancers. However, in spite of such recent improvement in the clinical diagnosis of cancer, patients with advanced stage of cancer still have poor survival. Under this circumstance, there is an urgent need to better understand the biological mechanism via genetics of PXNneoplasm so as to guide patient management and develop novel therapeutic strategies.

Keywords: *Cancer, PXN gene, Variants, Genetic risk factors, Management*

Abstract ID: ICIS A21

Screening for IEM in Uttar Pradesh : A Pilot Study

[1]Nazmin Fatima, [2]Gyanendra Kumar Sonkar, [3]ShaliniTripathi, [2]Sangeeta Singh

[1]Department of Biochemistry, Integral Institute of Medical Sciences, Integral University, Lucknow

[2]Department of Biochemistry, King George's Medical University, Lucknow

[3]Department of Paediatrics, King George's Medical University, Lucknow

ABSTRACT

Monogenic diseases are the result of a single defective gene on the autosomes. Inborn errors of metabolism (IEM) are a heterogeneous group of monogenic diseases that affect the metabolic pathways. It relies on a high index of clinical suspicion and coordinated access to specialized laboratory services. The first approach to the diagnosis is by a multi-component analysis of body fluids in clinically selected patients, referred to as metabolic screening tests. Quantification of total and individual amino acids in biological fluids such as plasma, urine and cerebrospinal fluid has an important diagnostic implication in laboratory medicine. Nutritional status of an individual is clearly reflected from the analysis of its total amino acids content of plasma and urine. This helps to rule out the suspected amino acidopathies. The present pilot study presents the amino acid profile using HPLC in cases suspected for IEM. Method: A total of 142 suspected cases of IEM were recruited in the age group of 3 months to 15 years. Besides physical examinations, general biochemical testing for CBC, serum electrolytes, blood gluscose level and plasma ammonia, HPLC for amino acids were done in suspected cases for IEM or having characteristic features of IEM or upon request of the clinicians.

Results: At the screening level, out of 142, we found, 56 cases to be positive for reducing sugar, 54 for ketone bodies, 3 cases for phenolic compounds (i.e. Tryptophan, Phenylanine and Tyrosine). None of the cases were found to be positive for branched chain amino acids (i.e. Leucine, Isoleucine and Valine) and Homogentesic acid. Only one case was found positive for Tyrosine.Conclusion: Early recognition of IEM by screening tests in combination with strong clinical suspicion will help the clinicians to initiate prompt early treatment to prevent lethal neurological complications and developmental delay.

Keywords: *Inborn errors of Metabolism, Monogenic, Amino acidopathy, HPLC*

Abstract ID: ICIS A22

Exogenous supplementation of nitric oxide regulates the levels of connexins, pro-apoptotic and angiogenic factors and accelerates diabetic wounds healing

Mallikarjuna Rao Gedda, Rakesh K. Singh

Department of Biochemistry,Institute of Science,Banaras Hindu University, Varanasi, India

ABSTRACT

Dysfunction of various cell types at the site of wounds in hyperglycemia leads to the delay in wound closure albeit responsible factors are not well known. In the present study, we elucidated the role of nitric oxide (NO) donors on wound closure, fibroblasts proliferation and expression levels of Cx31, Cx31.1, Cx43,bax, caspase-3 and VEGF in diabetic wounds. The level of NO was found comparatively less ($p<0.01$)in diabetic wound tissuesas compared to non-diabetics. The expression levels of connexins and apoptotic factors were found up-regulated ($p<0.001$) in diabetic wounds as compared to non-diabetics. The topical application of s-nitroso glutathione (SNOG) embedded pluronic F-127 hydrogel on wounds accelerated healing through down regulation ($p<0.01$) of connexins and apoptotic factors in both, wound tissues and in vitro cultured wound fibroblasts. In addition, SNOG supplementation significantly ($p<0.01$) increased the rate of fibroblast proliferation, and VEGF expression ($p<0.001$) in diabetic wounds. These findings suggest that topical application of SNOG expedite wound closure rate in diabetic conditions through regulation of connexins, and enhanced proliferation of fibroblasts.

Keywords: *Diabetes, nitric oxide, connexins, apoptosis, fibroblasts*

Abstract ID: ICIS A23

Exploring Near Infrared (NIR)-Active Gold Nanorods in PhotothermalLysis of Thrombus with a Multimodal Perspective

Nitesh Singh

Banaras Hindu University, Varanasi, India

ABSTRACT

Fibrinolytic therapy for arterial or venous thrombotic disorders involves thesystemic administration of thrombolytics such as streptokinase, which isassociated with serious bleeding complications. With this study, we provide aproof-of-concept of photothermal thrombus ablation with gold nanorodsexposed to near-infrared irradiation, both in vitro using materials generatedfrom purified fibrinogen or plasma and in vivo in murine blood vessels. This isthe first report of the application of photothermal therapy as an anti-thromboticmeasure. Remarkably, the addition of streptokinase had a multimodal additiveeffect with regard to acceleration of photothermallysis of thrombi even at adose significantly below the therapeutic concentration, thus minimizing the lifethreatening side effects and adverse complications. This combinatorial approachexhibits great promise for lysing pathological clots while effectively overcomingthe drawbacks of existing therapies.

Keywords: *Fibrinolytic therapy, venous thrombotic disorders, photothermal therapy*

Abstract ID: ICIS A24

Variable association pattern of non-coding RNA gene (LOC284889) polymorphism with infectious diseases (malaria and visceral lesihmaniasis) among Indians – Evidence from independent studies.

[1]Sundaravadivel P,[1, 2] Aditya N Jha, A Mishra1, [1]Vipin K Singh, [1]Pradeep K Patra, [1]Kumarasamy Thangaraj

[1]CSIR-Centre for Cellular and Molecular Biology, Hyderabad, India.

[2]Pt. Jawaharlal Nehru Memorial Medical College, Raipur, Chhattisgarh, India.

ABSTRACT

The host genetic factors play important role in determining the outcome of the infectiousdiseases.Non-coding RNA is emerging as key regulator of cellular homeostasis. The non-coding RNA gene (LOC284889) located on chromosome 22q11.23 is largely uncharacterised and the polymorphism (rs34383331T > A) present in this gene is found to be showing variable association patterns among patients with malaria and visceral leishmaniasis (VL) in India. These studies comprised of 160 cases of severe malaria, 101 of mild malaria and 164 ethnically matched asymptomatic controls; 214 visceral leishmaniasis patients and 220 ethnically matched controls. The allele A (rs34383331T > A) is significantly associated with increased risk to P. falciparum malaria [severe: OR = 2.08, p = 0.002 and mild: OR = 2.09, P = 0.005]. However, no significant difference has been attained among visceral leishmaniasis case-controls [χ2 =0.78; p=0.37; OR=0.86; 95%CI=0.61-1.20)]. This variable association pattern implies complex and heterogeneous nature of the diseases. Also, at population level, Indian are unique at their genetic makeup. Hence, outcome of these studies reiterates the complexity existing at disease as well as the host genetics.

Keywords: *infectiousdiseases.Non-coding RNA , visceral leishmaniasis (VL), host genetics*

Abstract ID: ICIS A25

Interaction of Coffee Consumption and Thyroid Cancer Risk

Manish Mishra*, Ranjan Solanki, Raju Panta

Trinity School of Medicine, Ratho Mill, St. Vincent and the Grenadines

* Corresponding Author

ABSTRACT

Cancer is a major public health problem world-wide, there were 14 million new cases and 8.2 million cancer-related deaths recorded all over the world in 2012. As per 2017 American Cancer Society projection, the number of new cancer (all types) cases and thyroid cancer cases are 1,688,780 and 56,870 with mortality rates of 600,920 and 2,010 respectively in the United States. A number of hereditary variations foster the growth and advancement of carcinogenesis. For example, the altered expression of oncogenes (up-regulation) and tumor suppressor genes (downregulation) cascades are favorable for the expansion of neoplastictissues. Coffee is one of the most commonly consumed beverages in the world. Coffee consists of many components including caffeine, caffeic acid, cafestol, kahweol, chlorogenic acid, hydroxylhydroquinone, and antioxidants. An inverse association has been reported between coffee consumption and the risk of several cancers. Several components of coffee have been reported for their anti-carcinogenic properties and reduction of the harmful oxidation process via regulating various cell-signaling cascades. Further studies that include more details about thepatterns and habits of coffee consumption (coffee type, amount, preparation methods, etc) and the dose-response relationships are required to understand the impact of coffee consumption on thyroid cancer risk.

Keywords: *carcinogenesis, oncogenes, suppressor genes*

Abstract ID: ICIS A26

Controlled Synthesis of Vertically Aligned NiMn-LDH as Faradaic material for High Performance Supercapacitor Application

Saurabh Singh

School of Materials Science & Engineering, Pusan National University, Busan, Republic of Korea

ABSTRACT

Herein, I am presenting an effective approach to synthesize the vertically aligned morphology of NiMn layered double hydroxide (NiMn-LDH) nanostructure via simple one step hydrothermal method on Ni-foam substrate.Growth kinetics of the synthesized material has been propounded to show the scientific background behind obtained morphology. We have also shown that by varying the net precursor concentration of NiMn it is possible to optimize the faradaic performance of NiMn-LDH material. Performed electrochemical measurement shows that at the specific net concentration of 0.08M high faradaic performance upto 1100 F.g-1 can be achieved. Further this material shows good rate capability with increasing current density upto 20A.g -1 and good cycling stability over 2000 cycles. Superior electrochemical performance of this material vindicates its potential applicability as high performance Supercapacitor application.

Keywords: *vertically aligned morphology, hydrothermal method, faradaic performance*

Abstract ID: ICIS A27

Plasmodium falciparum SUFs system as a promising drug target against cerebral malaria

[1,2]BijayKumar and [1, 2] SamanHabibb

[1]Molecular Biology Unit, Institute of Medical Sciences, Banaras Hindu University Varanasi, India

[2]Division of Molecular and Structural Biology, CSIR-Central Drug Research Institute, Lucknow, India

ABSTRACT

The plastid of Plasmodium falciparum, the apicoplast, performs metabolic functions essential to the parasite survival that composed of several pathways of bacterial origin measured to be striking drug target. Among these is the sulfur mobilization (SUF) pathway of Fe-S cluster biogenesis one of the promising drug target. Functional mechanisms of the Plasmodium SUFs in the maintenance of apicoplast and survival of parasite have not been elucidated. Biochemical investigation of its components and inhibitors of Plasmodium SUFs provided thrust in plasmodium biology and drug discovery. Various reactions in the plastid require the assembly of [Fe–S] prosthetic groups on participating proteins as well as the reductant activity of ferredoxin that is converted from its apo-form by the assembly of [Fe–S] clusters inside the apicoplast. The [Fe–S] assembly pathway involving sulphurmobilisingSuf proteins has been predicted to function in the apicoplast with one component (PfSufB) encoded by the plastid genome itself. We demonstrate the ATPase activity of recombinant P. falciparum nuclear encoded SufC and its localisation in the apicoplast. Further, an internal region of apicoplastSufB was used to detect PfSufB–PfSufC interaction in vitro; co-elution of SufB from parasite lysate with recombinant PfSufC on an affinity column also indicated an interaction of the two proteins. As a departure from bacterial SufB and similar to reported plant plastid SufB, apicoplastSufB exhibited ATPase activity, suggesting the evolution of specialised functions in the plastid counterparts. Our results provide experimental evidence for an active Suf pathway in the Plasmodiumapicoplast. We further reported the characterization of two proteins, Plasmodium falciparumSufS (PfSufS) and PfSufE that mobilize sulfur in the first step of Fe-S cluster assembly and confirm their exclusive localization to the apicoplast. The cysteine desulfurase activity of PfSufS is greatly enhanced by PfSufE, and the PfSufS-PfSufE complex is detected in vivo. Structural modeling of the complex reveals proximal positioning of conserved cysteine residues of the two proteins that would allow sulfide transfer from the PLP (pyridoxal phosphate) cofactor-bound active site of PfSufS. Sulfide release from

the L-cysteine substrate catalyzed by PfSufS is inhibited by the PLP inhibitor D-cycloserine, which forms an adduct with PfSufS-bound PLP. D-Cycloserine is also inimical to parasite growth, with a 50% inhibitory concentration close to that reported for Mycobacterium tuberculosis, against which the drug is in clinical use. Our results establish the function of two proteins that mediate sulfur mobilization, the first step in the apicoplast SUF pathway,and provide a rationale for drug design based on inactivation of the PLP cofactor of PfSufS.

Keywords: *Plasmodium SUFs, pyridoxal phosphate, Mycobacterium tuberculosis*

Abstract ID: ICISA28

Further studies to understand the mechanism of LEDGF/p75-dependent splicing and LEDGF/p75 dependent enrichment of H3K36me3 in gene bodies are needed to develop a better picture of this triangle of splicing, H3K36m3 and HIV-1 integration. Assessment of genetic diversity of the diverse aromatic rice germplasm collections from India

[1]Gagandeep Singh, [1*]Gopala Krishnan S, [2]Sheshu Madhav M, Shobha Rani N[2], [3]Robin S, Kuldeep Singh[4], [5]Nagarajan M and [1]AK Singh

[1]Division of Genetics, ICAR-Indian Agricultural Research Institute, New Delhi 110 012, India;

[2]ICAR- Indian Institute of Rice Research, Hyderabad 500 030, Telangana, India;

[3]Department of Rice, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India;

[4]School of Biotechnology, Punjab Agricultural University, Ludhiana, Punjab, India;

5Rice Breeding and Genetics Research Centre, ICAR- Indian Agricultural Research Institute, Aduthurai 612 101, Tamil Nadu, India

**Corresponcence:gopal_icar@yahoo.co.in*

ABSTRACT

Aromatic rices are cultural heritage of India, possessing characteristics flavor, exquisite grain and cooking quality. Inspite of being unique, their per se improvement as well as utilization in rice improvement have been minimal due to limited research on characterization both at morphological and molecular level. Therefore the present study was conducted with the objective of characterizing the extent of genetic diversity in a set of 556 aromatic rice germplasm collections from different

geographical regions of India, comprising of aromatic short grain rice, landraces, indigenous Basmati accessions as well as exotic collections. The molecular diversity of 556 aromatic rice germplasm lines

was assessed using a set of 40 simple sequence repeat (SSR) markers from GCP panel representing 12 chromosome of the rice. The number of alleles detected among these

aromatic germplasm varied from 2 to 4 as many as 23, 11, 2 markers amplifying 2, 3 and 4 alleles, respectively. The Polymorphic Information Content (PIC) of the markers varied from 0.0 to 0.63. Molecular marker analysis helped in assessing the diversity in the aromatic rice germplasm and some of the aromatic rice germplasm are being utilized in diversification of the aromatic rice germplasm.

Keywords: *Polymorphic Information Content (PIC), germplasm, simple sequence repeat (SSR)*

Abstract ID: ICIS A29

An event based approach using twitter sentiment analysis for predicting the economy of India

SatyabrataAich

Pusan National University, Busan, South Korea

ABSTRACT

Several meaningful studies have been done on sentiment analysis of tweets for predicting real life case studies as well as predicting the economy of a country. In some cases some big events makes the real time tweets more important and meaningful for prediction of stock market, as well as the economy of a country. In this case we took the demonitization, as a big event and collected the real time tweets based on that event to predict the Indian stock market as well as economy. We have collected over several thousands of tweets around the demonetization period. We have analyzed the financial indices based on the sentiment scores of the tweets. We have found a significant correlation between the sentiments and financial indices, which interpret the impact of events and public sentiments towards the events on the economy of the country

Keywords: *Stock Market , demonetization , sentiments and financial indices*

Abstract ID: ICIS A30

A probabilistic simulation of collision between ship and offshore installation

M.P. Mujeeb Ahmed[1,2], JeomKee Paika[1,2,3]

[1]Department of Naval Architecture and Ocean Engineering, Pusan National University, Busan 46241, Republic of Korea

[2]The Korea Ship and Offshore Research Institute (The Lloyd's Register Foundation Research Centre of Excellence), Pusan National University, Busan 46241, Republic of Korea

[3]Department of Mechanical Engineering, University College London, London WC1E 7JE, UK * Corresponding author: jeompaik@pusan.ac.kr (J.K. Paik)

ABSTRACT

While in operation, offshore installations are subjected to various accidents. Over the years, collision of offshore supply vessel (OSV) has been identified as the most frequent type of accidents. A design value based on the past collision accidents and expert opinions are followed by the classification societies and regulatory committees. However, these values are sometimes proven to be conservative or inadequate, considering that the most of the current sailing ships have not upgraded the safety measures. Also, most of the minor collision accidents are not reported and recorded. Therefore, in this study, a probabilistic approach to foresee the real collision accident scenarios are simulated using sampling techniques and a time domain and structural analysis of the selected scenario is carried out to study the structural redundancy and reliability of the offshore installation. The probabilistic method followed in this study will provide an efficient and prudent design of installation against ship collision.

Keywords:_Ship-installation collision, probabilistic approach, collision scenario, Offshore supply vessel (OSV)._

Abstract ID: ICIS A31

Optimization study and batch production of citric acid using Aspergillus niger isolated from rotten orange with pineapple peel and corncob as a substrate

Smriti Pandey[1], Dr. Raghvendra Raman Mishra[2]

[1]Phage-X Technologies Private Limited, Varanasi, India

[2]RGSC, Banaras Hindu University, Varanasi, India

ABSTRACT

Citric acid is the most important organic acid produced by fermentation, widely used in food, pharmaceutical and chemical industries.Aspergillus niger, one of the most important fungi used in industrial microbiology has been employed for many years for the commercial production of citric acid. The present study was aimed to investigate the potential of Aspergillus niger to convert pineapple peel and corncob powder into citric acid through fermentation carried out for few days. Since Aspergillus niger is the traditional producer of citric acid. Although, strain of Aspergillus niger is isolated from rotten orange. Environmental factors that have been shown to exert an effect on citric acid production are the type and concentration of carbon source of the fermentation medium, initial pH, temperature and substrate. Besides the regulation of product formation by environmental conditions, strain selection and improvement has become the important factor. Because of annual growths in demand of citric acid, using alternative processes and strains for its production are in progress. Hence, the techniques developed to maintain a good ecological report too besides reducing the overall market production price of citric acid. Implementation of the proposal will not only make India the leading producer of citric acid, but also a model for ecological welfare.

Keywords: *Aspergillus niger, orange, pineapple, corncob, citric acid, batch production*

Abstract ID: ICIS A32

Large Scale production of nsP2 protease of Chikungunya virus

Pallavi Das[1] **, Raghvendra Raman Mishra**[2] **, P.K. Dash**[3]

[1]Phage-X Technologies Private Limited, Varanasi, India

[2]DDU Kaushal Kendra, RGSC, Banaras Hindu University, Varanasi, India

[3]Division of Virology, DRDE, Gwalior

ABSTRACT

Chikungunya represents a classic example of global expansion of an arboviral infection in last decades (1). In spite of its global reemergence, no approved drugs or vaccines are available till date. Effective countermeasures including development of promising therapeutics against CHIKV remain one of the important public health priorities. Currently, targeting of viral enzymatic activities that are crucial for the viral replication cycle are believed to be attractive target for development of antiviral therapy.

We have developed batch fermentation processes for high yield production of rCHIKV-nsP2 protease from E. coli. The cell growth and rCHIKV nsP2 protease yield was affected by culture conditions. From economic point of view, it is essential to enhance volumetric and specific product yield by development of efficient fermentation and purification strategies. In the present study, batch cultivation was adopted to increase the product yield. The batch fermentation strategy employed in this work is probably one of the cost-effective means to improve the cell biomass and recombinant protein production.

Keywords: *arboviral infection, CHIKV, antiviral therapy, protein*

Abstract ID: ICIS A33

Determination of nano/trace elements from Spirlina maxima auxenic culture extract by FT-Raman Spectroscopy

Pragya Mishra
Centre of Food Technology, University of Allahabad, Allahabad, 221003, U.P., India

ABSTRACT

Spirulina species is a rich source of nutraceutical components. The full grown auxenic culture may contain green nano particle with other elements. In the present work we used FT-Raman Spectroscopy to prevent elemental loss. Confirmed pure culture of Spirulina maxima (S. maxima) isolates were grown and extract was prepared to analyze its nutraceutical value and elemental component. The chemical constituents of soluble mobile phase and non volatile fraction of S. maxima extracts were identified by High-performance liquid chromatography (HPLC) method and total volatile biomass was used to find out its nutraceutical profile including, amino acids, fatty acid and vitamin using Gas chromatograph (GC) technique. HPLC profile of S. maxima extracts showed that there were several pigments such as chlorophyll with in significant relative percentages (% of total area). GC analysis of S. maxima extract shows diversity in its nutraceutical capacity. Extract was enriched with various amino acids, fatty acids and Vitamins. A non-destructive Raman spectroscopic analysis of extract has been conducted by laser excitation at 1064 nm, with the objective of direct measurement while preserving the integrity of the more representative chemicals. FT-Raman spectra of extract have been recorded by exciting 1064 nm laser in the spectral region 50-4000 cm-1 at a resolution of 4 cm-1. The observed Raman bands are attributed to (S-S) bridges of cysteine and methionine amino acids, beta fructose and beta glucose monosaccharide and unsaturated fatty acids. The curve fitting analyses have been used for the quantitative analysis of various biochemicals and their distribution.

Keywords: *Spirulina maxima, FT-Raman Spectroscopy, HPLC, GC, curve fitting.*

Abstract ID: ICIS A34

Development of a promissing nanocomposit for osteomyelitis using Raghs ø Bacteriophage powder with Bone Cement Based nano hybrid

Raghvendra Raman Mishra
Medical Laboratory Technology, Deen Dayal Upadhyay Kaushal Kendre, Banaras Hindu University, Varanasi, 221005, U.P., India,

ABSTRACT

Due to emergence of superbugs such as Methicillin resistant Staphylococcus aureus (MRSA) the treatment of infections especially of bone (osteomyelitis) is extremely difficult. The aim of this study was to evaluate the role of an adjutant alternative therapeutic implant material i.e. application of S. aureus specific bacteriophages Raghs ø in cases of osteomyelitis caused by MRSA in animal model. We used previously developed Poly methyl methacrylate (PMMA) based bone cement and its nanocomposites with layered double hydroxide (LDH) with bacteriophages Raghs ø powder. A total 22 rabbits were included in this study. The first two rabbits were used to test the safety of phage cocktail while rest twenty rabbits were divided into: Group A (n=4) to assess the establishment of osteomyelitis, Group B (n=4) osteomyelitis developed but implant therapy started only after 6 weeks and Group C (n=12) osteomyelitis developed and implant therapy started after 3 weeks. Group B and C rabbits were treated with 4 doses of cocktail of seven virulent bacteriophages at the interval of 48 h. Comparison between three groups was made on the basis of observation of clinical, radiological, microbiological, and histopathological examinations. Total duration of observation was 14 weeks. Experimental group rabbits recovered well from the illness in the next two weeks of the therapy. Appetite and activity of the rabbits improved, local oedema, erythema and induration subsided. There were minimal changes associated with osteomyelitis in X-ray and histopathology also showed no signs of infection with new bone formation. Control B group rabbits also recovered well from infection. Phage therapy has very good potential to treat difficult infections caused by multidrug resistant bacteria.

***Keywords**: Methicillin resistant Staphylococcus aureus (MRSA), Osteomylitis, Bacteriophage, PMMA*

Abstract ID: ICIS A35

Ber (Zizyphus mauritiana): An Underutilized Fruit

Sonika Pandey and Amrita Poonia

Centre of Food Science & Technology, Institute of Agricultural Sciences, Banaras Hindu University.Varanasi.

Email- sonika.pandey@rediffmail.com

Mobile No – 9919715759

ABSTRACT

Ber is also known as Indian jujube, desert apple or Indian plum. It belongs to family Rhamnaceae and genus Zizyphus. Zizyphus mauritiana Lamk. is commercially important in India. It is considered as an underutilized crop. It is widely cultivated in different states of India, i.e. Madhya Pradesh, Rajasthan, Gujarat, Punjab, Haryana, Uttar Pradesh, Maharashtra and to limited extent in several other states. The content of nutrients in Ber fruit is found to be higher than that of some other fruits like mango, guava, orange and strawberry. It is very rich in protein, phosphorous, calcium, carotene and vitamin C. However they are often under valued and underutilized as more exotic fruits become available. Ber fruit also contain good source of antioxidants and phenols. This fruit has many medicinal uses like it can be consumed as a digestant, laxative, used in chest complaints etc. Ber fruit is mainly eaten fresh and in a dehydrated form. The fruits are highly seasonal and available in plenty at particular times of the year. During peak season, the price decreases and a glut in the market may result in the spoilage of large quantities, to avoid this spoilage, the fruits can be processed into various products like ber fruit powder, candy, jelly, jams etc. Fruit powder can used in development of value added products contribute significantly to the therapeutic as well as nutritive value.

Keywords: *Ber fruit, Antioxidants, Medicinal value, Value addition.*

Abstract ID: ICIS A36

Novelmutations inNR5A1 and ARgenesof individuals with 46,XY causesdisorders of sex development

D V S Sudhakar[1], Phanindranath R[1], Anubhav Bhardwaj[1],Usha Kabilan[1], Sree N[1], Raghvendra S[1], Lakshmi Rao K[1], Mamta Deendayal[2], Purnima Bhargava[1], Chaitanya A Datar[3], Rima Dada[4],Satyamoorthy K5,Thangaraj K[1]

1CSIR - Centre for Cellular and Molecular Biology, Hyderabad-500007, India
2Infertility Institute & Research Centre, Secunderabad, India
3Sahyadri Medical Genetics & Tissue Engineering Facility, Pune, India
4All India Institute of Medical Sciences, New Delhi,India
5Manipal University, Manipal, India

ABSTRACT

Disorders of sex development (DSD) are a group of rare congenital conditions defined by atypical phenotypic sex and gonadal dysgenesis. 46,XY DSD is heterogeneous and clinical phenotypes include ambiguous genitalia, hypospadias, hermaphroditism and complete sex reversal. Most often the underlying cause of DSD is a variant in gene(s) related to gonadal development or steroidogenic pathway. Approximately, 64 candidate genes have been found to be associated with DSD; of which, the most commonly associated genes are androgen receptor (AR)and steroidogenic factor 1 (also known as NR5A1). In the present study, initially exome sequencing was performed in two families with 46,XY DSD.Later, entire coding regions ofNR5A1and ARweresequenced, in an additional 61 sporadic cases of 46,XY DSD. A total of three novel mutations in NR5A1were identified in the DNA binding domain of the proteinin unrelated individuals. Wild type and mutant NR5A1proteins were expressed invitro using rabbit reticulocyte lysate system (TNT system,Promega). Protein binding to target promoter sequence (CYP11A1) was assessed by electrophoretic mobility shift assay (EMSA) using P32labeled DNA probes.To confirm the results of EMSA we performed dual luciferase assays using pGL3-hNROB1 and pCMV6-hNR5A1 vectors. All the three mutant proteins showed complete absence of binding to target promoter sequence in EMSA.

Dual luciferase assays further confirmed the EMSA results and there was a significant decrease in the reporter gene expression in Hek293 cells co-transfected with mutant proteins compared to cells co-transfected with wild pCMV6-hNR5A1constructs. In addition to the above, 5 mutations were identified in ARgene of which, 2 were novel (p.Lys823Asn and p.Ile842Ser) and three were earlier reported in androgen receptor database (rs137852569, rs754201976, p.Asp733Asn). In conclusion, 5% of DSD individuals had NR5A1 mutations and 8.2% individuals showed mutations in androgen receptor gene.

Keywords: *phenotypic, gonadal dysgenesis, steroidogenic pathway, androgen receptor gene.*

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