

*Journal of*  
**PROTEINS AND PROTEOMICS**



International Conference on Advances in Biosciences and  
Biotechnology – ICABB-2018  
(February 01-03, 2018)



A Journal of the  
PROTEOMICS SOCIETY, INDIA

IS International Science Press

**Editorial Board — Journal of Proteins and Proteomics (JPP)**  
**A Journal of the Proteomics Society, India (PSI)**

**EDITOR-IN-CHIEF**

**Suman Kundu**

Department of Biochemistry, University of Delhi  
South Campus, New Delhi, India  
E-mail : [jppindia@gmail.com](mailto:jppindia@gmail.com)

**EDITORS FOR PROTEINS SECTION**

**Alo Nag**

Department of Biochemistry,  
University of Delhi (DU), South Campus  
New Delhi, India

**Amal Kanti Bera**

Department of Biotechnology, Indian Institute of  
Technology Madras (IITM), Chennai, India

**Arvind M. Kayastha**

School of Biotechnology, Banaras Hindu  
University (BHU), Varanasi, India

**Debashis Mukhopadhyay**

Biophysics and Structural Genomics Division,  
Saha Institute of Nuclear Physics (SINP), India

**Gulsah Sanli**

Department of Chemistry, Izmir Institute of  
Technology, Izmir, Turkey

**Himangshu S. Bose**

Mercer University School of Medicine &  
Memorial Health University, Medical Center,  
Savannah, USA

**Michael Blaber**

Department of Biomedical Sciences,  
Florida State University, Tallahassee, USA

**Monica Sundd**

National Institute of Immunology (NII),  
New Delhi, India

**N. Srinivasan**

Molecular Biophysics Unit, Indian Institute of  
Science (IISc), Bangalore, India

**Rizwan Hasan Khan**

Interdisciplinary Biotechnology Unit, Aligarh  
Muslim University (AMU), Aligarh, India

**Vikash Kumar Dubey**

Department of Biosciences and Bioengineering,  
Indian Institute of Technology Guwahati (IITG),  
Guwahati, India

**EDITORS FOR PROTEOMICS/BIOINFORMATICS SECTION**

**Abhijit Chakrabarti**

Crystallography and Molecular Biology Division,  
Saha Institute of Nuclear Physics (SINP),  
Kolkata, India

**Debasis Dash**

CSIR-Institute of Genomics and Integrative  
Biology (IGIB), New Delhi, India

**Harsha Gowda**

Institute of Bioinformatics (IOB), Bangalore;  
Centre for Systems Biology and Molecular  
Medicine, Yenepoya University, Mangalore, India

**K Dharmalingam**

Aravind Medical Research Foundation (AMRF),  
Madurai, India

**Kalpana Bhargava**

Defence Institute of Physiology & Allied Sciences  
(DIPAS), DRDO, Delhi, India

**T. S. Keshava Prasad**

Institute of Bioinformatics (IOB), Bangalore;  
Centre for Systems Biology and Molecular  
Medicine, Yenepoya University, Mangalore, India

**Mahesh J Kulkarni**

CSIR-National Chemical Laboratory (NCL),  
Pune, India

**Niranjan Chakraborty**

National Institute of Plant Genome Research  
(NIPGR), New Delhi, India

**Rakesh K Mishra**

CSIR-Centre for Cellular and Molecular Biology  
(CCMB), Hyderabad, India

**Ravi Sirdeshmukh**

Institute of Bioinformatics (IOB); Mazumdar  
Shaw Medical Foundation and Centre for  
Translational Research, Bangalore, India

**Renu Deswal**

Department of Botany, University of Delhi (DU),  
Delhi, India

**Sanjeeda Srivastava**

Department of Biosciences and Bioengineering,  
Indian Institute of Technology Bombay (IITB),  
Mumbai, India.

**Shantanu Sengupta**

CSIR-Institute of Genomics and Integrative  
Biology (IGIB), New Delhi, India

**Srikanth Rapole**

National Centre for Cell Science (NCCS), Pune,  
India

**Subhra Chakraborty**

National Institute of Plant Genome Research  
(NIPGR), New Delhi, India

**Surekha M. Zingde**

Formerly from Advanced Centre for Treatment,  
Research and Education in Cancer (ACTREC),  
Mumbai, India

**Utpal Tatu**

Department of Biochemistry, Indian Institute of  
Science (IISc), Bangalore, India

**ASSOCIATE MEMBERS**

**G. Hariprasad**

Department of Biophysics, All India Institute of  
Medical Sciences (AIIMS), New Delhi, India

**K. Balamurugan**

Department of Biotechnology, Alagappa  
University (AU), Karaikudi, India

**Lipi Thukral**

CSIR-Institute of Genomics and Integrative  
Biology (IGIB), New Delhi, India

**Md. Imtiyaz Hassan**

Centre for Interdisciplinary Research in Basic  
Sciences, Jamia Millia Islamia (JMI), New Delhi,  
India

**Neel Sarovar Bhavesh**

International Centre for Genetic Engineering and  
Biotechnology (ICGEB), New Delhi, India

**INTERNATIONAL ADVISORY BOARD**

**Aragula Guru Rao**

Iowa State University, Ames, USA

**Faizan Ahmad**

Jamia Millia Islamia, New Delhi, India

**Jiban K. Dattagupta**

Saha Institute of Nuclear Physics, Kolkata, India

**Mark S Baker**

Macquarie University, NSW, Australia

**M.A. Vijayalakshmi**

VIT University, Vellore, India

**Maurizio Brunori**

Sapienza- University of Rome, Rome, Italy

**Michael I. Oshtrakh**

Ural Federal University, Russian Federation

**Rajiv Bhat**

Jawaharlal Nehru University, New Delhi, India

**Tapan K. Chaudhuri**

Indian Institute of Technology Delhi,  
New Delhi, India

**Tej P. Singh**

All India Institute of Medical Sciences,  
New Delhi, India



**INTERNATIONAL SCIENCE PRESS**

F-2562, Ansal's Palam Vihar, Gurgaon, Haryana  
INDIA, Phone: 91-124-2365193  
E-mail: [internationalsciencespress@gmail.com](mailto:internationalsciencespress@gmail.com)



**PROTEOMICS SOCIETY, INDIA**

c/o CSIR-CCMB, Uppal Road, Hyderabad  
Telengana 500007, E-mail: [proteomicsociety@ccmb.res.in](mailto:proteomicsociety@ccmb.res.in)  
[www.psindia.org](http://www.psindia.org); [www.jpp.org.in](http://www.jpp.org.in)

## **GENERAL INFORMATION, GUIDELINES AND POLICIES**

**The Journal:** Journal of Proteins and Proteomics (JPP), administered by Proteomics Society, India (PSI), is a peer reviewed international journal envisaged to serve the world wide community of researchers and teachers dealing with the challenges of proteins and proteomics research resulting in an improved understanding of protein science in general. Published quarterly, the aim is also to supplement the regular issues with special issues annually in selected, relevant topics of protein science. The journal has an online presence at <http://www.jpp.org.in>. The journal publishes wide array of articles at no cost, whatsoever, to authors and provides free access to all articles through its website. Hard copies of the journal are available at nominal subscription charges.

**Copyright:** Journal Articles by JPP is licensed under a Creative Commons Attribution-ShareAlike 4.0 International License (<https://creativecommons.org>). Under the CC BY-SA license, JPP allows free access to its publications and one can copy, use, analyze, perform and present information publicly and produce and distribute derivative literature in any digital medium for any reasonable purposes, subject to appropriate acknowledgement of the authors and the journal with a link to the license. The journal allows rights to re-produce printed copies in accordance to the Creative Commons policies. If any content of the journal is re-mixed, transformed or built upon then it must be distributed with the same license as the original. Submission of an article implies that the authors agree to the copyright laws and principle followed by the journal in this regard.

**Permissions:** Please write to [jppindia@gmail.com](mailto:jppindia@gmail.com) for information on how to request permissions to reproduce articles or any other information from the journal.

**Disclaimer:** The information and opinions presented in this journal reflect the views of the authors and not of the Proteomics Society or journal or its editors or international advisors or publisher and does not constitute endorsement by the journal or the society in any way. The journal or society does not assume any liability or responsibility for authenticity, correctness, accuracy, completeness or usefulness of the information published here and is the sole responsibility of the authors.

**Plagiarism:** The authors must ensure that they shun plagiarism in any form, whether in text material or data presented. Authors must thoroughly check their articles for plagiarism using standard, international tools and available practice and the journal assumes no responsibility for plagiarism committed by authors. Articles will be rejected or withdrawn if ever found guilty of plagiarism.

**Ethical Issues, Rights:** Authors are requested to conform to their institutional and country specific ethical guidelines and policies with respect to any biological sample. The society, journal or publisher carries no responsibility of any ethical mis-conduct. Proper ethical clearances must be obtained by the authors from appropriate authorities and the same must be declared in the published articles along with reference number and date of the clearance certificates. For human subjects and patient samples informed consent must be duly obtained by the authors as per regulations of the concerned authority and a statement to this effect should be included in the manuscript. Human and animal rights should not be violated and a statement to this effect must be included in the manuscript as well. All documents related to ethical issues must be readily available with the authors and must be produced on demand.

**Conflict of interest:** The authors must declare conflict of interests, if any.

**Advertising Guidelines:** JPP does accept classified advertisements from legal and well established agencies to promote the journal, as long as they conform to set policies of the journal and are related to the subject matter of the journal publications. Inquiries may be directed to [jppindia@gmail.com](mailto:jppindia@gmail.com). Advertisements do not however suggest that the journal endorses any of the products.

**Supplementary Issue****International Conference on Advances in Biosciences and Biotechnology – ICABB-2018**

(February 01-03, 2018)

**CONTENTS**

Scientific Programme

Day Programme

Message from Executive Chairman

Message from Vice-Chancellor

Message from Organizers

Abstracts for Keynote/Invited talk .....	JPP 3-21
Abstracts for Oral Presentations .....	JPP 23-47
Abstracts for Poster Presentations .....	JPP 49-144

## **ABOUT THE INSTITUTE**

Jaypee Institute of Information Technology, Noida was established in the year 2001 and has been declared as a “Deemed to be University” under Section 3 of UGC Act 1956 in the year 2004.JIIT’s state-of-the-art, environmentally conditioned campus comprises smart buildings with Wi-Fi connectivity covering the Academic Block, Business School cum Research Block, Faculty Residences, Student Hostels and Annapurna. Well equipped modern laboratories and an intellectually stocked Learning Resource Centre with books and E-Resources provide a pleasant and stimulating ambience.JIIT has been constantly ranked amongst the top engineering Institutes in Delhi NCR. Recently it has been ranked among top Engineering Institutes in India by Edu Rand 2014 Engineering College Rankings.

## **ABOUT THE HOST DEPARTMENT**

The Department of Biotechnology at JIIT, NOIDA, established in 2002, remains committed to provide research-informed teaching and learning, and vibrant R & D environment. Faculty with rich research exposure in academia and industry both in India and abroad contributes to the department academic core.

The biotechnology scope is never ending as the power to alter life has just seen its beginning. The field of biotechnology is steadily growing in India. Biotech industry achieves record (15 %) growth in 2012-13. In response to continuously evolving technology and industry needs, curriculum is designed to impart skill sets enabling adaptation to academia, research, and industry. The curriculum provides engineering interface and integrates core subject area knowledge with professional development; focusing on entrepreneurship, analytical and research skills. The research emphasis is reflected in the active doctoral program (30 students pursuing PhD and 09 completed), publications in international/national journals, and sponsored research projects totaling approximately INR-6.28 Crores from premier national funding agencies namely, the Department of Biotechnology (DBT), the Department of Science and Technology (DST), All India Council for Technical Education (AICTE), Indian Council for Medical Research (ICMR) and Department of AYUSH. Interaction with leading scientists from academia and industry through invited lectures, workshops and conferences ensures all-round development of the students. Our students continue to secure positions in graduate schools for MS/Ph.D at universities of international/National repute such as Max Planck Institutes, John Hopkins, Georgia Tech, Keck Graduate Institute, Penn State, IITs etc. among others. Many students have been selected in core biotechnology firms Panacea Biotech, Cadilla Biotech, Ranbaxy, and Premas Biotech Ltd.

## **ABOUT THE CONFERENCE**

**The International Conference on Advances in Biosciences and Biotechnology (ICABB-2018- 1<sup>st</sup> to 3<sup>rd</sup> Feb., 2018)** aims to amalgamate multi-disciplinary fields of biology, biosciences and medical biotechnology. It will provide a platform to academicians, researchers, scholars, technocrats from academia and industry to share their knowledge and experience. An additional one day Pre-Conference **WORKSHOP on Emerging Trends in Target Identification and Drug Design (31<sup>st</sup> Jan., 2018)** is a key feature of the event which would give an opportunity to selected participants to hone their practical skills and interact with International Faculties/Experts.

The Conference focuses on five principal themes defining the advancements in the fields of biotechnology:

- Disease & Omics Technology;
- Pharmaceutical & Medical Biotechnology,
- Industrial Biotechnology,
- Agriculture & Environmental Biotechnology;
- Molecular Biology, Nanobiotechnology & Bioinformatics.

All accepted abstracts will be published online under the umbrella of Journal of Proteins and Proteomics ISSN No. 0975-8151, which is a Journal of the Proteomics Society, India. (An online link will be provided for the same) Selected abstracts from poster and oral presentations will be considered for publication as full length manuscripts by the Conference Technical Committee and the Editorial Members of the following UGC listed Journals.

1. 3Biotech; ISSN: 2190-5738 (electronic version) Impact Factor: 1.361 (Special issue Title: Biotechnology for Medical Interventions)
2. Journal of Proteins & Proteomics; ISSN No. 0975-8151
3. International Journal of Engineering, Technology, Science and Research



# Scientific Programme

For

*Workshop on Emerging Trends in Target Identification and Drug Design (31<sup>st</sup> Jan, 2018)*

## Programme

09:00-09:30	Spot Registration and Distribution of workshop Kit <i>(In front of Auditorium)</i>
09:30-09:40	Inauguration and Welcome Note
<b>09:40-10:20</b>	<b>Invited Talk - Use of probiotic yeast in Crohn's disease against AIEC - Adeline Sivignon, University of Auvergne, France</b>
10:20-10:45	Tea/Coffee Break
<b>10:45-11:25</b>	<b>Invited Talk - Inhibitor screening against the b-clamp of H. pylori. - Dr. Samudrala Gourinath, School of Life Sciences, JNU, New Delhi</b>
<b>11:25-12:05</b>	<b>Invited Talk - Synthetic glycoconjugates as <i>E. coli</i> and <i>A. fumigatus</i> antiadhesives - Sébastien Gouin, University of Nantes, France</b>
<b>12:05 -12:45</b>	<b>Invited Talk - Cryoelectron microscopy: Recent advances and applications - Dr. Manidipa Banerjee, IIT, New Delhi</b>
<b>12:45-13:25</b>	<b>Invited Talk - Design and Screening of Sugar-Derived Small Molecule Inhibitors of Galectins - Cyrille Grandjean, Université des Sciences et Techniques de Nantes, France</b>
13:30-14:30	Lunch
<b>14:30-15:00</b>	<b>Invited Talk - NMR and Calorimetry techniques for Protein interactions - Dr. Neel S. Bhavesh, ICGEB, New Delhi</b>
15:00-15:30	Tea/Coffee Break
<b>15:30-16:00</b>	<b>Invited Talk - Challenges in Protein Crystallization &amp; Data processing - Dr. Ethayathulla Abdulsamath, AIIMS, New Delhi</b>
<b>16:00-16:30</b>	<b>Invited Talk - Surface Plasmon Resonance: Introduction and Application to Drug Discovery - Dr. Likhesh Sharma, GE Healthcare</b>
16:30-17:00	Valedictory & Vote of Thanks



# Scientific Programme

For

**International Conference on Advances in  
Biosciences and Biotechnology – ICABB-2018**  
(February 01-03, 2018)



## DAY 1- THURSDAY, 1<sup>ST</sup> FEBRUARY, 2018

**08:30 am onwards      Conference Registration (in front of Auditorium)**

**09:30-10:30              Inauguration and Welcome Note**

**10:30-11:00              Tea/ Coffee Break**

### **Technical Session : Disease and Omics technology (Chair person: Prof. Nicolas Barnich)**

**11:00-11:35              Invited talk - Structure, mechanism, and antagonism of protein assemblies pivotal to inflammation, autoimmunity, and allergy - Prof. Savvas Savvides, Belgium**

**11:35-12:10              Invited talk - CAPRI: The Diverse Challenges of Computational Protein-Protein Docking. Dr. Marc F Lensink, University of Lille, France**

**12:10-12:45              Invited talk - Sites for Dynamic Protein-Carbohydrate Interactions of *o*-, *n*-, *s*- and *c*-linked Mannosides on the *E. coli* FimH Adhesin - Dr. Julie Bouckaert, France**

**12:45 -13:30              Oral presentations (7 min duration including Q & A) and poster session  
OP1-OP5**

**13:30-14:30              Lunch Break**

### **Technical Session : Industrial Biotechnology & Molecular Biology (Chair person: Prof. Savvas Savvides)**

**14:30-15:05              Invited talk - Human Antibodies: Generation & Applications - Prof. V.K. Choudhary, UDSC, New Delhi**

**15:05-15:40              Invited talk - NMR of Complex Biological Systems and Mixtures- Prof. R.V. Hosur, TIFR, Mumbai**

**15:40-16:10              Tea/ Coffee Break**

**16:10-17:30              Oral presentations (7 min duration including Q & A) and poster session  
OP6-OP13**

**18:00-19:30              Cultural program**

**20:00-21:00              Gala Dinner**

## DAY 2- FRIDAY, 2<sup>ND</sup> FEBRUARY, 2018

### Technical Session : Pharmaceutical & Medical Biotechnology (Chair person: Dr Amit Tyagi, INMAS, Delhi)

09:00-09:35	<b>Invited talk - Adherent-invasive <i>Escherichia coli</i> in inflammatory bowel disease - Prof. Nicolas Barnich, University of Auvergne, France</b>
09:35-10:10	<b>Invited talk - Understanding Disease Heterogeneity in Era of Personalized Medicine - Dr. Anup Madan, USA</b>
10:10-10:45	<b>Invited talk - Diagnostics for the Developing World: A look at the challenges and opportunities - Dr. Shikha Sharma, Abbott, Mumbai</b>
10:45-11:15	Tea/Coffee Break
11:15-11:50	<b>Invited talk - Mr. Rajiv Maini, Pharmcovigilence, Sun Pharmaceuticals, Gurgaon</b>
11:50-13:30	<b>Oral presentations (7 min duration including Q &amp; A) and poster session <u>OP14-OP23</u></b>
13:30-14:30	Lunch Break

### Technical Session : Agricultural and Environmental Biotechnology (Chair person: Dr Pammi Gauba)

14:30-15:05	<b>Invited talk - Optimizing Plant Feedstock for Biofuel Production - Dr. Rita Sharma, School of Computational and Integrative Sciences, JNU, New Delhi</b>
15:05-15:30	<b>Oral presentations (7 min duration including Q &amp; A) and poster session <u>OP24-OP25</u></b>
15:30-16:00	Tea/Coffee Break
16:00-17:30	<b>Oral presentations (7 min duration including Q &amp; A) and poster session <u>OP26-OP40</u></b>

## DAY 3- SATURDAY, 3<sup>RD</sup> FEBRUARY, 2018

### Technical Session : Molecular Biology, Nanotechnology and Bioinformatics (Chair person: Prof. Punit Kaur, Head, Biophysics Dept., AIIMS)

09:00-09:35	Invited talk - Prof. T. P. Singh, AIIMS
09:35-10:10	<b>Invited talk - Synthetic Biology: Emergence of a novel drug discovery platform - Prof. Pawan K. Dhar, School of Biotechnology, JNU, New Delhi</b>
10:10-10:30	<b>Oral presentations (7 min duration including Q &amp; A) and poster session <u>OP41-OP42</u></b>
10:30-11:00	Tea/Coffee Break
11:00-12.00	<b>Oral presentations (7 min duration including Q &amp; A) and poster session <u>OP43-OP51</u></b>
12:00-1:30	<b>Valedictory, Vote of Thanks &amp; Closing Ceremony followed by Lunch</b>

## ORAL PRESENTATIONS

### Technical Session : Disease and Omics technology (Chair person: Prof. Nicolas Barnich)

<b>Day 1</b>	<b>12:45 -13:30</b>	<b>Oral presentations and evaluation session</b>
<i>OP No.</i>	<i>ICABB ID</i>	<i>Title</i>
OP1	275	An <i>in vitro</i> model for <i>M. tuberculosis</i> persistent infection drug discovery studies
OP2	235	Investigating the effect of sugars on antimicrobial peptide Indolicidin
OP3	031	Members of PHISTc protein family localize to different sub-cellular organelles and bind major virulence factor 'PfEMP-1'
OP4	163	The Human Oral Cancer microbiome database
OP5	082	Genome Wide Analysis of Repetitive DNA Sequences of Four Indian Drosophila Species <i>Zaprionus Indianus</i>

### Technical Session : Industrial Biotechnology & Molecular Biology (Chair person: Prof. Savvas Savvides)

<b>Day1</b>	<b>16:10-17:30</b>	<b>Oral presentations and evaluation session</b>
<i>OP No.</i>	<i>ICABB ID</i>	<i>Title</i>
OP6	252	Screening and Identification of potential inhibitors against UDP-N-acetylglucosamine enolpyruvyl transferase (MurA) in <i>Streptococcus pneumoniae</i> : An <i>In silico</i> approach
OP7	081	Lipidomics- an emerging tool to redefine the role of lipids in combating MDR-TB
OP8	006	<i>In-silico</i> prediction of high specificity inhibitors against HpGGT: Implications of divergent sites in drug design
OP9	104	Functional Food: Probiotic as health booster
OP10	166	Screening Selective Estrogen Beta Receptor Modulators against Breast Cancer: An <i>in silico</i> Approach
OP11	113	Metal ions modulated response of sweeteners
OP12	039	Virtual Screening of Chikungunya Virus Envelop Glycoprotein Inhibitors
OP13	057	Expression, Purification and Functional Characterzation of Recombnant Hypervariable Region (HVR) of CHIKV nsp3 Protein

### Technical Session : Pharmaceutical & Medical Biotechnology (Chair person: Dr Amit Tyagi, INMAS, Delhi)

<b>Day2</b>	<b>11:50-13:30</b>	<b>Oral presentations and evaluation session</b>
<i>OP No.</i>	<i>ICABB ID</i>	<i>Title</i>
OP14	001	Nano emulsion based etoposide formulation for improved oral bio availability
OP715	121	Regulation of biosimilars in India: Role of National Institute of Biologicals (NIB)

OP16	137	Pro-resolvin lipid mediators from dietary flax seed oil potentiate the polarization of ATMs from M1 to M2 phenotype High Fat Diet fed Insulin resistant Murine model
OP17	149	Complementary and Alternative Therapies Targeting Oxidative Stress in Inflammatory Bowel Disease
OP18	280	Altered serum proteome profiles in mammary tumorigenesis in Wistar rats: the prognostic signatures
OP19	279	Resveratrol suppressed brain inflammation and oxidative stress during experimental epilepsy
OP20	218	Designing of functionality active smaller palindromic analogues of an antimicrobial peptides : Tritpticin
OP21	220	Antimicrobial and Cytotoxicity evaluation of Polyphenon 60 and Ciprofloxacin loaded Nano emulsion against Uropathogenic strains
OP22	100	Baclofen-loaded PLGA nanoparticles for neuropathic pain management: <i>in-vitro</i> and <i>in-vivo</i> Evaluation
OP23	136	Curcumin mediated effects on anti-diabetic drugs induced cardiotoxicity

**Technical Session : Agricultural and Environmental Biotechnology (Chair person: Dr Pammi Gauba)**

Day2	15:05-15:30 & 16:00-17:30	Oral presentations and evaluation session
OP No.	ICABB ID	Title
OP24	138	Dissecting the Role of á-Tocopherol in Plants: Potential Application for Human Health and Abiotic Stress Alleviation in Plants
OP25	123	Genome wide cytosine methylation in response to dehydration stress modulating the expression pattern of genes in foxtail millet ( <i>Setaria italic</i> )
OP26	092	Analysing the therapeutic potential of <i>Syzygium cumini</i> : A Novel Cardioprotective Agent
OP27	253	Gauging of pollution in river Ganga at Varanasi
OP28	144	Introgression of <i>xa13</i> , <i>Xa21</i> , <i>sd1</i> genes in Indian Basmati using marker assisted backcross breeding
OP29	134	Quality characteristics of underutilized, non-conventional <i>Amorphophallus paeoniifolius</i> flour and starch
OP30	021	<i>In-silico</i> genome wide identification and characterization of glutathione S-transferase gene family in <i>Cajanus cajan</i> (L.)
OP31	096	Conservation of <i>Rheum emodi</i> through <i>in vitro</i> approaches
OP32	131	Various Facets of Histone Modifications
OP33	270	Synergetic effect of metatopolin and benzyladenine on axillary shoots bud induction and proliferation in <i>Rauvolfia tetraphylla</i> (L.) by using nodal explants

OP34	012	Gold Nanoparticles: One-Pot Synthesis through Green Route and Antibacterial Application
OP35	203	Photosynthesis and Growth in Salinity Exposed Mungbean Cultivars- Role of Sulfur, Glutathione, Proline and Glucose
OP36	184	Hydrogen - urea fuel: the dream that won't die
OP37	154	Pathological Interaction of <i>M. incognita</i> , <i>P. betavescularum</i> & <i>R. solani</i> on Growth and Biochemical Changes of Beetroot ( <i>Beta vulgaris</i> )
OP38	108	<i>Usnea longissima</i> Ach: A promising source of nutraceutical
OP39	109	Prophylactic Detection of Pathogenic Bacteria Using PCR And Real Time PCR in Municipal Supplied Drinking Water, Jaipur, India
OP40	215	Abiotic Parameter Mediated Transcriptional Regulation of HMGCoA Reductase in <i>in Vitro</i> Culture of <i>Bacopa monnieri</i>

**Technical Session : Molecular Biology, Nanotechnology and Bioinformatics**  
**(Chair person: Prof. Punit Kaur, Head, Biophysics Dept., AIIMS)**

**Day 3    10:10-10:30 &  
 11:00-12.00      Oral presentations and evaluation session**

OP No.	ICABB ID	Title
OP41	230	Multistage unfolding dynamics of TDP-43 to characterize the intermediate Ensembles involve in amyotrophic lateral sclerosis
OP42	112	Chemical synthesis of novel antimicrobial peptide against MDR (multidrug resistant) strains of <i>E. coli</i>
OP43	168	Development of QSAR Model for ICL Inhibitors
OP44	187	Recombinant TPI and PGAM based ELISA for detecting anti-TPI and PGAM antibodies in mammary tumors of Dog
OP45	259	<i>In silico</i> screening for identification of novel CysE inhibitors: Targeting the $\beta$ -helix cap of the LâH domain
OP46	119	Fetal Heart MicroRNA Profiling and Functional Annotation: An Indication Towards Gene Reprogramming in Cardiac Pathologies
OP47	111	tRNA Structure Analysis across <i>Wolbachia</i> Endosymbionts
OP48	171	Characterization of antimicrobial protein with antibiofilm activity from the goat milk isolate
OP49	037	Standardization Studies on Surface Sterilization, <i>in vitro</i> Shoot Induction and Multiplication of <i>Thrysostachys Oliveri</i>
OP50	038	Exploration of novel adhesive bandage for Accelerated and Scar-free Wound Healing
OP51	268	Identification of drug target for multidrug resistant biofilm forming <i>Acinetobacter baumannii</i>

## POSTER PRESENTATIONS

- The printed Poster hard copies should be taken to the conference by the delegates, and will be posted to the poster area in the designated position according to the "registration Number".
- Tacks and technical equipment will be available for the hanging of posters.
- Authors who are presenting the poster are required to stand by their poster during each poster session but posters should be placed before the beginning of the session
- **Please remove your poster after the assigned date and time.** The Organizing Committee will not be responsible for posters that are not removed on time.

### Technical Session : Disease and Omics technology (Chair person: Prof. Nicolas Barnich)

<b>Day 1</b>	<b>12:45 -13:30</b>	<b>Poster presentations and evaluation session</b>
<i>PP No.</i>	<i>ICABB ID</i>	<i>Title</i>
PP1	003	Effective therapies for third generation resistant non-small cell lung cancer
PP2	010	Lp-23: a potential antibacterial lipopeptide against <i>Mycobacteria smegmatis</i>
PP3	019	Therapeutic treatment of lung cancer : micro RNA
PP4	023	Epigenetic therapy approaches in non-small cell lung cancer
PP5	032	Reviewing the inhibitor approaches targeted against plant viruses
PP6	033	Emerging and resurging encephalitis viruses : the Indian scenario
PP7	070	The impact of Next Generation Sequencing technology on health and disease
PP8	071	Potential effects of nicotine on the health of female foetus and passive smokers
PP9	072	EGB761 an active component of <i>Ginkgo biloba</i> : treating alzheimer disease
PP10	074	Smoking cessation: an analysis of currently available methods to quit smoking
PP11	080	MiRNA : epigenetic biomarkers in cardiac disease
PP12	098	Challenges and strategy in the era of multidrug resistance
PP13	132	Rheumatic heart disease: impact of socioeconomic factors on disease outcome in Assam, India
PP14	135	Effects of aging and camkii regulation on cardiovascular functionality of <i>Drosophila melanogaster</i>
PP15	141	Viral encephalitis in India
PP16	142	Omega3 fatty acids as therapy for multiple sclerosis treatment
PP17	177	Immunotherapy: cancer treatment
PP18	180	Transfection of EGFP tagged recombinant CHIKV protein in mammalian cells
PP19	186	Molecular link between obesity and breast cancer in menopause women
PP20	192	Application of Next Generation Sequencing in cardiovascular diseases: A revolutionized approach

PP21	193	Tools for processing of Next Generation Sequencing large dataset
PP22	196	Alterations of cell membrane integrity and extracellular polysaccharide matrix of <i>Cryptococcus neoformans</i> biofilm of exposure to essential oil active components
PP23	212	Mesenchymal stem cell tissue engineering
PP24	223	High grade brain tumor and drug resistance
PP25	224	Phylogenetic & conservation analysis of MFS transporters
PP26	236	Effect of anti-leishmanial drug amphotericin B on transcription factors STAT3 and ROR $\alpha$ in experimental visceral leishmaniasis
PP27	237	<i>Leishmania donovani</i> infection in BALB/C mice: modulation of key innate immunity genes TLR2 and TLR4 via MyD88 signalling pathway during infection and after treatment with amphotericin B.
PP28	243	Analysis of <i>Aedes aegypti</i> interactome mediated by arboviruses
PP29	245	Role of innate immunity in the process of neurodegeneration
PP30	256	Next generation sequencing analysis pipeline
PP31	262	Sequencing technologies for transcriptomic analysis
PP32	268	Identification of drug target for multidrug resistant biofilm forming <i>Acinetobacter baumannii</i>
PP33	272	Cloning, large scale purification and characterization of crystallization grade CysF from <i>Klebsiella pneumoniae</i>
PP34	274	Identification of biofilm associated genes of <i>Mycobacterium</i> species: a review of technique and strategies
PP35	097	Targeting active site flexibility of <i>Mycobacterium Tuberculosis</i> Isocitrate Lyase for Potent Inhibitors
PP36	084	Mining for novel cellulases using metagenomics, metatranscriptomics and metaproteomics

**Technical Session : Industrial Biotechnology & Molecular Biology (Chair person: Prof. Savvas Savvides)**

Day 1	16:10-17:30	Poster presentations and evaluation session
PP No.	ICABB ID	Title
PP37	60	The emerging role of DHA in Parkinson's disease
PP38	172	Molecular Docking of Insulin Receptor Against Natural Bioactive Compounds and their Derivatives with Hypoglycemic Effect
PP39	173	Comparative Analysis of Alkaloids and its Derivatives as Binding Ligands of B-DNA : A Computational Approach
PP40	239	Unfolding dynamics of TDP-43 RRM-1 domain involved in frontotemporal lobar degeneration revealed by Atomistic Simulations
PP41	49	Enhanced lipid production using fed-batch fermentation of Oleaginous yeast isolates for future biodiesel

PP42	52	3D - Bioprinting: promising future of medicine
PP43	54	Organic leather as a startup
PP44	59	Mycoremediation: an approach to remediate heavy metals
PP45	61	Green Food Processing techniques
PP46	79	Microalgae in commercial market
PP47	86	Latest trends in Cosmeceuticals
PP48	95	Algae biofuel production
PP49	103	Optimization strategies for maximal bacteriocin production from lactic acid bacteria
PP50	158	Active cosmetic ingredients obtained through biotechnology for skin care
PP51	178	Biofabrication for product development
PP52	195	Designing principle of photobioreactor: an approach of mass microalgae cultivation
PP53	214	The Glycerol biorefinery for industrially important chemicals
PP54	258	Optimization of PVA gel technology for non-segregated MSW leachate treatment.
PP55	269	Pre-bleaching of unbleached bamboo pulp with Laccase enzyme produced by <i>Pseudomonas</i> sp. PBS-2 from North-East Indian Bio-resource
PP56	271	Effects of probiotics on gut-brain axis
PP57	278	Development of An Anti-Fungal Drug Loaded Nanoemulgel For The Treatment Of Oral Candidiasis
PP58	77	Fault in our gut: obesity, diabetes and gut microbiota
PP59	105	A facile composite comprising of encapsulated <i>Citrobacter Freundii</i> LCJ002 and Iron oxide nanoparticles for the removal of toxic diazo dye congo Red
PP60	140	The emerging trend: Bioremediation of organic and inorganic air pollutant
PP61	148	Biodegradation of dimethoate residue by native Rhizobacterial isolates
PP62	156	Studies on optimization of siderophore production by microbial isolate obtained from aquatic soil and its antibacterial activity
PP63	161	Optimization of indole acetic acid produced by bacterium isolated from Rhizospheric region of <i>Triticum aestivum</i> (wheat plant)
PP64	206	Using synthetic biology for biofuel production
PP65	228	Application of glucomannan
PP66	234	Irradiated chitosan mediated changes on growth, biochemical processes and menthol production in <i>Mentha arvensis</i> L. In Northern Himalayas
PP67	260	Eco-friendly wastewater treatment- use of a microalgae
PP68	277	Handmade paper making by eco-friendly processes: production of acid free, chlorine and azo free paper

**Technical Session : Pharmaceutical & Medical Biotechnology (Chair person: Dr Amit Tyagi, INMAS, Delhi)**

<b>Day 2</b>	<b>11:50-13:30</b>	<b>Poster presentations and evaluation session</b>
<b>PP No.</b>	<b>ICABB ID</b>	<b>Title</b>
PP69	249	Irritable bowel syndrome: a gut brain axis disorder?
PP70	085	DHA Supplementation and Alzheimer's Disease
PP71	233	Morphene and its similars: overcoming the side effects
PP72	013	Antiulithiatic properties of <i>Bryophyllum pinnatum</i>
PP73	014	Macrotyloma uniflorum and its medicinal properties
PP74	016	Micro RNAs As Biomarkers For Diagnosis Of Cancer
PP75	018	Effect of inhibitor and stimulator in nephrolithiasis
PP76	024	Phytotherapy: emerging trends for ros induced urolithiasis
PP77	026	Preparation of oil in water nanoemulsions of donepezil for the treatment of alzheimer's
PP78	281	Evidence based validation of Herbal Medicines
PP79	045	Antibody drug conjugate- a targetted approach to cancer
PP80	046	Antimicrobial and Cytotoxicity evaluation of Polyphenon 60 and Ciprofloxacin loaded Nano emulsion against Uropathogenic strains
PP81	047	Treatment of alzheimer: natural remedies versus synthetic drugs
PP82	067	Biomedical & pharmaceutical applications of chitosan based material
PP83	087	Therapeutic potential of Cannabis
PP84	091	Gut microbiota and metabolic syndrome
PP85	094	Current cancer vaccines
PP86	110	Assessment of Vitamin D in type II Diabetic patients
PP87	116	Media optimization for Bacteriocin production
PP88	120	Method validation of CDC bioassay for assuring efficacy of Anti- CD20 monoclonal antibody Biosimilars
PP89	126	Molecular characterization of glycoprotein D(GD) of bovine Herpes virus - 1 as a potential diagnostic antigen
PP90	128	Expression of Methionine Sulfoxide Reductase A: Protein Repair Enzyme in Prokaryotic system
PP91	130	Medicinal plants for prevention and treatment of Parkinson's disease
PP92	152	Exploring mechanism of action of opioids
PP93	157	Screening of Carotenoid producing bacteria from various sources
PP94	159	Resistance to wonder drugs- antibiotics: A Review
PP95	165	Targeting of Natural compounds as Potential Anticancer agents against G-Quadruplex structure

PP96	182	Recent applications of bacterial cellulose and its composites
PP97	198	Advancement in the Ovary Freezing Technique for the Treatment of Ovarian Diseases
PP98	211	Genital and urinary tract infections in Diabetes
PP99	213	Comparative toxicity analysis of anti-diabetic drugs in cardiac cell lines
PP100	217	Improved yield attributing traits and quinonic compounds in <i>Nigella sativa</i> L. - A phytotherapeutic herb of India
PP101	222	Effects of Benzidine as aromatic spacer in enzyme conjugate on bridge heterologous ELISA for Prednisolone
PP102	227	Animal model development of anti-ovulatory study
PP103	238	Oxidative stress: cause of infertility
PP104	241	Role of antioxidant coenzyme Q and vitamin E in neuroprotection of glutamate induced damage in retinal ganglion cells
PP105	247	Development and stability analysis of essential oil loaded micro-emulsion for transdermal application
PP106	264	Screening of multidrug resistant bacteria from sewage from different sites in Delhi/NCR
PP107	265	Understanding cable bacteria: a biogeobattery
PP108	273	Role of DHA in brain development
PP174	145	Analysis of L6 skeletal muscle cells proteins expressed on exposure to diverse glucose concentration using MALDI-TOF
PP176	160	Cloning and expression of truncated ORF-2 as a vaccine candidate against Hepatitis E virus
PP203	058	Evaluation of Boswellic acid derived from <i>Boswellia serrata</i> as anti-inflammatory and anti-oxidant agent

**Technical Session : Agricultural and Environmental Biotechnology (Chair person: Dr Pammi Gauba)**

Day2	16:00-17:30 & 15:05-15:30	Poster presentations and evaluation session
PP No.	ICABB ID	Title
PP109	150	Therapeutic uses of common Indian plants for treatment of brain tumor
PP110	225	Herbal remedies for Rheumatoid artheritis: A review
PP111	008	Antifungal properties of bacterial isolates from Firoz shah kotla fort against phytopathogens
PP112	011	A biological approach for rapid synthesis of silver nanoparticle for waste water treatment
PP113	020	Epigenetic changes in glioblastoma and targeted therapies
PP114	022	<i>Withania somnifera</i> : the rejuvenator

PP115	029	Carbon sequestration: a solution to global problem
PP116	030	Gut-Brain Connection and Mental Health
PP117	034	Decolourization of textile azodye direct red 31 by immobilized <i>Scenedesmus rubescens</i> isolated from textile effluent
PP118	088	Pesticide Degradation by Micro-organisms
PP120	040	Allelopathic effect of <i>Syzygium cumini</i> and <i>Ocimum tenuiflorum</i> plants
PP121	041	Diatoms as a fuel: A futuristic approach
PP122	042	Screening and characterization of micro-organisms for anti microbial activity from the biodiversity rich Timli forest range India
PP123	048	Phytoremediation: A green solution for heavy metal degradation
PP124	050	Role of probiotics in prophylaxis of <i>Helicobacter pylori</i> infection
PP125	051	Impact of antibiotics on plant growth
PP126	053	Remediation of nitrate by microorganisms
PP127	055	Fungal Chitosan and its application
PP128	068	Fighting depression with omega-3 fatty acids
PP129	073	Biological control of post harvest diseases in agricultural grains
PP130	075	Impact of Heavy metals on medicinal herbs
PP131	076	Gut emotions: Psychobiotics as an adjuvant therapy in depression and anxiety disorders
PP132	078	Rutin: extraction & biological activities
PP133	089	Effect of different lights on the growth and development of endangered medicinal herb <i>Rhodiola imbricate</i>
PP134	114	Optimization of carotenoid production by yeast strains from different sources using agro-renewable waste
PP135	117	Chitinolytic bacteria: as biocontrol agent
PP136	127	Brassinosteroid-seed treatment regulates biochemical responses of <i>Brassica juncea</i> seedlings under insecticide stress
PP137	146	Interdependancy of soil quality and microbial activity: A Review
PP138	147	A study on dynamic association between soil quality and microbial activity in selected regions of North India
PP139	153	Investigation of Alternative Splicing Modulation Occurring on Infection of <i>Tomato leaf curl New Delhi</i> virus (tolcndv) in Tomato ( <i>Solanum lycopersicum</i> L.)
PP140	155	Bio Chemical and phytoconstituents study of plants grown in fly ash amended soil: A waste management approach
PP141	179	Impact of lead on Leguminous plants
PP142	185	Equilibrium studies of pb2+ ions biosorption from aqueous solution using <i>S.filipendula</i>

PP143	190	Expression Analysis of Chitinase class-IV gene of <i>Brassica juncea</i> in response to hormonal treatments and <i>Alternaria brassicae</i>
PP144	199	Analysis of transcriptome and metabiome responses during cr(vi) stress in roots of <i>Oryza sativa</i>
PP145	201	Production of proinsulin in milk of transgenic animals
PP146	204	<i>Azotobacter vinelandii</i> strain SRIA23 influences <i>Piriformospora indica</i> growth under <i>in vitro</i> conditions
PP147	205	Advantages of genetically modified phytase producing crops
PP148	207	<i>In vitro</i> assessment of <i>Piriformospora indica</i> under salinity stress
PP149	229	Estrogen toxicity
PP150	254	Auxin priming and induction of S phase kinase associated protein 1 SKP1 during terminal heat stress in wheat ( <i>Triticum aestivum</i> )
PP151	278	Development of a Antifungal Drug Loaded Nanoemulgel for the Treatment of oral Candidiasis
PP152	017	Wheat Gluten and Puroendolin as Edible food coating
PP153	066	Impact of Antibiotics on Plants
PP154	276	Evaluation of anti-microbial property of heparin binding domain of goat vitronection
PP155	007	Molecular cloning and functional characterization of fatty acid hydroxylase from plants

**Technical Session : Molecular Biology, Nanotechnology and Bioinformatics**  
**(Chair person: Prof. Punit Kaur, Head, Biophysics Dept., AIIMS)**

Day3	10:10-10:30 & 11:00-12.00	Poster presentations and evaluation session
PP No.	ICABB ID	Title
PP156	093	Essentiality of Methylisocitrate lyase
PP157	101	Understanding CysK for developing Future Therapeutics
PP158	107	Role of Isocitrate lyase: adaptation to best environment
PP159	232	Application of nanotechnology for nitric oxide gas in therapeutics
PP160	002	Analysis of pilin biosyntheses genes in virulence of <i>Arromonas hydrophila</i>
PP161	004	Comprehending the patterns for co-existence of Rheumatoid Arthritis and Ankylosing spondylitis through gene expression profiling
PP162	009	Identification of a differentially expressed genetic signature in obstructive sleep apnea
PP163	027	<i>In silico</i> studies of uncharacterized genes of <i>Bramia Juncea</i> L.
PP164	043	Colon cancer: Resistance and Treatment
PP165	056	Identification and manipulation of FNR promoter of <i>Salmonella typhimurium</i>

PP166	069	Advancement of Nanotechnology in Tuberculosis
PP167	083	Role of micro RNA as oncomir and tumor suppressor
PP168	099	Applications of nanotechnology in cosmetics
PP169	102	Mycobacterial Rv1916 has Isocitrate Lyase activity: A controversy resolved
PP170	106	Molecular imaging and their potential use in Nanotechnology
PP171	124	Focused Ultrasound used to deliver nanoparticles across blood brain barrier
PP172	125	Nanotechnological revolution in food industry
PP173	129	Challenges in changes disease vaccine development role of Bioinformatics and networks
PP175	151	Investigation of interactions of camphene molecule with oxidative enzymes: Docking studies
PP177	162	Use of Nanotechnology for the treatment of Schizophrenia
PP178	164	Tobacco stem silver nanoparticles: A Neuroprotective Agent
PP179	167	Nano-forensics: a tighter knot for criminals
PP180	169	<i>In silico</i> molecular docking studies of azols against lanosterol-14-alpha-demethylase protein (ERG11P) from <i>Candida tropicalis</i>
PP181	282	Substituent structure-solubility relationship for prodrug designing with improved solubility profile
PP182	175	Induced pluripotent stem cells - a step forward in stem cell therapy
PP183	176	Ras oncogenes as emerging therapeutic targets and potential biomarkers for cancer
PP184	181	Association of Serotonin (5-HT) with drugs/substance abuse addictive behavior
PP185	188	Chikungunya polymerase: a potential targets for inhibitors <i>in silico</i> study
PP186	189	Biology and competitive genome analysis of <i>Acinetobacter baumannii</i> : an emerging nosocomial pathogen
PP187	191	Characterization of MIR-30 family member in Norepinephrine induced cardiac hypertrophy
PP188	197	Study on drug formulation on Neuropathic pain
PP189	202	Expanding the repertoire of amino acid
PP190	216	Dramatic increase in the Expression of recombinant CysE from <i>Streptococcus pneumoniae</i> by codon Optimization
PP191	219	The role of Nanotechnology in stem cell therapy
PP192	226	Analysis of exemestane from lipid polymer hybrid Nano particles
PP193	231	Phycoobiotics :pirates of Gut microbiota
PP194	242	Bioinformatics and Drug Discovery

PP195	244	Nano-carriers for Vaccine Designing- updates and concerns
PP196	246	Fabrication, Validation and Optimization of polymeric Nanoparticles for enhancing neural activity
PP197	248	Applications of the NGS in deciphering human gut microbiome
PP198	250	Detection of copy number variations through Next Generation Sequencing to identify genetic basis of cancer
PP199	251	<i>In silico</i> studies of FDA approved drugs against <i>Salmonella typhi</i> FTSZ dimension protein
PP200	261	Standardization of virtual screening and Post-analysis protocols relevant to <i>in-silico</i> drug discovery
PP201	266	<i>In silico</i> studies of natural compounds against Japanese Encephalitis Virus N53 protein
PP202	221	Identification and analysis of mobile genetic elements in Gibbon genome

January 25, 2018



### Message

It is indeed a matter of great pleasure for me to know that the **Department of Biotechnology, Jaypee Institute of Information Technology, Noida** is organizing an "**International Conference on Advances in Bio-sciences and Biotechnology (ICABB)**", from **1<sup>st</sup> - 3<sup>rd</sup> February, 2018**.

I am certain that this International Conference will provide an opportunity to all the participants to share their research outcomes and pick up new ideas to get valuable feedback and suggestions in their research studies. I am confident that the outcome of this conference will be of great value to all researchers, academicians and scientists working in various areas of the Biotechnology.

I express my best wishes to all the organizers and participants of the conference and wish them a grand success in the organization of this event.



Manoj Gaur



# Jaypee Institute of Information Technology

(Declared Deemed to be University u/s 3 of the UGC Act)

January 25, 2018

**Prof. (Dr.) S. C. Saxena**  
Vice-Chancellor



## Message

It gives me great pleasure to know that the **Department of Biotechnology, Jaypee Institute of Information Technology, Noida** is organizing an "**International Conference on Advances in Bio-sciences and Biotechnology (ICABB)**", from **1<sup>st</sup>-3<sup>rd</sup> February 2018**. The conference will provide an excellent platform for exchange of research findings and new advances in the thematic areas of the conference. I am certain that the deliberations during the conference will be of enormous value to all the participating delegates and will bring out new ideas and solutions to the challenging problems related to the themes. I am sure that the conference will prove a highly rewarding experience for the participants.

I convey my best wishes to the organizers and participants and wish a grand success to the event.

With best wishes,

  
(S.C. Saxena)



## Message from organizers



It gives us great pleasure in handing over this memoir of our International event ICABB-2018 to you. We welcome you all to International Conference on Advances in Biosciences and Biotechnology (ICABB-2018), being organized by Department of Biotechnology, Jaypee Institute of Information Technology, Noida from February 1st-3rd 2018. On behalf of the Organizing Committee we wish you a comfortable stay and a fulfilling research experience during the conference.

The Conference focuses on five principal themes defining the advancements in the fields of biotechnology: Disease & Omics technology; Pharmaceutical & Medical biotechnology, Industrial Biotechnology, Agriculture & Environmental Biotechnology; Molecular Biology, Nanobiotechnology & Bioinformatics. It aims to amalgamate these multi-disciplinary fields of biology, biosciences and medical biotechnology by providing a platform to academicians, researchers, scholars, technocrats from academia and industry for sharing their knowledge and experience. An additional one day Pre-Conference WORKSHOP (31st Jan 2018) on Emerging Trends in Target Identification and Drug Design is a key feature of the event which would give an opportunity to participants to hone their practical skills and interact with International Faculties/ Experts. Participants can look forward to recent developments and brain storming sessions.

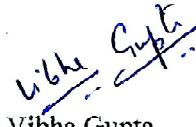
This event is a result of continuous and sincere efforts of all the faculty members of Department of Biotechnology involved in the planning and execution of this conference. We are highly grateful to all international and national speakers who agreed to come and deliver talks for the conference. We are extremely thankful to our Advisory committee members for their guidance.

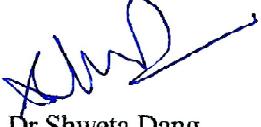
We thank Prof S. C. Saxena, Hon'ble Vice Chancellor, for his constant motivation, guidance, valuable inputs and support extended to make this conference a success. Without his cooperation and full support, this conference would not have been possible.

We also take this opportunity to thank our publishing partners, sponsors and extend our sincere thanks to Indian Council of Medical Research, Government of India for partially funding this conference.

Thank you all once again, and we look forward to a productive event.

  
Dr Pammi Gauba  
Co-Chair

  
Dr Vibha Gupta  
Convener

  
Dr Shweta Dang  
Convener

# **Keynote/Invited talk**

*for*

***Workshop on Emerging Trends in Target  
Identification and Drug Design***

***(31st Jan, 2018)***

*&*

***International Conference on Advances in  
Biosciences and Biotechnology - ICABB-2018***

***(February 01-03, 2018)***

---

## PROBIOTICS AND BACTERIOPHAGES IN CROHN'S DISEASE: TWO STRATEGIES TO TARGET ADHERENT-INVASIVE ESCHERICHIA COLI BACTERIA (AIEC)

Adeline Sivignon

M2iSH, U1071, Inserm/ Université Clermont Auvergne, Clermont-Ferrand, France



**Objective.** Adherent-invasive *Escherichia coli* (AIEC) are abnormally predominant on Crohn's disease (CD) ileal mucosa. AIEC are pathobiont bacteria able to induce inflammatory responses that could initiate or perpetuate the chronic gut inflammation. Probiotics or bacteriophages (viruses infecting bacteria) represent two different ways to eliminate these bacteria from the gastro-intestinal tract, without disturbing the microbiota homeostasis. Here, we evaluated the potential of these two methods to reduce AIEC gut colonization and the signs of colitis.

**Methods.** 1/Bacteriophages: Three bacteriophages were selected to efficiently target AIEC bacteria isolated from CD patient. Efficacy of this bacteriophage cocktail was investigated using two *in vivo* experimental models: transgenic mice expressing CEACAM6 ('CEABAC10 mice') colonized by AIEC strain LF82 and the DSS chemically-induced colitis model infected with AIEC LF82.2/Probiotics: The effect of *Saccharomyces cerevisiae* CNCM I-3856 was assessed *in vitro* on the T84 cell line, and *ex vivo* on ileal enterocytes from CD patients, both infected with LF82 bacteria. Then, yeasts were daily administered to LF82-infected CEABAC10mice. Bacterial colonization, severity of diarrhea and intestinal pro-inflammatory cytokine release were analyzed. Intestinal permeability was assessed by measuring 4 kDa dextran-FITC flux in serum and claudin-2 expression was visualized by immune fluorescence on proximal colon.

**Results.** 1/ In LF82-colonized CEABAC10 mice, 24h after the oral administration of the cocktail of bacteriophages, the fecal concentration of LF82 bacteria has significantly dropped by two log in the bacteriophage group and stays significantly lower than in control group four days post-treatment. The colonization level of LF82 bacteria reduced progressively over a period of five days through the entire gut. Bacteriophage treatment reduced colitis symptoms in the DSS-induced model with a reduction of LF82 bacterial levels in feces, compared to the control group. 2/*S. cerevisiae* CNCM I-3856 decreased the AIEC LF82 gut colonization in CEABAC10 mice. This probiotic effect was accompanied by an improvement of the signs of colitis, a prevention of intestinal mucosa injuries and a decrease in the release of pro-inflammatory cytokines. Interestingly, yeast cell wall derivatives demonstrated similar preventive effects on LF82 colonization and signs of colitis.

**Conclusion.** The high efficacy of the bacteriophages targeting AIEC bacteria and of the probiotic *Saccharomyces cerevisiae* CNCM I-3856 in different cellular and murine models suggest that such treatments could reduce AIEC-associated symptoms in CD patients, providing an incentive to initiate clinical studies. These two strategies provide therefore, a new "microbiota friendly" way to efficiently target gut pathogens.

---

## INHIBITOR SCREENING AGAINST THE B-CLAMP OF *H. PYLORI*

**Dr. Samudrala Gourinath,**

*School of Life Sciences, JNU, New Delhi*

---

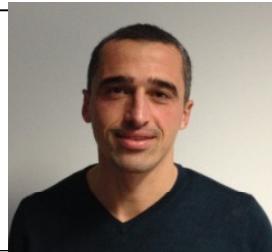


The  $\beta$ -clamp is the processivity-promoting factor for most of the enzymes in prokaryotic DNA replication; hence, it is a crucial drug target. In the present study, we investigated the  $\beta$ -clamp from Helicobacter pylori, aiming to seek potential drug molecules against this gastric-cancer-causing bacterium. An in silico screening of Food and Drug Administration (FDA) approved drugs against the *H. pylori*  $\beta$ -clamp, followed by its in vitro inhibition using a surface competition approach, yielded the drug diflunisal as a positive initial hit. Diflunisal inhibits the growth of *H. pylori* in the micromolar range. We determined the structure of diflunisal in complex with the  $\alpha$ -clamp to show that the drug binds at subsite I, which is a protein-protein interaction site. Successful identification of FDA-approved molecules against *H. pylori* may lead to better and faster drug development.

## SYNTHETIC GLYCOCONJUGATES AS *E.COLI* AND *A. FUMIGATUS* ANTIADHESIVES

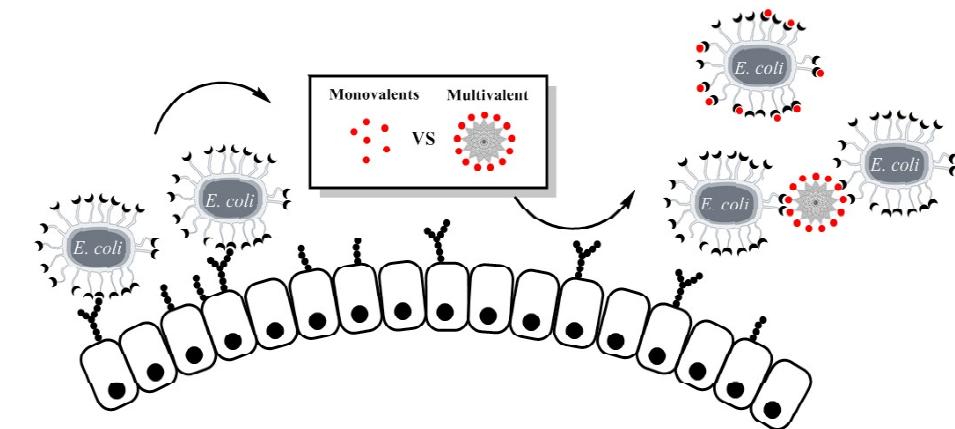
Sébastien G. Gouin

*University of Nantes, CEISAM, Chimie Et Interdisciplinarité, Synthèse, Analyse, Modélisation,  
UMR CNRS 6230, UFR des Sciences et des Techniques, 2, rue de la Houssinière,  
BP 92208, 44322 NANTES Cedex 3, France*



Increasing bacterial resistance to antibiotics is a serious health problem, which is worsening with the constant identification of strains resilient to commonly available chemotherapeutic agents. Among the therapeutic alternatives developed at the academic level, the anti-adhesive strategy has seen a growing interest in the last 25 years.<sup>[1,2]</sup> The concept is to disrupt the lectin-mediated adhesion of the pathogen to eukaryotic cells. This therapeutic approach should be less prone to bacterial resistance and selection pressures as the pathogens are not killed during the decolonisation process.

Several relevant bacterial targets have been identified, including the mannose-binding lectin FimH, displayed at the tip of long proteinaceous *E. coli* organelles called pili, and the AFL lectin from *A. fumigatus* at the surface of the spores (conidia). We developed potent FimH antagonists to disrupt the attachment of pathogenic *E. coli* to bladder and intestinal cells for the potential treatment of urinary tract infections and inflammatory bowel diseases (Crohn's disease), respectively.<sup>[3,4]</sup> More recently we extended this anti-adhesive concept to *A.fumigatus* conidia. We will discuss the design of mono- and multivalent lectin antagonists and their *in vitro* and *in vivo* potential in the treatment of specific infections.



- [1] A. Bernardi, J. Jimenez-Barbero, A. Casnati, C. De Castro, T. Darbre, F. Fieschi, J. Finne, H. Funken, K.-E. Jaeger, M. Lahmann, et al., *Chem. Soc. Rev.* **2013**, *42*, 4709–4727.
- [2] D. Deniaud, K. Julienne, S. G. Gouin, *Org. Biomol. Chem.* **2011**, *9*, 966–979.
- [3] J. Bouckaert, Z. Li, C. Xavier, M. Almant, V. Caveliers, T. Lahoutte, S. D. Weeks, J. Kovensky, S. G. Gouin, *Chem. – Eur. J.* **2013**, *19*, 7847–7855.
- [4] D. Alvarez Dorta, A. Sivignon, T. Chalopin, T. I. Dumych, G. Roos, R. O. Bilyy, D. Deniaud, E.-M. Krammer, J. de Ruyck, M. F. Lensink, et al., *ChemBioChem* **2016**, *17*, 936–952.

---

## CRYOELECTRON MICROSCOPY: RECENT ADVANCES AND APPLICATIONS

**Speaker: Dr. Manidipa Banerjee,**

*Associate Professor, Kusuma School of Biological Sciences,  
Indian Institute of Technology - Delhi*

---



The last few years has seen unprecedented progress in the field of cryoelectron microscopy and image processing, with the resolution and size barriers being broken. Central to these efforts has been the development of equipment and methods such as direct electron detector, phase plate and in-column filters, in addition to the availability of powerful microscopes and better algorithms for data collection and processing. Currently, cryoelectron microscopy can routinely generate detailed structural information of proteins at resolutions of 2 - 3 Å, which was previously possible only through X-ray crystallography. In addition, although cryoEM was previously applicable for larger proteins complexes exclusively, high resolution structure of biomolecules less than 100 KD are frequently being resolved. Since cryoEM based structural analysis requires significantly less sample and time compared to other structural biology methods, it is expected to revolutionize the field of structural biology and forever alter the landscape of structure-based drug design. The applications of cryoelectron microscopy in deciphering virus-host interaction and virus structure will be discussed.

## DESIGN AND SCREENING OF SUGAR DERIVED SMALL MOLECULE INHIBITORS OF GALECTINS

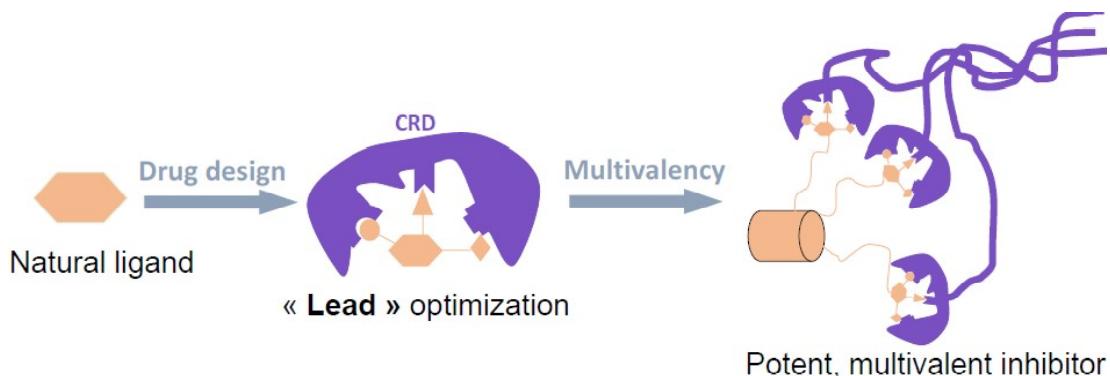
Johann Dion, Nataliya Storozhylova<sup>1</sup>, Samir Dahbi, Annie Lambert,  
Stéphane Téletchéa, Christophe Dussouy, Cyrille Grandjean

*Unité Fonction et Ingénierie des Protéines (UFIP), UMR CNRS 6286, Université des Sciences et Techniques de Nantes. Nantes. France. E-mail:cyrille.grandjean@univ-nantes.fr*



Galectins are key players of homeostasis and as such, their expression and function are finely tuned *in vivo*. Depending on the cell type and/or stage of differentiation, they can be found in the nucleus, in the cytoplasm and also extracellularly. Galectins have been shown to be either directly or indirectly associated to more than 100 human pathologies, spanning from inflammatory diseases, infectious diseases, diabetes, heart failure to cancer.<sup>1</sup> As a consequence, interfering with galectin/ligand interaction has been proposed as potential novel therapeutic strategies or, at least, as a practical mean to delineate the roles of the galectins played in fundamental biological processes.

We thus devised a strategy based on both drug-design and cluster-effect to design potent and specific sugar-related small molecule inhibitors of the galectins. (Figure 1).



**Figure 1:** Overall strategy to obtain potent and specific inhibitors starting from natural sugar-based ligand of the galectins.

Binding affinities of these derivatives are characterized using a set of biophysical methods including microarray screening, fluorescence anisotropy measurements, isothermal microcalorimetry and X-ray crystallography.<sup>2,3</sup> Most affine or selective derivatives are selected and their functional utility assessed both *in vitro* and *in vivo*.<sup>4,5</sup>

1. Klyosov A.A.; Traber P.G. in *Galectins*, Ed. American Chemical Society, **2012**, pp. 3-43.
2. Atmanene, C.; Ronin, C.; Gautier, F.-M.; Djedaiñi-Pillard, F.; Téletchéa, S.; Ciesielski, F.; Vivat, V.; Grandjean, C. *Biochem Biophys Res Commun* **2017**, 489, 281-286.
3. Dion, J.; Advedissian, T.; Storozhylova, N.; Dahbi, S.; Lambert, A.; Deshayes, F.; Viguer, M.; Tellier, C.; Poirier, F.; Téletchéa, S.; Dussouy, C.; Tateno, H.; Hirabayashi, J.; Grandjean, C. *Chembiochem* **2017**, 18, 2428-2440.
4. Dion, J.; Deshayes, F.; Storozhylova, N.; Advedissian, T.; Lambert, A.; Viguer, M.; Tellier, C.; Dussouy, C.; Poirier, F.; Grandjean, C. *Chembiochem* **2017**, 18(8), 782-789.
5. Coppin, L.; Vincent, A.; Frénois, F.; Duchêne, B.; Lahdaoui, F.; Stechly, L.; Renaud, F.; Villenet, C.; van Seuningen, I.; Letourtre, E.; Dion J.; Grandjean, C.; Poirier, F.; Figeac, M.; Delacour, D.; Porchet, N.; Pigny, P.\* *Sci Rep*, **2017**, 7:43927.

---

## NMR AND CALORIMETRY TECHNIQUES FOR PROTEIN INTERACTIONS

**Neel Sarovar Bhavesh**

*Transcription Regulation group, International Centre for Genetic Engineering and Biotechnology (ICGEB), New Delhi 110 067, Email: neelsb@icgeb.res.in; Web: <http://www.neelsb.com>*

---



To carry out variety of biological processes in a complex and regulated manner, proteins generally interact with other molecules. Therefore an understanding of function depends on our ability to map the interaction networks that exist in different cellular processes. The study of protein interactions not only helps in understanding the molecular basis of human diseases but has immense applications in a number of therapeutic areas, particularly drug design. Protein interactions range from high affinity ( $K_d < nM$ ) to very low affinity ( $K_d > mM$ ). Though there are many tools for study of protein interactions, complete characterization of protein interaction can be obtained by determining the thermodynamic parameters and by description of interaction surface at a atomic level. Isothermal Titration Calorimetry (ITC) is a reliable, label-free and standard technique for measuring bio-molecular interactions. During the interaction, heat is either generated or absorbed. ITC is a thermodynamic technique that directly measures the heat released or absorbed during a biomolecular binding event. It simultaneously determines all binding parameters like dissociation constants ( $K_d$ ), reaction stoichiometry ( $n$ ), enthalpy ( $\Delta H$ ) and entropy ( $\Delta S$ ) in a single experiment. These parameters are used in elucidation of the mechanism of the molecular interaction and recognition processes. Among the techniques used for atomic-resolution structure determination of proteins and its complexes, NMR spectroscopy is unparalleled in providing atomic-resolution details of protein interactions in solution at close to physiological conditions and also in living cell. Additionally it provides dynamic features of the interaction, including the role of solvation. Various NMR parameters like Chemical Shift Perturbation (CSP), filtered NOESY, Saturation Transfer, Residual Dipolar Couplings (RDC), Paramagnetic Relaxation Enhancements (PRE), Pseudo-Contact Shift (PCS) help in determining if interaction occurs, map the site(s) of interaction and finally to determine the structure of the entire complex or the structure of one component. Use of both ITC and NMR spectroscopy including sample preparation, limitations, analysis and interpretation of data will be discussed.

---

## CHALLENGES IN PROTEIN CRYSTALLIZATION & DATA PROCESSING

**Dr. Ethayathulla Abdulsamath**

*AIIMS, New Delhi*

---



Crystallization is one of the bottle necks to determine structure of macromolecules and in the era of structure-based drug design we need to understand the process of protein crystallization. There is no defined protocol to crystallize a macromolecule but we need to understand certain thermodynamic nature of the macromolecule to be crystallized. Few examples will be discussed in detailed like challenges faced during crystallization. DNA binding protein is one of the example where two macromolecules need to be crystallized. p73 DNA binding domain crystallized with promoter sequence the challenges faced and strategies used to crystallize protein-DNA complexes. Second example: Strategies used to crystallize a 11-transmembrane helical protein Melibiose transporter; challenges faced in data processing and solving the protein phasing to solve the structure. A few examples for challenges faced for data processing will be discussed in detailed.

---

## SURFACE PLASMON RESONANCE: INTRODUCTION AND APPLICATION TO DRUG DISCOVERY

Likhesh Sharma, PhD

*Application Scientist, GE Healthcare LifeSciences*



Quantification of Drug-Target interaction is a very important step in characterization and development of new drugs. One of the well-established techniques to study these interactions is Surface Plasmon Resonance. Surface Plasmon Resonance (SPR) allows us to measure the kinetics of Drug-Targets and how fast and slow the two molecules interact which also helps determine their strength of binding. These numbers can be used both to screen new drug candidates and validate the putative drug-target interactions and evolutionary significance of these interactions. In this talk I would introduce SPR as a technique and its applications for drug discovery.

### Speaker's Bio

I did my Bachelors in microbiology from University of Delhi, thereafter I joined as an Integrated PhD fellow at Indian Institute of Science Bangalore. During PhD I worked in the area of protein folding, engineering and design. Currently I work as an Application Scientist in GE Healthcare-Life Sciences where I take care of our protein interaction and purification portfolio. I help scientists from both academia and industry to utilize SPR as a tool to carry out cutting edge research.

---

## STRUCTURE, MECHANISM, AND ANTAGONISM OF PROTEIN ASSEMBLIES PIVOTAL TO INFLAMMATION, AUTOIMMUNITY, AND ALLERGY

Savvas Savvides

Ghent University, VIBCenter for Inflammation Research, Belgium



We employ integrative structural biology in conjunction with molecular interaction studies, cellular interrogation and *in vivo* studies to elucidate the structural and mechanistic principles underlying the assembly, activation and pathophysiology of protein complexes pivotal to immunity, inflammation, and cancer. We have recently ventured into combining detailed structural and mechanistic insights from our studies of pro-inflammatory cytokine/receptor complexes with molecular design and engineering in order to harness their therapeutic potential.

My presentation will showcase our recent work on pro-inflammatory receptor complexes mediated by the human cytokines TSLP and IL-23, two validated clinical targets against widespread inflammatory diseases such as asthma and atopic dermatitis (TSLP), and psoriasis and rheumatoid arthritis (IL-23). In particular, I will illustrate how structure-function studies have inspired and provided a wealth of insights to fuel the development of potent protein-based antagonists that do not exist in nature. For instance, in the case of pro-allergic/inflammatory human TSLP we are developing a fusion protein comprising the ectodomains of the cognate receptors, whereas to combat the pro-inflammatory activity of IL-23 we have worked with an industrial partner to develop a novel protein scaffold therapeutic. Together, our work shows that basic research at the frontline of molecular structural biology enables the generation of unanticipated insights, which in turn become inextricably linked to the design and further development of innovative molecular tools and protein-based therapeutics.

---

## CAPRI: THE DIVERSE CHALLENGES OF COMPUTATIONAL PROTEIN-PROTEIN DOCKING

**Marc F. Lensink**

*University of Lille, CNRS UMR8576 UGSF, F-59000, Lille, France*

---



Protein-protein interactions play a central role in all biological processes. These processes result from the physical interaction of two or more protein molecules, forming a macromolecular assembly. Computational protein docking is the process of obtaining the three-dimensional coordinates of a macromolecular assembly. The CAPRI experiment has been catalyzing the development of protein docking methods by organizing blind predictions experiments for over 15 years. The targets in CAPRI follow the demand of the experimentalists and thus represent a wide variety of biological processes. In the last 5 years the experiment has diversified and now includes the prediction of multi-component assemblies, of protein-peptide, protein-nucleic acid and protein-polysaccharide binding, and the prediction of binding affinities and positions of interfacial water molecules. A parallel experiment is dedicated to the scoring of docking poses. The CAPRI project gives a fair assessment of the performance of present-day protein docking methods for the more difficult targets and therefore provides an upper limit of what can be expected from docking algorithms.

---

## SITES FOR DYNAMIC PROTEIN-CARBOHYDRATE INTERACTIONS OF O-, N-, S- AND C-LINKED MANNOSIDES ON THE *E. COLI* FIMH ADHESIN

Dr. Julie Bouckaert

*Unité de Glycobiologie Structurale et Fonctionnelle, UMR 8576 of the Centre National de la Recherche Scientifique and the University of Lille, 50 Avenue de Halley, 59658 Villeneuve d'Ascq, France*



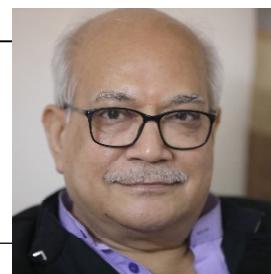
Nowadays high-resolution structures solved by X-ray crystallography are often combined with binding affinity data, molecular dynamics simulations and quantum chemical calculations, to allow unravelling the molecular mechanism of a target protein of interest. Curiously, the knowledge of the protein's mode of action is often obtained by employing a similar bundle of methods that are used to rationally design and analyze new chemical compounds, some of the latter that might represent future drugs against the protein of interest. We will introduce the case of FimH, a mannose-specific lectin at the tip of type-1 pili of *E.coli* and a major instigator of urinary tract infections as well as implied in dysbiosis in Crohn's disease. Targeting this protein through new mannoside-based anti-bacterial antiadhesives represents a promising alternative to the standard antibiotic treatments of such infections.

---

## HUMAN ANTIBODIES: GENERATION & APPLICATIONS

**Vijay K. Chaudhary, Amita Gupta and Vaishali Verma**

*Centre for Innovation in Infectious Disease Research, Education and Training (CIIDRET),  
University of Delhi South Campus, New Delhi 110021, India.  
(vkchaudhary@south.du.ac.in, +919811800434, +911124115883).*



The pioneering experiment of German Scientist Emil Behring, demonstrating the protection of guinea pigs from the effects of diphtheria toxin by injection of cell-free material of blood from a convalescent guinea pig is one of the earliest documented therapeutic applications of antibodies. This natural substance was named as "Antibody". This work led Paul Ehrlich to hypothesize that blood must contain a myriad of antibodies capable of fitting around and blocking the action of foreign substances that the body encounters and that these magic bullets can be used to cure diseases. This led to the concept of passive immunotherapy in which the antibodies derived from the blood of hyper-immunized animal can be used as therapeutic molecules to neutralize infections such as Diphtheria, Tetanus, Rabies or even snake bites. The discovery of Hybridoma technology was another major breakthrough in the antibody research and paved way to produce specific monoclonal antibodies and marked the beginning of use of mouse monoclonal antibodies for the treatment of cancer. However, it was learnt that mouse-derived monoclonal antibodies (MAbs) result in human anti-mouse antibodies (HAMA). To reduce the HAMA response, the mouse MAbs were engineered to produce chimeric (carrying mouse-derived variable domains fused to human-derived constant domains) or humanized antibodies (with mouse-derived complementarity determining regions implanted on a human antibody framework). However, this requires careful engineering of antibodies making the process time-consuming and difficult. Meanwhile, the technologies were developed to produce fully human antibodies for therapy. These technologies include: (a) use of phage-displayed antibody libraries, where *in vitro* selection of antibody library is carried out against the target antigen followed by production of full-length bivalent antibodies in mammalian cells; and (b) use of transgenic humanized mouse, where the mouse immune repertoire is replaced by that of human and immunization with the target antigen followed by hybridoma production leads to production of human antibodies. Another technology involves immortalization of human B cells with Epstein Barr virus (EBV) transformation. Since the introduction of first successful mouse monoclonal antibody, OKT-3 for preventing kidney transplant rejection, there are 74 US-FDA approved antibodies which include 5 Mouse, 9 Chimeric, 26 humanized and 23 fully human antibodies with first fully human MAb 'Adalimumab' being introduced in 2002. These antibodies are targeted against a number of oncology, neurobiology, inflammatory, autoimmune targets, etc. and comprise a total market of more than 80 billion US dollars. In addition, nearly 645 Antibody molecules are in different stages of clinical development. In conclusion, the antibody-based therapeutics are an important form of biologics serving as wonder drugs. Given their importance in the global scenario, the Indian research institutes should make sincere efforts and impart training for antibody research to help in nation building.

---

## NMR OF COMPLEX BIOLOGICAL SYSTEMS AND MIXTURES

Ramakrishna V. Hosur<sup>1,2</sup>

<sup>1</sup>*Department of Chemical Sciences, Tata Institute of Fundamental Research, 1-Homi Bhabha Road, Colaba, Mumbai-400005, India*

<sup>2</sup>*UM-DAE Centre for Excellence in Basic Sciences, University of Mumbai, Kalina Campus, Santa Cruz, Mumbai- 400098, India*



Nuclear Magnetic Resonance (NMR) spectroscopy has come a long way since its discovery seven decades ago and continues to evolve unabated with new applications emerging in many areas of biology and chemistry, such as, structural biology, metabolomics, proteomics, drug discovery, to name a few prominent ones. We have been involved in developing NMR methods for various aspects of these applications over the last two decades. This includes, enhancing the speed of structure determination, pushing the size limits to higher and higher molecular weights, elucidation of structure-function relationships, investigation of large molecular assemblies, intrinsically disordered proteins, folding intermediates, molten globules, drug-protein interactions, protein fibrillation etc. The latest in this endeavour is NMR of complex mixtures as in metabolomics and in herbal drug preparations. This talk will highlight the major accomplishments over the years.

---

## ADHERENT-INVASIVE *ESCHERICHIA COLI* IN INFLAMMATORY BOWEL DISEASE

Nicolas Barnich

M2iSH Unit 1071, Inserm/Université Clermont Auvergne



Intestinal microbiome dysbiosis has been consistently described in patients with inflammatory bowel disease (IBD). In the last decades, *Escherichia coli*, and the adherent-invasive *E. coli* (AIEC) pathotype in particular, has been implicated in the pathogenesis of IBD. Since the discovery of AIEC, two decades ago, some progress has been made in unraveling these bacteria characteristics and its interaction with the gut immune system. The mechanisms of adhesion of AIEC to intestinal epithelial cells (via FimH and cell adhesion molecule 6) and its ability to escape autophagy when inside macrophages will be presented. We also explore the existing data on the prevalence of AIEC in patients with Crohn's disease and ulcerative colitis, and the association between the presence of AIEC and disease location, activity and post-operative recurrence. Finally, we highlight potential therapeutic strategies targeting AIEC colonization of gut mucosa, including the use of phage therapy and anti-adhesive molecules. These strategies may open new avenues for the prevention and treatment of IBD in the future.

---

## UNDERSTANDING DISEASE HETEROGENEITY IN THE ERA OF PERSONALIZED MEDICINE

Anup Madan, PhD.

Covance Genomics Laboratory, 9911 Willows Road NE, Redmond, WA-98052.



The ability to characterize molecular features of cancer with more widespread implementation of advanced sequencing technologies is resulting in the development of innovative health care for patients. The analyses of high throughput genomics data sets in our laboratory and others have provided remarkable insights into the genetic complexity of malignant tumors. There is also growing evidence of a relationship between intra tumor heterogeneity and clinical outcome. The presence of intra-tumor heterogeneity has implications for the development of cancer therapeutics, patient recruitment for clinical trials and treatments in the era of personalized medicine. Our laboratory has been investigating changes in genomic aberrations associated with multiple tumor types in longitudinal studies to better understand and mitigate the impact of tumor heterogeneity. To further increase the resolution of our analysis, we have also profiled circulating tumor DNA (ctDNA) and performed single cell analysis using circulating tumor cells (CTCs) in selected patient samples. This has increased the sensitivity of detection and identified additional targets that could have been used for therapeutic intervention. In addition to single nucleotide variants, we have also used copy number variations, gene expression changes etc. to monitor disease progression and response to therapeutics. These data sets are being further analyzed in combination with TCGA data and other publicly available datasets for the functional prediction of significant candidate alterations and the results of these analyses will be presented.

---

## DIAGNOSTICS FOR THE DEVELOPING WORLD:A LOOK AT THE CHALLENGES AND OPPORTUNITIES

**Dr. Shikha Sharma**

*Scientific Affairs Manager, Abbott Point-of-Care, Abbott Healthcare Pvt Ltd.  
Godrej BKCI, Bandra (E), Mumbai, India*



The countries and communities of the developing world, with inadequately resourced healthcare systems, struggle with multiple health challenges mainly associated with their poor socioeconomic development. In addition to trans-global diseases, such as diabetes, cardiovascular issues, and cancer, they face huge challenges from tropical, nutrition deficiency related, waterborne, and respiratory diseases<sup>1</sup>. Furthermore, diseases such as malaria, pneumonia, diarrhea, and HIV/AIDS, are estimated to kill more than 15 million people annually. With the growing population and upsurge in both communicable and non-communicable diseases in India, the healthcare industry plays key role in the country's development. The expenditure on the healthcare sector is amongst the lowest in the world both from public funds as well as private sources. Reliable and accurate diagnostic investigations play a vital role in healthcare decisions, choice of treatment, and achievable survival. Although more than 50% of treatment decision-making is based on some diagnostics, it still accounts for less than 3% of the cost of healthcare. The existing central lab diagnostic instrumentation usually requires sophisticated infrastructure, stable electrical power, expensive reagents, long assay times, and highly trained personnel which is not often available in limited resource settings. Unfortunately, a major aspect in developing countries is that they often lack modern laboratories, fully automated instruments that provide highly reproducible, quantitative, and hence sensitive and accurate diagnostic results. Rural areas often lack access to even basic diagnostic devices and trained personal<sup>2</sup>. The scarcity of running water and reliable electrical services are additional challenges for delivering healthcare in these areas. The presentation will provide an overview of the healthcare related challenges involved in rural areas and suggestion strategies to address them including the emerging rapid and easy-to-use point-of-care (POC) tests that can dramatically enhance a physician's ability to diagnose patients' diseases rapidly and accurately<sup>3</sup>.

### Reference

1. Sharma, S., Crawley, A. and O'Kennedy, R., 2017. Strategies for overcoming challenges for decentralised diagnostics in resource-limited and catastrophe settings. *Expert review of molecular diagnostics*, 17(2), pp.109-118.
2. Urdea, M., Penny, L.A., Olmsted, S.S., Giovanni, M.Y., Kaspar, P., Shepherd, A., Wilson, P., Dahl, C.A., Buchsbaum, S., Moeller, G. and Burgess, D.C.H., 2006. Requirements for high impact diagnostics in the developing world. *Nature*, p.73.
3. Sharma, S., Zapatero-Rodríguez, J., Estrela, P. and O'Kennedy, R., 2015. Point-of-care diagnostics in low resource settings: present status and future role of microfluidics. *Biosensors*, 5(3), pp.577-601.

---

## OPTIMIZING PLANT FEEDSTOCK FOR BIOFUEL PRODUCTION

**Manoj K. Sharma<sup>1</sup> and Rita Sharma<sup>2</sup>**

<sup>1</sup>*Crop Genetics & Informatics Group, School of Biotechnology, Jawaharlal Nehru University, New Delhi-110067, India.*

<sup>2</sup>*Crop Genetics & Informatics Group, School of Computational and Integrative Sciences, Jawaharlal Nehru University, New Delhi-110067, India.*



Depleting fossil fuels and growing environmental concerns demand for a green and alternate energy revolution. Since plant cell walls are the most abundant source of biomass on Earth; they provide an excellent opportunity for generating greener biofuels. However, establishing a sustainable and economically-viable biofuel industry require optimized crop plants with improved sugar yields and low input requirements. Research in our laboratory is focused on understanding the genetic basis of cell wall composition in rice and identifying key strategies for improved saccharification yields in grasses.

---

**CURRENT TRENDS IN NEW DRUG DISCOVERY****T.P. Singh***Department of Biophysics, All India Institute of Medical Sciences, New Delhi*

Considering the alarming rise in the incidence of bacterial resistance to known antibiotics, there is a desperate need to develop bacterial resistance-free antibiotics. There are efforts to design new antibacterial agents using natural products, combinatorial chemistry approach, structure based design and using synthetic compound libraries. In order to overcome the problem of antibiotic resistance, new approaches such as exploitation of innate immunity proteins is very promising. The proteins of the innate immune system provide the first line of defense against infecting microbes. These proteins recognize the conserved motifs that are present on the cell walls of bacteria. Thus the success of the innate immune system depends on the affinity of the proteins of innate immune system towards the bacterial cell wall molecules. The conserved motifs of microbial cell walls are called pathogen associated molecular patterns (PAMPs) that include the well known peptidoglycans (PGN) and lipopolysaccharides (LPS) of Gram-negative bacteria, PGN and lipoteichoic acid (LTA) of the Gram-positive bacteria and mycolic acid (MA) and other fatty acids of *Mycobacterium tuberculosis*. These PAMPs are classified into two groups: (i) those which contain glycan moieties such PGN, LPS, LTA etc. and (ii) those that are derivatives of fatty acids such as MA. Therefore, there should be two independent binding sites for the two different types of PAMPs. The PAMPs are specifically recognized by innate immunity molecules which are historically known as peptidoglycan recognition proteins (PGRPs).. The epidemiological data showed that camels have the lowest rates of infections. Structurally, PGRP-S from camel exists in the form of two dimers whereas the human protein acts as a monomer. As a result of dimerization, a deep binding cleft is formed in the camel protein whereas only a shallow cleft is present in the case of human monomeric protein. Because of dimerization, the potency of camel protein is much higher than the same protein from other species. Thus if camel protein is used or a suitably mutated human protein is prepared and used, the fight against bacterial infection will improve.

The mechanism of action of PGRP-S involves an effective sequestration of bacteria which leads to the killing of bacteria. Since PGRP-S interacts with bacterial cell wall, the kinetics of bacterial cell death appears to be similar to those of antibiotics which inhibit the biosynthesis of PGN. Due to this similarity, PGRP-S protein from innate immune system is termed as "protein antibiotics" and since they bind to bacterial cell wall molecules the issues of side effects and resistance will not arise and if the potencies are high, the invading bacteria can be tackled rapidly.

---

## SYNTHETIC BIOLOGY: EMERGENCE OF A NOVEL DRUG DISCOVERY PLATFORM

Pawan K Dhar

*School of Biotechnology, Jawaharlal Nehru University, New Delhi*

---



Synthetic Biology is a rational design and construction of biological components leading to useful applications. In June 2004 at MIT, Synthetic Biology was launched as a formal scientific discipline, though its foundation was laid much earlier. Concepts like logic gates, truth table, data sheet, applets that were part of the engineering domain found their imprints in biology for the first time. Suddenly the focus changed towards construction of novel biological systems, instead of studying existing ones. For the last ten years, the scientific community has understood various advantages and limitations of building biological systems. Turns out that the grand challenge of booting up a cell from rationally designed parts, devices and circuits is non-trivial. However, the payoffs have far more depth due to limitations in the current technologies. In the first part of my talk, I shall outline key concepts of Synthetic Biology from its origin to the present evolution and beyond.

In the second part, I shall describe our work and plans for the Indian community. Broadly three kinds of functional DNA sequences exist: one that encodes proteins, another that encodes only RNA (non-coding DNA) and third that does not transcribe at all (NOT coding DNA). Historically people have paid attention to protein coding genes. For the last two decades, non-coding RNA biology has taken the center stage. However, the role of not-coding DNA (the dark matter of genome) is still unknown. We asked a simple question: Why did nature allocate protein coding and RNA coding jobs to a specific set of sequences. Did she sample all possibilities, retained good results, retired not-so-relevant results and left some genome sequences untouched. To address this issue, we have developed a novel approach for designing lab made genes towards therapeutic applications. The second part of my talk will focus on health applications generated from technology developed in-house.

# **Oral Presentations**

*International Conference on Advances in  
Biosciences and Biotechnology - ICABB-2018  
(February 01-03, 2018)*

## **AN IN VITRO MODEL FOR MYCOBACTERIUM TUBERCULOSIS PERSISTENT INFECTION DRUG DISCOVERY STUDIES\***

**Rahul Shrivastava<sup>1\*</sup>, Shivani Sood<sup>2</sup> and Gopal Singh Bisht<sup>1</sup>**

<sup>1</sup> Department of Biotechnology & Bioinformatics, Jaypee University of Information Technology, Waknaghat -173234, (H.P.), India

<sup>2</sup> Viral Vaccine Laboratory, National Institute of Biologicals (NIB), A-32, Sec- 62, NOIDA, India

E-mails: shivanisoodcri@gmail.com, bisht.gopal@gmail.com,

\*Corresponding author: juit.rahl@gmail.com

Persistent form of tuberculosis remains major hurdle in absolute and effective control of the disease. Study of model systems using *M. tuberculosis* are associated with constraints in terms of cost (establishment and maintenance of BSL3) as well as screening period (longer generation time). Aim of the present study was to develop a rapidly growing mycobacteria based model mimicking *M. tuberculosis* persistent infection which may offer advantages in terms of cost effectiveness and comparatively faster screening time for potential drugs and drug targets. *M. fortuitum* was selected on the basis of shorter generation time, ease of handling, non-requirement for biosafety level-3 and closer homology with *M. tuberculosis* genome sequence. *M. fortuitum* showed constant CFU for extended periods of time, the most important characteristic feature of a persistent infection. Further validation of the model also confirmed that it exhibited all physiological features of a persistent infection. Identification of five novel gene sequences of *M. fortuitum* was done as homologues of *M. tuberculosis* genes involved in persistence and submitted to GenBank database. Upregulation of these *M. fortuitum* homologues studied by real-time PCR showed their involvement in persistence of *M. fortuitum*. Our studies indicate a conserved mechanism of persistence in *M. fortuitum* and *M. tuberculosis*, suggesting *M. fortuitum* as potential surrogate organism for studies related to *M. tuberculosis* persistence.

## **INVESTIGATING THE EFFECT OF SUGARS ON ANTIMICROBIAL PEPTIDE INDOLICIN**

**Rohini Dwivedi and Kanwal J. Kaur\***

National Institute of Immunology, Aruna Asaf Ali Marg,  
New Delhi -110067, India

E-mails: rohiniidwivedi@niit.ac.in,

\*Corresponding author: kanwal@niit.ac.in

Antibiotic drug resistance presents one of the biggest challenges worldwide and raises an urgent need for the development of alternate class of therapeutics. Antimicrobial peptides with small length and broad spectrum activity offer a strong potential to combat this emerging concern. The present study focuses on indolicidin a potent antimicrobial peptide which has a sequence ILPWKPWPPWRR-NH<sub>2</sub> and belongs to cathelicidin family of antimicrobials. High hydrophobicity of indolicidin attributed to the presence of 5 tryptophans seems crucial for its membrane active mode of action, but is also speculated to be a prime cause of the cytotoxicity and aggregation propensity exhibited by indolicidin, thereby limiting its prospective therapeutic potential. Glycosylation with an established effect on modifying the pharmacokinetic properties of the molecule was used as a tool to design therapeutically improved analogues of indolicidin. Earlier study from our lab, showing structural correspondence between the aromatic ring and the sugar ring made us adopt the strategy of substituting tryptophan with the sugar moiety. The study undertaken to generate the indolicidin analogue with increased therapeutic index led us to explore the effect of sugar at different tryptophan positions viz. W6, W9 and W11 of the indolicidin. The results suggested that substitution of tryptophan with sugar was able to significantly reduce the haemolytic activity of indolicidin, irrespective of the position or the nature of sugar involved. However, the effect of sugar on antimicrobial activity of the peptide appeared to depend on the position of tryptophan substituted, when tested against different strains of gram negative and gram positive bacteria. The study thus led to the identification of W9 position of indolicidin which upon substitution with sugar generated glycosylated analogue having an improved therapeutic index. To the best of our knowledge, the use of glycosylation strategy for reducing the cytotoxicity of indolicidin has not been reported earlier.

**Keywords:** Drug resistance, Antimicrobial peptides, Indolicidin, Cytotoxicity, Glycosylation

OP3

ICABB-031

## MEMBERS OF PHISTc PROTEIN FAMILY LOCALIZE TO DIFFERENT SUB-CELLULAR ORGANELLES AND BIND MAJOR VIRULENCE FACTOR 'PfEMP-1'

Vikash Kumar<sup>1</sup>, Jasweer Kaur<sup>1</sup>, Amrit P. Singh<sup>2</sup>,  
 Vineeta Singh<sup>3</sup>, Anjali Bisht<sup>4</sup>, Jiban J. Panda<sup>4</sup>,  
 Prakash C. Mishra<sup>5</sup> and Rachna Hora<sup>1\*</sup>

1. Department of Molecular Biology and Biochemistry, Guru Nanak Dev University, Amritsar, India, 2. Department of Pharmaceutical Sciences, Guru Nanak Dev University, Amritsar, India, 3. National Institute of Malaria Research, New Delhi, India, 4. Institute of Nano Science and Technology, Mohali, India, 5 Department of Biotechnology, Guru Nanak Dev University, Amritsar, India  
 \*Corresponding author: rachnahora@gmail.com

Plasmodium falciparum (Pf) exports numerous proteins to the host erythrocytes collectively called as malaria 'exportome'. Several reports suggest that most of the exported proteins are translocated across host cell via an intermediate parasite originated membranous structures called Maurer's cleft (MCs). Plasmodium helical interspersed sub-telomeric (PHIST) is one of the novel family of exported proteins that play diverse role in infected red blood cells (iRBCs) including trafficking of exported proteins and their stabilization in iRBCs. Here, we have attempted to understand the function and localization of two unexplored proteins of PHISTc sub-family viz. PFD1140w and PF11\_0503. Both these members containing conserved Phist domain were successfully expressed and purified using various chromatography techniques. Size exclusion chromatography suggests Phist domains have different oligomeric states in solution. Polyclonal antibodies against recombinant PHIST proteins were raised in rabbit whereas antibodies against acidic terminal segment (ATS) of major virulence factor 'PfEMP-1' and MCs signature protein 'PfSBP-1' were raised in mice. Co-localization assays with 'PfEMP-1' and 'PfSBP-1' revealed PHIST proteins localize to different sub-cellular organelles in iRBCs. Our in vitro protein binding studies reveal PFD1140w interacts with PfEMP-1 and PfSBP-1 whereas PF11\_0503 binds to only PfEMP-1. Kinetic analyses of the interaction of recombinant PFD1140w and PF11\_0503 with ATS domain of PfEMP-1 depict significantly different binding strengths for these members. In-vitro complex binding assays suggest PFD1140w binds simultaneously to both PfEMP-1 and PfSBP-1 leading to formation of a complex. Our competitive binding assays depict that both PHIST

proteins bind to distinct binding sites on PfEMP-1 despite sharing common conserved domain. Collectively, our data support the hypothesis that PHIST proteins play crucial role in cytoadherence, thereby contributing to the pathology of the disease. Since Pf EMP-1 is a major cytoadherence ligand, a comprehensive understanding of PHIST-PfEMP-1 interaction may form the basis for development of newer drugs against lethal malaria.

OP4

ICABB-163

## THE HUMAN ORAL CANCER MICROBIOME DATABASE

Nadia and Jayashree Ramana

Department of Biotechnology and Bioinformatics, Jaypee University of Information Technology, Waknaghat, Solan, Himachal Pradesh, 173234, India

\*Correspondence author: jayashree.ramana13@gmail.com

The Microbiome is the total microbial community and biomolecules within a defined environment. The oral cavity is inhabited by many of the bacterial species. Some of them have a key role in the development of oral disease. Interrelationships between oral microbiome and systemic conditions such as head-and-neck cancer have become increasingly appreciated in recent years. Emerging evidence also suggests a link between periodontal disease and oral cancer. Bacteria have been linked to cancer through several mechanisms such as production of toxins, chronic inflammation, and carcinogenic metabolites. We have developed the Human Oral Cancer Microbiome Database (HOCMD) which provides the scientific community with comprehensive information on the species that are present in the human oral cancer microbiota. It is manually curated, searchable, metagenomic resource to facilitate investigation of human oral cancer microbiota and will make it publicly accessible through web interface. This is achieved by combining a manually curated list of bacterial genomes from human fecal samples. The HOCMD enables detailed analysis of human microbial communities and supports research from basic microbiology and immunology to therapeutic development in human Oral Cancer. Our database HOCMD is different from Human Oral Microbiome database (HOMD) as the latter provides the comprehensive information about species that are present in the human oral cavity while the former is with regard to the species that are present in the Human Oral Cancer microbiota.

**Keywords:** Microbiome, Metagenome, HOCMD, Oral Cancer.

## GENOME WIDE ANALYSIS OF REPETITIVE DNA SEQUENCES OF FOUR INDIAN *DROSOPHILA* SPECIES AND *ZAPRIONUS INDIANUS*

**Radhika Khanna and Sujata Mohanty\***

Jaypee Institute of Information Technology, Sector 62, Noida,  
Uttar Pradesh

\*Corresponding author: sujata.mohanty@jiit.ac.in

Majority portion of the eukaryotic genome consist of long stretches of highly repetitive DNA sequences in form of simple repeats, tandem repeats, segmental duplications and interspersed repeats. These repetitive DNA sequences are vital component of genome as they play important role in proper organization of genomic information. Studying these sequences is helpful in gaining in-depth knowledge about the evolutionary pattern in genomic architectural variations in an organism. For past few decades, repetitive DNA sequences have been analyzed in order to gain insight into structural, molecular organization, evolution and function of the genomes. The recent advancement of sequencing technology has led to introduction of Next Generation Technology, where whole genome sequencing has produced an unprecedented amount of information about the origin, diversity and genomic significance of repetitive sequences. *Drosophila* serves as an ideal model organism for evolutionary studies. Previous studies have reported about 9% of the *Drosophila* genome is composed of repetitive elements out of which 20% comprises of transposable elements. In the present study, repetitive elements were identified and characterized in the whole genome assembly of Indian *Drosophila* (*Drosophila biarmipes*, *Drosophila bipectinata*, *Drosophila takahashii* and *Drosophila nasuta*) and *Zaprionus* (*Zaprionus indianus*) species using Repeat Masker. The results have shown about 8-9% of Indian *Drosophila* genome comprises of repetitive DNA sequences which is quite similar to the earlier findings. The most abundant repetitive DNA families in Indian species were simple repeats followed by low complexity sequences and transposable elements where retrotransposons were found to be predominant class. The knowledge inferred from the study can be further applied for understanding the nature and consequences of genome size variation among different *Drosophila* species.

**Keywords:** *Drosophila*, *Zaprionus*, Repetitive DNA sequences, Whole genome assembly, India

## SCREENING AND IDENTIFICATION OF POTENTIAL INHIBITORS AGAINST UDP-NACETYLGLUCOSAMINE ENOLPYRUVYL TRANSFERASE (MurA) IN *STREPTOCOCCUS PNEUMONIA*: AN *IN-SILICO* APPROACH

**Dr. K. Peera<sup>1</sup> and Dr. M. Abdul Kareem<sup>2\*</sup>**

1. DBT -Bioinformatics Infrastructure Facility, Department of Zoology, Sri Venkateswara University Tirupati 517502. Andhra Pradesh. 2. Dept. of Biochemistry, School of Sciences, IGNOU, New Delhi-68.

E-mails: drkutagollapeera2014@gmail.com, Corresponding author: abdul.kareem@ignou.ac.in.

*Streptococcus pneumoniae* are the most common cause of pneumonia and meningitis in infants and adults. Peptidoglycan layer is an essential component of cell wall composed of alternating units of N-acetylglucosamine (GlcNAc) and N-acetylmuramic acid (MurNAc). UDP-N-acetylglucosamine enolpyruvyl transferase (MurA) is a key enzyme involved in peptidoglycan synthesis. The Biosynthesis of peptidoglycan in cytoplasm is catalysed by MurA which transfer enolpyruvyl group from phosphoenol pyruvate (PEP) to UDP-N-acetylglucosamine to form UDP-N-acetylglucosamine. Present study was aimed to develop novel antimicrobial agents against MurA enzyme through *insilico* analysis approach. The three-dimensional structure of MurA enzyme was modelled computationally by using Modeller9v10. Later this enzyme model subjected to molecular dynamics simulations using NAMD 2.5 software with CHARMM27 force field tip 3p model of water. Initially energy minimization carried 5000 runs for 10 ps time and subsequent minimized model was simulated with 1,00,000 runs for 2 ns time period. The final resolved model reliability was assessed by procheck using Ramchandran plot calculations, verify 3D and WHATCHECK programs. From Zinc database 5000 similar structure compounds with fosfomycin were virtually screened against MurA by Autodock vina in PyRx virtual screening tool. The docking results reveal that the compounds Zinc50247, Zinc3020559, Zinc1884559, Zinc3154681, Zinc19286884, Zinc58219 and Zinc3978065 have -10.3, -10.1, -9.8, -9.8, -9.2, -9.1 and -9.0 k.cal/mol binding affinity respectively, with MurA enzyme. We found that, the Amino acids Asp306, Tyr329, Gly115, Arg121, Arg322, Ser125, Leu91 and Phe125 present in the enzyme binding pocket are showing molecular interactions with ligands. MurA being a potential drug target in treating

*Streptococcus pneumoniae* infections, in this study we found that Zinc50247 effectively inhibits the MurA enzyme and can act as potential therapeutic agent.

**Keywords:** *Streptococcus pneumoniae*, MurA enzyme, Molecular modeling, Molecular dynamics and Zinc.

OP7

ICABB-081

## LIPIDOMICS – AN EMERGING TOOL TO REDEFINE THE ROLE OF LIPIDS IN COMBATING MDR-TB

Zeeshan Fatima

Amity Institute of Biotechnology, Amity University Haryana, Gurugram (Manesar)-122413, India

Tuberculosis (TB) still remains a major health problem globally and multidrug resistance (MDR) acquired by *Mycobacterium tuberculosis* (MTB) through continuous deployment of antitubercular drugs warrants immediate search for novel drug targets. Although the technologies such as transcriptome, proteome have gained considerable attention, lipidomes still remain relatively uncharacterized and at rudimentary level. In the era of newly developed ‘omics’ based technologies, our knowledge has gained significant leap and recently improved our insight to understand lipids to great extent. The emerging field of lipidomics in the recent times has considerably enhanced the awareness about lipid molecules to have some unique biological roles that is distinct from their usual functions. Considering the fact that 30% of MTB genome codes for lipid which are among most adaptable molecules that acclimatize to the development of MDR, deciphering the role of lipids in development of MDR in MTB is emerging as new strategy in current scenario. In this study we have employed high throughput mass spectrometric approach to analyze differential lipidome profile in response to isoniazid (INH). Total cell lipid was extracted by modified Folch method and processed by UPLC coupled with a tandem quadrupole detector mass spectrometer. Data generated in m/z peaks were processed and analysed by mass spectrometry based lipid(ome) analyzer and molecular platform (MS-LAMP) software. All the 6 classes of lipid present in MTB were analysed including 3 main classes viz. Fatty acyls (FA), Glycerolipids (GL), Glycerophospholipids (GPL). The data generated unravels the complete remodeling of MTB lipids and we could confirm that INH treated cells have distinct lipid imprints. MTB lipids are potential candidates for diagnostic and therapeutic biomarkers owing to their limited

structural similarity with human lipids. Since lipid compositional changes are significant for the sustenance of MDR, this study points towards compositional variation in INH treated bacilli. Further intricate studies are warranted for its implication in biomarker(s) identification. The present lipidomic approach will serve as resource for further validation so that assessment of various strategies aimed at disrupting the function of MTB lipids and thereby MDR could be employed for TB management.

OP8

ICABB-006

## “IN-SILICO PREDICTION OF HIGH SPECIFICITY INHIBITORS AGAINST HpGGT: IMPLICATIONS OF DIVERGENT SITES IN DRUG DESIGN”

Ved Vrat Verma<sup>1</sup>, Rani Gupta<sup>2</sup> and Manisha Goel<sup>1\*</sup>

1. Department of Biophysics, University of Delhi, South Campus, New Delhi-110021, India 2. Department of Microbiology, University of Delhi, South Campus, New Delhi-110021, India

E-mails: vedvratverma@gmail.com, ranigupta15@rediffmail.com, manishagoel@south.du.ac.in, \*Corresponding author: manishagoel@south.du.ac.in

$\gamma$ -glutamyltranspeptidase (GGT: EC 2.3.2.2) is a N-terminal nucleophile hydrolase, ubiquitously present in all three domains of life: prokaryotes, eukaryotes and archaea. It catalyzes the cleavage and transfer of  $\alpha$ -glutamyl moiety of glutathione to either water (hydrolysis) or substrates like peptides (transpeptidation). GGTs exhibit significant variability in their enzyme kinetics. In mammalian, GGT inhibition prior to chemotherapy has been shown to sensitize tumor cells to the therapy. In pathogenic bacteria like *Helicobacter pylori* and *Bacillus anthracis* GGT be an important virulence factor. *Helicobacter pylori* is a common human pathogen (affecting about 50% of the world population) which persistently colonizes human mucosa causing gastritis, ulcer and gastric. GGT of *Helicobacter pylori* (HpGGT) has been shown to contribute to the bacteria’s colonization potential, and its inhibition has been shown to be effective in decreasing the pathogenicity of the bacteria. Since, GGT has direct influence on human health; both human and bacterial GGTs are promising drug targets. The present study essentially describes our efforts towards the screening of novel drug like molecules which can recognize, bind and inhibit HpGGT with higher affinity than GGT from other species, especially humans. In the current work, we have explored the possibility of using type 2 divergent sites within the substrate cavity of HpGGT for designing such species-

specific inhibitors. We therefore performed virtual screening of HpGGT as target against the ZINC database. Based on glide score values, a large number of drug-like compounds were predicted to have high affinity for HpGGT. The top binders were then docked with the Human GGT and glide scores of each compound for the two targets were compared. Compounds with show higher affinity for HpGGT than HsGGT, were studied further. We conclude that such molecules show higher interactions with the predicted type 2 divergent sites as compared to the other molecules; therefore, these could be species-specific inhibitors for HpGGT.

**Keywords:** HpGGT, type 2 divergence sites, virtual screening, species-specific

OP9

ICABB-104

## FUNCTIONAL FOOD: PROBIOTIC AS HEALTH BOOSTER

Priyanka Roy

Department of Basic and Applied Sciences, National Institute of Food Technology Entrepreneurship and Management, Kundli, Sonipat (India)  
E-mails: namaskar.kolkata14@gmail.com

A good food habit plays an important role for healthy life. In order to immunize various lifestyle disorders, consumers were switch to functional food that helps is fulfil the nutritional requirement of the body as well as provides protection from various diseases. Probiotic microorganism which also known as friendly microorganism, play an important role in this regard. As it has enormous potential to produced verity of products such as vitamins, proteins, antioxidants. Moreover, it helps in leading healthy life by symbiotic association with the host. In this current study are focussing on the potential of probiotics microorganism for improving the health conditions in metabolic disorders as well as in reducing the risk of developing pathogenic diseases. This review includes various probiotic microorganism and their metabolites, with a focus on human health benefits.

**Keywords:** Probiotic microorganism, functional food, lifestyle disorders, health benefits, nutrition

OP10

ICABB-166

## SCREENING SELECTIVE ESTROGEN BETA RECEPTOR MODULATORS AGAINST BREAST CANCER: AN IN SILICO APPROACH

Harmeet Dhiman and Manpreet Kaur Paintal

Department of Biotechnology, Guru Nanak Girls College (Affiliated to Punjab University), Model Town, Ludhiana Punjab 141 002  
E-mails: pearl4aug@yahoo.com, harmeetdhiman0019@gmail.com

Estrogen receptors are a group of proteins found inside cells. Various studies have indicated that elevated levels of estrogens leads to breast cancer. Flavonoids or phytoestrogens are a class of plant secondary metabolites and their role has been exploited for cancer prevention. Present study is a computational based docking method to evaluate the role of flavanoids targeted against breast cancer receptor. The sequence of target protein ER $\beta$  for docking was selected from Protein Data Bank. Docking calculations was performed using AutoDock suite of programs. Drug or ligand library was generated for structural analogues of for three classes of flavanoid based compounds, namely, Benzopyran, Raloxifene, Tamoxifene using ZINC which is a free database of commercially available potential drug like candidates for virtual screening. The results were evaluated primarily on the basis of binding energy, hydrogen bond formation, hydrophobic interactions and inhibition constants (Ki). The interactions between receptor and ligand was analysed through LIGPLOT and UCSF Chimera softwares. The main aim of this study was to screen a potent flavanoid based drug with minimal toxicity against breast cancer.

**Keywords:** Estrogen receptor, Benzopyran, Raloxifene, Tamoxifene, AutoDock, ZINC, LIGPLOT, UCSF Chimera

OP11

ICABB-113

## METAL IONS MODULATED RESPONSE OF SWEETNERS

Aditi Shrivastav and Sudha Srivastava\*

Department of Biotechnology, Jaypee Institute of Information Technology, Noida  
E-mails: aditishrivastav96@gmail.com,  
\*Corresponding author:sudha.srivastava@jiit.ac.in

Designing safe sweet molecules remains an unresolved problem due to non availability of common

pharmacophores for sweeteners belonging to widely different chemical classes. It becomes a further uphill task in the absence structure of human sweet taste receptor. We have exploited the taste experiments findings of sweet taste suppression of all sweet molecules by  $Zn^{2+}$  ions while differential suppression was observed in presence of other ions  $Na^+$  and  $Mg^{2+}$ . We have predicted the structure of human sweet taste receptor using homology modeling tools followed by docking analysis of sweet molecules (natural sugars (sucrose, fructose, glucose, maltose), amino acids (D-tryptophan, D-serine, D- alanine), sugar alcohols (xylitol), sulphonyl amides (Saccharin), cyclamate) in presence of metal ions. Mode of sweetness inhibition by metal ion receptors was analyzed and Crucial residues for sweetness have been identified. Results show that AH-B-X theory of glucophores for sweetners is not applicable to a wide class of sweetners.

**Keywords:** Glucophores, sweetners, sweet molecules, hSTR (human sweet taste receptor)

OP12

ICABB-039

### VIRTUAL SCREENING OF CHIKUNGUNYA VIRUS ENVELOPE GLYCOPROTEIN INHIBITORS

Garima Agarwal<sup>1</sup>, Vandana Gupta<sup>2</sup>, Reema Gabrani<sup>1</sup>, Amita Gupta<sup>3</sup>, V.K. Chaudhary<sup>3</sup> and Sanjay Gupta<sup>1\*</sup>

1. Center for Emerging Diseases, Department of Biotechnology, Jaypee Institute of Information Technology, Noida, UP 201309, India., 2. Department of Microbiology, Ram Lal Anand College, University of Delhi South Campus (UDSC), Benito Juarez Marg, New Delhi 110021, India., 3. Department of Biochemistry, University of Delhi South Campus, Benito Juarez Marg, New Delhi 110021, India.  
E-mails: garima0913@gmail.com, vandanagupta72@rediff.com, reema.gabrani@jiit.ac.in, ag0907@yahoo.com, vkchaudhary@south.du.ac.in, \*Corresponding author: sanjay.gupta@jiit.ac.in

Chikungunya virus (CHIKV) is a re-emerging mosquito-borne Alphavirus that had caused numerous well documented outbreaks of debilitating chikungunya fever in the recent years globally, particularly Africa, Asia, Europe and America with its devastating effects. Non availability of specific therapeutics and preventive vaccine has led to highly challenging situation. Therefore, the development of anti-CHIKV treatment is a requisite. In recent years drug repositioning has gained recognition for the curative interventions as it is much more cost effective and time saving in comparison to conventional drug discovery process. The envelope glycoproteins of

CHIKV E1 and p62 (precursor of E2 & E3) forms hetero-dimer, three such hetero-dimers combine together to form one trimeric spike on viral surface. These envelope proteins are considered to be promising target for drug discovery because of their vital role in viral attachment, entry and assembly in the host cells. In the current study, we propose structure based virtual screening of drug molecule on crystal structure of mature chikungunya envelope protein (PDB 3N41) using a library of FDA approved drug molecules active on the cell wall and envelope of bacteria. Group of Cephalosporin drugs docked successfully within pockets prepared between the E1 domain II and E2  $\alpha$  ribbon at E1-E2 interface of CHIKV envelope protein complex made up of E1, E2 and E3 proteins, with significantly low binding energies. With the top hits selection based on ranking score, sixteen drugs seemed to be best. Out of these 16 leads, five are identified as top leads with -67.67, -63.78, -61.99, -61.77 and -61.65 as cumulative score within Pocket 1 and Pocket 2. This *in-silico* study reveals that these shortlisted leads are potential inhibitors of E1-E2 hetero-dimer formation in CHIKV.

OP13

ICABB-057

### EXPRESSION, PURIFICATION AND FUNCTIONAL CHARACTERIZATION OF RECOMBINANT HYPER VARIABLE REGION (HVR) OF CHIKUNGUNYA VIRUS NSP3 PROTEIN

Ipsita Nandi<sup>a</sup>, Reema Gabrani<sup>a#</sup>, Amita Gupta<sup>b</sup>, Vijay k. Chaudhary<sup>b</sup>, Vandana Gupta<sup>c</sup>, Sanjay Gupta<sup>a#</sup>

a. Center for Emerging Diseases, Department of Biotechnology, Jaypee Institute of Information Technology, Noida, U.P. 201309, India b. Department of Microbiology, University of Delhi South Campus (UDSC), Benito Juarez Marg, New Delhi 110021, India c. Department of Microbiology, Ram Lal Anand College, University of Delhi South Campus (UDSC), Benito Juarez Marg, New Delhi 110021, India  
a#. Department of Biotechnology Jaypee Institute of Information Technology Centre for Emerging Diseases A-10, Sector-62, Noida, Uttar Pradesh, India-201 307  
#Corresponding author: sanjay.gupta@jiit.ac.in, sjay1908@gmail.com, reema.gabrani@jiit.ac.in

One of the most important rapidly re-emerging mosquito borne alphavirus is Chikungunya virus (CHIKV). Chikungunya infection often leads to self-limited febrile illness with prolonged myalgia and arthralgia leading to significant morbidity in infected individuals. There is a pressing need for development of anti-CHIKV therapeutics, as neither antiviral drug

nor vaccines has been licensed yet. The potential targets can be CHIKV proteins as they are associated with viral life cycle. Several CHIKV proteins are being studied worldwide, but Non-structural protein 3 (nsP3) has been less explored. This protein consists of three domains: Macro domain, alphavirus unique domain (AUD) and hyper variable region (HVR). HVR of nsP3 protein contains proline rich clusters, which are functional SRC homology 3 (SH3) domain interaction motifs. Interaction of these motifs with host amphiphysin protein is crucial for viral RNA replication. Present study focuses on purification of HVR protein for structural and functional assay. In order to obtain purified protein, HVR region was amplified from TOPO clones of nsP3 of IND-06-Guj strain and cloned into expression vector. Expression and solubilization of the protein was optimized at various different conditions before purification. The soluble recombinant HVR (His-HVR) protein was purified using affinity chromatography. Purified protein was analyzed for structural studies and functional assays. Circular dichroism of His-HVR protein was performed for structural study and it was observed that it consists of mostly random coils. For functional assay, co-pull down of His-HVR protein was performed with endogenous amphiphysin-I protein of N2a cells and was analyzed using western blotting. This purified protein will find applications as a target for novel therapeutic interventions in future.

**Keywords:** Amphiphysin-I; Circular dichroism; IND-06-Guj; N2a cells; SRC homology 3 (SH3) domain

OP14

ICABB-001

## NANOEMULSION BASED ETOPOSIDE FORMULATION FOR IMPROVED ORAL BIOAVAILABILITY

**Mrigendra Mahato and Saima Amin\***

Department of Pharmaceutics, School of Pharmaceutical Education and Research, Jamia Hamdard, New Delhi 110062

E-mails: [mrigendramahato@gmail.com](mailto:mrigendramahato@gmail.com),

\*Corresponding author: [samin@jamiahmdard.ac.in](mailto:samin@jamiahmdard.ac.in)\*

Etoposide is an epipodophyllotoxin antineoplastic agent, which acts by forming a ternary complex with topoisomerase II and DNA, causing DNA breaks and cell death. It is used in the treatment of several tumors including small cell lung cancer, testicular cancer, lymphomas, and leukemias. However, the problem associated with etoposide is its poor aqueous solubility (water solubility is only 0.03mg/ml) and low permeability. It is also recognized as P-glycoprotein

(P-gp) and cytochrome P450 3A (CYP3A) substrate. Nanoemulsion is considered as an ideal approach to enhance to solubility and permeability of such drugs to improve their bioavailability, therefore, the purpose of the present study was to enhance the oral bioavailability of etoposide through lipid based drug delivery. Process parameters (stirring time, stirring speed and duration of sonication) were optimized for the preparation of formulation using Labrafac Lipophile WL 1349, Labrasol, Propylene glycol and Solutol HS 15. The globule size in nanoemulsion was found to be 170 nm with polydispersity index 0.129 and the zeta potential -35.8 mV. A very significant increase in percentage drug release was achieved in the case of nanoemulsion ( $87.427 \pm 0.82\%$ ) as compared to marketed capsule-Posid ( $50.877 \pm 1.33\%$ ) and drug suspension ( $41.374 \pm 1.69\%$ ) in simulated intestinal fluid of pH 6.8. The release was almost similar in simulated gastric fluid of pH 1.2. The nanoemulsion formulation of etoposide showed maximum absorption within 2h per oral administration to Wistar albino rats with  $AUC_{0-t}$  4359.289 ng/ml.h. The formulation showed shorter half-life (9 hours) than the corresponding capsule and drug suspension. The shelf-life of the developed nanoemulsion formulation was found to be 1.9 years through accelerated stability study.

**Keywords:** nanoemulsion, bioavailability, solubility, p-glycoprotein, stability.

OP15

ICABB-121

## REGULATION OF BIOSIMILARS IN INDIA: ROLE OF NATIONAL INSTITUTE OF BIOLOGICALS (NIB)

**Subhash Chand\*#, Nripendra N. Mishra\*,  
Richi V. Mahajan\*, Surinder Singh\***

\*National Institute of Biologicals, (Ministry of Health and Family Welfare) Sector-62, Institutional Area, Noida, Uttar Pradesh 201309.  
# Presenting Author

The global biosimilars market is expected to reach USD 10.90 Billion by 2021 from USD 3.39 Billion in 2016, at a CAGR of 26.3%. A Biosimilar product is the one, similar in terms of quality, safety and efficacy to an already licensed reference bio-therapeutic product. The expiry of patent protection for many biological medicines has led to the development of biosimilars. Similar Biologics were first developed in the 1980s using recombinant techniques to synthesize or improve naturally occurring complex peptides, proteins, and glycoproteins. Biosimilars products have to undergo

extensive analytical characterisation & comparability testing against Reference bio-therapeutic Product (RBP) to ensure product's quality, safety and efficacy. The first Biosimilar Guidelines in India were released in June 2012. Revised Biosimilar Guidelines has been released by CDSCO in March 2016. The Indian guidelines on similar biologics address the pre-marketing and post-marketing regulatory requirement, and also address the requirements related to manufacturing process and quality control. India has adopted a "sequential approach" (like "stepwise approach" - US and EU) to market Biosimilar products. National Institute of Biologicals (NIB) is as an apex autonomous Institute under the administrative control of Ministry of Health and Family welfare, Government of India. NIB is ensuring the quality of biological drugs like diagnostics, Vaccines and Biotherapeutics, including therapeutic monoclonal antibodies by undertaking high end quality control testing. CDSCO/ State FDA forwards various biological products including biosimilars for quality evaluation at NIB before marketing authorisation or post marketing surveillance to ensure the quality, safety and efficacy of the various biological products marketed in India.

OP16

ICABB-137

### **PRO-RESOLVIN LIPID MEDIATORS FROM DIETARY FLAXSEED OIL POTENTIATE THE POLARIZATION OF ADIPOSE TISSUE MACROPHAGES [ATM] FROM M1 TO M2 PHENOTYPE IN HIGH-FAT DIET FED INSULIN RESISTANT MURINE MODEL**

**Farah Khan, Samina Bashir, Yadhu Sharma and Md. Nematullah**

*Department of Biochemistry, Faculty of Science, Jamia Hamdard, New Delhi-110062, India.*

Specialized pro-resolving mediators are a group of lipid mediators that include lipoxins, resolvins etc. and have been delineated for resolution of acute inflammation. Altered resolution of inflammation as observed in obesity, a state of chronic low-grade inflammation, especially in the adipose tissue, has been linked to peripheral insulin resistance that involves enhanced macrophage switching from M2 [anti-inflammatory] to M1[pro-inflammatory] phenotype. Resolvins gain importance owing to their potential use as exogenously delivered therapeutic agents that may modulate macrophage switching. Flaxseed oil,

obtained from the seeds of, *Linumusitatissimum*, *L.*, is evidenced to posses anti-inflammatory potential, and may act a rich source of resolvins [E and D series]. In the present study, we evaluated the levels of E and D series resolvins in ATMs upon FXO supplementation and observed the effect FXO has on adipose tissue macrophages. High-fat diet fed obese insulin resistant *c57bl/6* mice (HFD-IR) were orally supplemented with FXO (4, 8 or 16 mg/ kg BW). LC-MS analysis of adipose tissue macrophages upon FXO supplementation revealed the increased concentration of pro-resolving factors like D and E series resolvins. Improved insulin sensitivity and lowered inflammation in adipose tissue were observed as suggested by NF- $\kappa$ B/ P65 expression by immunohistochemistry, cytokine profile, and macrophages surface markers (CD-80/86) and, TLR-4/2 expression by flow cytometry. Both by western blotting and real-time PCR, elevation in the expression of arginase 1, a marker of M2 macrophages, was observed on FXO supplementation in a dose dependant manner. Conclusively, our study suggested that Flaxseed oil may dose dependently switch M1 ATMs towards M2 through Resolvins mediated inhibition of TLRs/Nf- $\kappa$ B pathway.

**Keywords:** Resolvins, macrophage polarization, inflammation, EPA and DHA

OP17

ICABB-149

### **COMPLEMENTARY AND ALTERNATIVE THERAPIES TARGETING OXIDATIVE STRESS IN INFLAMMATORY BOWEL DISEASE**

**Mythily Subramaneyaan<sup>1\*</sup>**

*1. Division of Biochemistry, School of Basic and Applied Sciences, Galgotias University, Plot No-2, Sector-17A, Yamuna Expressway, Greater Noida, India*

\* Corresponding author: drmythily.s@gmail.com

Inflammatory bowel disease (IBD) is a common and chronic gastrointestinal disorder characterized by intestinal inflammation and mucosal tissue damage. Although the mechanisms underlying the etiology of IBD have not been thoroughly illuminated, it is commonly accepted that numerous factors including genetic susceptibility, alterations in intestinal epithelial cells, dysregulation of immune responses, intolerance to the microbiota, and environmental factors in a background of oxidative stress together contribute to IBD development. The conventional treatment of IBD includes the use of corticosteroids, immunosuppressant, antibiotics and biologic agents.

However, the use of these drugs is accompanied by a certain number of side effects such as GI problems, anaemia, and hypersensitivity. Recent reports indicate that at least 40% of IBD patients have used complementary and alternative medicines (CAMs). Because the pathomechanism of oxidative stress in IBD has been suggested by many laboratory reports and clinical trials, regulating Nrf2 signalling and suppressing ROS generation by targeting NOX or mitochondria are both potential treatment options for IBD. Furthermore, some nonconventional therapeutic methods with antioxidant effects, such as ROS generation inhibitors, functional dietary interventions, and natural or synthetic substances that activate antioxidant enzymes, have attracted increasing attentions as CAMs for IBD. These antioxidant therapies may have fewer side effects, lower costs, and better treatment responses, offering new hopes to IBD patients, especially those with UC in both the active phase and the remission stage of the disease and could be developed into potential medications for IBD.

**Keywords:** Inflammatory bowel disease, oxidative stress, redox signalling, complementary and alternative medicines.

OP18

ICABB-280

### ALTERED SERUM PROTEOME PROFILES IN MAMMARY TUMORIGENESIS IN WISTAR RATS: THE PROGNOSTIC SIGNATURES

Saima Wajid

Department of Biotechnology, School of Chemical and Life Sciences,  
Jamia Hamdard, New Delhi- 110062  
E-mails: swajid@jamiahAMD.ac.in

Breast cancer is regarded as the major cause of cancer death in females. It is the 2<sup>nd</sup> most prevalent cancer in humans and is a matter of deep concern for females, needs efficient and accurate prognostic strategies more importantly for the sporadic cases so that its early detection is possible before the manifestation (histopathological confirmation) of disease. The present study was conducted to identify the prognostic signatures developed as preliminary events in mammary tumorigenesis. We developed a breast cancer model using Wistar rats. The serum proteome of rats was analysed by virtue of 1D and 2D electrophoresis, followed by PD Quest software analysis, which revealed the altered expression (upregulation and downregulation) of several proteins at different stages bearing prognostic significance. The

proteins in question were subjected to MALDI-TOF MS characterization and thereby identified. These proteins can hence serve as important tools in the search of prognostic markers for the early detection of breast cancer, and may thus be recognized as prognostic signatures.

**Keywords:** Breast cancer; Wistar rat; MALDI- TOF MS; Proteins; Tumorigenesis

OP19

ICABB-279

### RESVERATROL SUPPRESSED BRAIN INFLAMMATION AND OXIDATIVE STRESS DURING EXPERIMENTAL EPILEPSY

Nidhi B. Agarwal and Md. Ubedul Hoda

Centre for Translational and Clinical Research, School of Chemical and Life Sciences, Jamia Hamdard, New Delhi-110062  
E-mails: nidhiagarwal@jamiahAMD.ac.in

**Objective:** Presently available antiepileptic drugs remain refractory to one third of patients. Thus, there is an urge to identify new molecules which can modulate process of epileptogenesis. Therefore, the present study was conducted to evaluate the effects of Resveratrol (RESV) on epileptogenesis in pentylenetetrazole (PTZ)-induced kindling in mice. Further, its effects on oxidative stress and brain inflammation during epileptogenesis were also assessed.

**Method:** Swiss albino mice were administered RESV (10, 20 and 40 mg/kg,p.o). For the development of kindling PTZ was administered in a dose of 25 mg/kg, i.p. on every alternate day and RESV in all the three doses was administered daily. Seizure score was continuously monitored till the development of kindling and cognition tests were performed in the end of the study. The animals were sacrificed and levels of inflammatory biomarkers (Interleukins) and oxidative stress were observed in the hippocampus and cortex of the kindled animals.

**Results:** RESV in all the tested doses suppressed the development of kindling and reduced the levels of interleukin and oxidative stress (MDA, glutathione, GPx) in kindled mice.

**Conclusion:** RESV suppressed the epileptogenesis and decreased brain inflammation. It can be potential candidate for epilepsy disease but further studies are required to ascertain the same.

OP20

ICABB-218 OP21

ICABB-220

**DESIGNING OF FUNCTIONALLY ACTIVE SMALLER PALINDROMIC ANALOGUES OF AN ANTIMICROBIAL PEPTIDE: TRITRPTICIN**

Gagandeep Kaur and Kanwal J. Kaur\*

National Institute of Immunology Aruna Asaf Ali Marg,  
New Delhi-110067, India

E-mails: gagan@niit.ac.in, \*Corresponding author: kanwal@niit.ac.in\*

Tritrpticin, Trp-rich or Pro/Arg-rich peptide, is a member of cathelicidin family. Since Trp, Pro and Arg residues play vital role in membrane disruption and in cell entry, tritrpticin can act as an attractive template around which novel antimicrobial peptides can be designed. Although effective against a broad spectrum of microorganisms, tritrpticin has strong haemolytic activity, which may suppress its therapeutic potential. Previous structure-activity analysis based on various deletion analogues in our lab, led to the identification of two minimal functional palindromic peptides namely CT7(WWWFPRR) and NT7(RRFPWWW) from tritrpticin, which by themselves exhibit adequate antibacterial activity against *Escherichia coli* and *Salmonella typhimurium*. To further improve the antimicrobial potency of these peptides, we designed analogues with C-terminus amidation (CT7-NH2 and NT7-NH2). We observed that perfectly palindromic analogues of tritrpticin with C-terminal amidation showed 2.5-fold higher antibacterial activity with comparison to that of CT7 and NT7 and led to faster killing of bacteria. The designed analogues displayed increased membrane permeability in concentration dependent manner. The higher antibacterial activity can be correlated to faster rate of internalization into bacterial cells. Circular dichroism spectroscopy suggested that there was no alteration in structure of peptides upon amidation. Moreover, CT7-NH2 and NT7-NH2 showed similar trend to CT7 and NT7 in context of exhibiting reduced RBC lysis and increased cell viability in comparison to that of tritrpticin. Since the two amidated analogues, CT7-NH2 and NT7-NH2 possess short peptide sequence, increased antibacterial activity and reduced cytotoxicity, they may work as promising candidates of antimicrobial peptides to fight various microbial pathogens.

**Keywords:** palindromic analogues, antibacterial activity, toxicity, membrane permeability

**ANTIMICROBIAL AND CYTOTOXICITY EVALUATION OF POLYPHENON 60 AND CIPROFLOXACIN LOADED NANO EMULSION AGAINST UROPATHOGENIC STRAINS**

Atinderpal Kaur, Sonal Jain, Reema Gabrani and Shweta Dang\*

Department of Biotechnology, Jaypee Institute of Information Technology, Sector 62, Noida, UP.

E-mails: atinderkahlon9@gmail.com; jain.sonal0208@gmail.com; reema.gabrani@jiit.ac.in, \*Corresponding author: shweta.dang@jiit.ac.in

Ciprofloxacin (Cipro) is a broad spectrum synthetic antibiotic that can be used to treat many bacterial infections. Combining it with a natural antimicrobial compound can enhance the therapeutic value, as non-specific action of natural compounds does not allow bacteria to become resistant. The preliminary antibacterial activity of both Polyphenon 60 (P60) and Cipro was evaluated against *E. coli* and it was found that both showed synergistic behaviour with FICindex value of 0.424. With the aim to enhance stability and antibacterial action P60 and Cipro were encapsulated in a single nanoemulsion (NE). In the present work, microtiter dish assay was performed to study the antibacterial potential of P60+Cipro loaded NE. The % cell viability was studied via 3-(4,5-Dimethylthiazol-2-Yl)-2,5-Diphenyltetrazolium Bromide (MTT assay). Adhesion assay was performed to explore the mechanism of antibacterial action. In addition growth curve analysis of *E. coli* in the presence of NE was performed. To further understand the mechanism of action of NE, Confocal Laser Scanning Microscopy was performed. The antibacterial study via microtiter dish assay showed that the NE formulation could inhibit the growth more effectively (% inhibition ~89%) as compared to corresponding aqueous formulation (% inhibition ~67%) and placebo (% inhibition ~76%) at their MIC values. The cytotoxicity analysis showed that the optimized formulation was nontoxic to Vero Cells. Moreover, it was observed that the NE was able to inhibit bacterial adhesion to mammalian cells as compared to aqueous formulation. Growth curve of *E. coli* indicated the inhibitory action of NE at the 5th h of inoculation. Confocal Laser Scanning Microscopy showed that the formulation exerts its antibacterial activity by disrupting the bacterial cell membrane. Hence, from the results it was concluded that developed P60+Cipro NE had enhanced antibacterial

activity and could further be explored for the treatment of urinary tract infection.

**Keywords:** Adhesion assay; Biofilm; Ciprofloxacin; Confocal laser microscopy; Polyphenon 60; Uropathogens

OP22

ICABB-100

## BACLOFEN-LOADED PLGA NANOPARTICLES FOR NEUROPATHIC PAIN MANAGEMENT: IN-VITRO AND IN-VIVO EVALUATION

Kuldeep Nigam<sup>1</sup>, Atinderpal Kaur<sup>1</sup>, Amit Tyagi<sup>2</sup>, Kailash Manda<sup>2</sup>, Reema Gabrani<sup>1</sup> and Shweta Dang<sup>1\*</sup>

1. Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sector-62, NOIDA, U.P., India 2. Institute of Nuclear Medicine & Applied Sciences, DRDO, Delhi, India  
E-mails: shweta.dang@jiit.ac.in

Baclofen (BAC) is a GABA derivative, which is used as muscle relaxant and CNS depressant and offers positive results for strong opioid resistant chronic pain conditions. Repetitive daily dosages cause multiple side effects because of peripheral interactions such as neuropsychiatric problems, hypertension, gastrointestinal and genitourinary problems etc.

In the present work, PLGA nanoparticles of baclofen (PLGA-BAC-NP) were developed to enhance brain uptake using nanoprecipitation method followed by homogenization at 10,000 rpm and ultra-sonication. The average particle size of the PLGA-BAC-NP was found to be 128.8 nm, polydispersity index of 0.225 and zeta potential was found to be in the range of 0.79 mv. In-Vitro dissolution studies were carried out using USP-Type II dissolution apparatus in simulated nasal fluid and simulated CSF to study the release of the baclofen from the polymeric matrix of PLGA and it was observed that BAC loaded NPs showed sustained release as compared to the aqueous drug. Further, cytotoxicity studies were done using MTT (3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide) assay on Neuro-2a neuroblastoma cell line and results showed comparably low cytotoxicity of PLGA-BAC-NP as compared to aqueous solution of Baclofen at reported Cmax values of the drug 722 ng/ml (IV). In-vivo studies were carried to study the path of PLGA-BAC-NP from nose to brain in Sprague-Dawley rats by radiolabelling of Baclofen with technetium-99m (99mTc). Stability of radiolabelled NPs were observed in normal saline and serum for 24

h. Upon intranasal administration to rats, the uptake of radiolabelled PLGA-BAC-NP via nose to brain was evident from the Gamma scintigraphy images. Biodistribution studies confirmed brain uptake via intranasal route as the NPs were dispersed in brain (3.5%/g) as measured by radioactivity at 3 h. It can be concluded from in vivo results that the developed PLGA NPs could serve as a potential carrier for the BAC in the treatment of neuropathic pain.

**Keywords:** Baclofen, PLGA, nanoparticles, MTT-assay, gamma-scintigraphy, bio-distribution

OP23

ICABB-136

## CURCUMIN MEDIATED EFFECTS ON ANTI-DIABETIC DRUGS INDUCED CARDIOTOXICITY

Aditi Jain and Vibha Rani\*

Transcriptome Lab, Department of Biotechnology, Jaypee Institute of Information Technology, Sector-62, NOIDA, Uttar Pradesh-201309, India  
E-mails: aditijain506@gmail.com, \*Corresponding author: vibha.rani@jiit.ac.in

Cardiovascular diseases are the major reason for mortality worldwide and cardiotoxicity associated with present day therapeutics of various chronic and lifestyle diseases has emerged as an important factor for developing cardiovascular complications. Different diabetic therapies are known to be associated with drug induced cardiotoxicity. There is a growing interest in supplementing diabetic medications with natural products having cardio-protective potential that could prevent heart from the dual stress of drug toxicity and glucose induced diabetic cardiomyopathy. The present *in vitro* study was designed to compare the cardiotoxicity associated with two most commonly used anti-diabetic drugs metformin and pioglitazone. Further, the role of Curcumin polyphenols was studied on these drugs induced cardiotoxicity in H9C2 cardiomyoblasts. The effects of the drugs was studied in hyper glycemic conditions with or without Curcumin by various dose and time dependent studies for cell viability, oxidative stress, and cell death. Qualitative microscopic analysis and quantitative assays were done to study morphological alterations, cell growth and ROS production followed by anti-oxidant enzymes and caspases activity assays. Effect of the drugs and Curcumin on the formation of advanced glycated end products was also measured using spectrofluorometer. The mechanism of action of the induced cardiotoxicity was studied by lipid

peroxidation and mitochondrial potential analysis. Oxidative stress studies showed a remarkable increase in ROS production with increasing dose of anti-diabetic drugs. Increased caspase activity and altered mitochondrial integrity was also witnessed in presence of metformin and pioglitazone. These alterations were found to be significantly reduced when treated with curcumin simultaneously. This study confirms that Metformin and Pioglitazone exert toxic effect on cardiac cells by generating oxidative stress. Curcumin, being an anti-oxidative molecule, can suppress the toxic effect generated by these drugs. Therefore, Curcumin can be used as a supplement with anti-diabetic drug to suppress the cardiac stress induced by the drugs.

**Keywords:** Cardiotoxicity, Metformin, Pioglitazone, Curcumin, Oxidative stress, anti-diabetic, cardioprotective

OP24

ICABB-138

---

### DISSECTING THE ROLE OF A-TOCOPHEROL IN PLANTS: POTENTIAL APPLICATION FOR HUMAN HEALTH AND ABIOTIC STRESS ALLEVIATION IN PLANTS

**Deepak Kumar and Neera Bhalla Sarin**

*Department of Botany, Central University of Jammu, Rahya-Suchani,  
Bagla-181143, J&K School of Life Sciences, Jawaharlal Nehru  
University, New Delhi-110067  
E-mails: deepakkumar@cujammu.ac.in*

---

Oxidative stress is one of the major manifestations of unfavorable environmental conditions faced by plants as also of several different diseases, including cancers, in humans. Alpha ( $\alpha$ )-tocopherol, the biologically most active form of vitamin E, is a major antioxidant that bulwarks the cells against oxidative damage. It constitutes a small fraction of the total tocopherol pool in most oilseed crops. We generated transgenic (TR) *Brassica juncea* plants with ~6-fold higher  $\alpha$ -tocopherol levels compared to the wild type (WT) plants by overexpressing  $\gamma$ -tocopherol methyl transferase. This enzyme catalyses a rate limiting step in the  $\alpha$ -tocopherol biosynthetic pathway. To better understand the roles of different tocopherol forms in plants we compared the performance of TR plants under conditions of abiotic stresses induced by NaCl (salinity), CdCl<sub>2</sub> (heavy metal) and mannitol (drought). This resulted in an increase in total tocopherol levels in both the WT and TR plants. Seed germination, shoot growth, and leaf disc senescence showed that TR *B.*

*junccea* had enhanced tolerance to these stresses. Damage caused by the induced stress was lower in TR plants compared to WT plants as assessed by their higher relative water content, lower MDA and H<sub>2</sub>O<sub>2</sub> accumulation and lower electrolyte leakage. Lesser superoxide and H<sub>2</sub>O<sub>2</sub> accumulation was observed in TR seedlings exposed to these stress. Enhanced levels of different antioxidant enzymes and molecules were present in TR plants when compared to WT plants under similar stress. We further checked the efficacy of feeding  $\alpha$ -tocopherol enriched seeds in securing the antioxidant defense in mice. We found significant increase in the content of various phase I and phase II detoxification enzymes with a corresponding decrease in the level of peroxidative damage. Also, the transgenic seeds were found to have chemopreventive effects against DMBA-induced skin papillomagenesis in mice model. Our results highlight the potential of increased  $\alpha$ -tocopherol in transgenic *B. juncea* in health of humans and agricultural crop plants.

OP25

ICABB-123

---

### GENOME WIDE CYTOSINE METHYLATION IN RESPONSE TO DEHYDRATION STRESS MODULATING THE EXPRESSION PATTERN OF GENES IN FOXTAIL MILLET (*Setaria italica*)

**Chandra Bhan Yadav\* and Manoj Prasad**

*National Institute of Plant Genome Research, New Delhi-110067  
E-mails: cbhayadav@nipgr.ac.in,  
\*Corresponding author: cbhayadav@nipgr.ac.in*

---

Cytosines methylation creates the epigenetic alteration of plant genomes in response to abiotic stress may influence the plant sensitivity. Foxtail millet (*Setaria italica*), an important forage crop that accounts for high nutritive value including Ca, Fe and starch content, small (~515 Mb), diploid, and less complex genome. We have quantified the genome-wide cytosine methylation and transcriptome analysis in the foxtail millet genome in two cultivars IC403579 (IC04- stress tolerant) and IC480117 (IC41- stress susceptible) under dehydration stress. Whole genome Methylation levels were also compared between both the cultivars under dehydration stress. The genome-wide methylation patterns for various sequence context such as CG, CHG, and CHH were quantified by bisulfite conversion followed with sequencing and visualization single cytosine level in both the contrasting cultivars of foxtail millet. The percentage of mCs in CG contexts

ranged from 53.0 – 68.0%, CHG contexts ranges from 41.0 – 52.0% and CHH contexts ranges from 7.1 – 14.6% in both the cultivars (with H being A, C or T). The hypo- and hypermethylated genes in response to dehydration stress were characterized all sequence contexts and found that the large fraction of genes (1998) were hypermethylated for the CpG sites in sensitive cultivars, whereas 1952 genes were highly affected in tolerant cultivars. Differentially methylated genes were also significantly and negatively correlated with transcript level for a subset of genes showing changes both in methylation and expression with dehydration stress. The comprehensive data of cytosine methylation and gene expression profiles in foxtail millet under dehydration stress provide a useful resource for future epigenomic regulation studies in plants under abiotic stresses.

**Keywords:** Abiotic stress, DNA methylation, Foxtail millet

OP26

ICABB-092

### ANALYZING THE THERAPEUTIC POTENTIAL OF *SYZYGIUM CUMINI*: A NOVEL CARDIO-PROTECTIVE AGENT

Neha Atale

Department of Biotechnology, ITS, Paramedical college,  
Muradnagar, Ghaziabad, UP, India

Diabetes associated cardiovascular disorders are pandemic diseases and became a major cause of mortality. Drugs based therapies are found to have toxic effects on human health and ultimately lead to multi-organ failure. In this regard, Plant extracts have gained an attention towards the remedy of such diseases due to availing the beneficial effects of polyphenols, secondary metabolites etc. Therefore, in the present study, we investigated the effect of *Syzygium cumini* methanol seed extract (MSE) on the glucose stressed cardiacmyocytes. The antiglycooxidative potential of *S. cumini* seed extracts was assessed by analyzing the scavenging activities for various free radicals and MSE was found to be powerful anti-glycooxidant. Doses of *S. cumini* MSE and glucose were optimized by MTT assay along with the gallic acid as positive control. Morphological analysis revealed the intact morphology of cells on MSE treatment, which was found to be enhanced on glucose administration. qRT -PCR studies explored the decrease in the expression of MMPs, IL-6 and TNF- $\alpha$

in MSE treated glucose stressed cells, upto the control cells. *In silico* docking studies showed the possibility of *S. cumini* polyphenols as natural MMPs inhibitors, significant and novel therapeutic targets. In our studies we found that crude methanol seed extract has adequate potential of combating the cardiac stress due to the synergistic effect of phytoconstituents of *S. cumini*.

**Keywords:** Anti-AGE agent, MMP, Glycooxidative, Cardioprotective, *S. cumini*

OP27

ICABB-253

### GAUGING OF POLLUTION IN RIVER GANGA AT VARANASI

Diva Raghuvanshi\*, Ruby Pandey,  
Harendra Singh, Vandana Srivastava and  
D.N. Shukla

Botany Department, University of Allahabad, Allahabad

\*Corresponding author: drdivyaraghuvanshi@gmail.com

Today to meet the needs of food requirements for growing population in the country, farmers of our country are using higher amounts of fertilizers and pesticides but at the cost of environment and health. Pesticides are very hazardous to the ecosystem and can cause severe illness when it enters the body. They do not remain at their target site but they often find their way to the aquatic environment via soil percolation, air drift or surface runoff. This affects abundance and diversity of non-target species producing complex effect on the ecosystems. Pesticide pollution in river Ganga at Kanpur is analyzed in the present work. Samples of water, sediment and plant were collected from the river. The results of the analysis of the water and soil and plant samples from river Ganga have shown the presence of both organochlorine and organophosphate pesticides. The organochlorine compounds detected were isomers of HCH ( $\alpha$ -,  $\beta$ -,  $\gamma$ - and  $\delta$ ), isomers of Endosulfan ( $\alpha$ - and  $\beta$ -), metabolites of DDT ( $o,p'$ -DDT,  $p,p'$ -DDT,  $p,p'$ -DDE and  $p,p'$ -DDD) and Aldrin. However, their contamination level was well within the permissible limit, but still their presence in the environment is a matter of great concern because of their persistency, bio magnification and toxicity. Hence, it is suggested that appropriate measures may be taken to protect the Ganga River from such contamination and an integrated effort should be made to prevent further contamination.

**Keywords:** Pesticides, Pollution, River Ganga, Varanasi, Organochlorine.

## **INTROGRESSION of *xa13*, *Xa21* and *sd1* GENES IN INDIAN BASMATI USING MARKER ASSISTED BACKCROSS BREEDING**

**R. K. Salgotra<sup>1</sup>, Deepak Kumar<sup>2</sup> and Meenakshi Raina<sup>1\*</sup>**

1. School of Biotechnology, Sher-e-Kashmir University of Agricultural Sciences & Technology of Jammu, Chatha, Jammu-190008 (Jammu & Kashmir), India, 2. Department of Botany, Central University of Jammu, Rahya-Suchani (Bagla), District: Samba - 181143 Jammu (Jammu & Kashmir), India  
E-mails: rks\_2959@rediffmail.com, deepakinjnu@gmail.com,  
\*Corresponding author: raina.kesar592@gmail.com

Two major bacterial blight (BB) resistance genes (*xa13* and *Xa21*) and a semi-dwarf gene (*sd1*) were introgressed into an Indian Basmati through marker-assisted backcross breeding. A high yielding introgressed line PAU148 carrying *xa13*, *Xa21* and *sd1* genes was used as donor parent. Marker-assisted backcrossing was continued till BC2 generation wherein gene specific markers specific for the resistance genes were used for foreground selection and a set of parental polymorphic microsatellite markers were used for background selection at each stage of backcrossing. In BC2F2 population 19 plants were found to be positive for all three genes whereas the maximum genome recovery of Ranbir Basmati in BC2F2 was 86.9 percent in introgressed line SBTIL121. The introgressed lines carrying resistance genes were further evaluated for bacterial blight resistance. The genotypes carrying both resistance genes exhibited very high level of resistance against bacterial blight while the lines containing either *Xa21* or *xa13* gene alone showed moderate resistance. The pyramided lines were also analyzed for agro-morphological characters in randomized block design (RBD) with two replications. All the lines were found to be significant for all the agro-morphological traits. The identified semi dwarf bacterial blight resistance lines were identified and advanced for further selection and evaluation.

**Keywords:** Bacterial blight, Marker assisted backcross breeding, Basmati, Semi-dwarf

## **QUALITY CHARACTERISTICS OF UNDERUTILIZED, NON-CONVENTIONAL AMORPHOPHALLUS PAEONIIFOLIUS FLOUR AND STARCH**

**Anuradha Singh and Neeraj Wadhwa\***

Division of Biochemistry, School of Basic and applied Sciences, Galgotias University, Plot No.2, Sector 17-A Yamuna Expressway, Gautam Buddha Nagar, Uttar Pradesh, India  
Department of Biotechnology, Jaypee Institute of Information Technology, Noida, Uttar Pradesh, India  
E-mails: anuradha.singh@galgotiasuniversity.edu.in, anuradhasingh.dr@gmail.com, \*Corresponding author: neeraj.wadhwa@jiit.ac.in

*A. paeoniifolius* commonly known as elephant foot yam is an underutilized, highly potential tropical tuber crop contains good source of protein as well as starch. The purpose of this study was to isolate and evaluate the physicochemical properties of flour and starch from Elephant foot yam. Establishing the quality characteristics of shelf-stable flour and starch from *A. paeoniifolius* will facilitate various industrial applications of the crop. Nutritional analysis revealed that the flour is fat and cholesterol free, high in fibre and may be suitable for celiac disease patients. SEM studies revealed that flour and starch granules are round, elliptical and polygonal in shape. The X-ray diffraction patterns of both flour and starch revealed A-type diffraction patterns. In addition starch yield, swelling power, water binding capacity, syneresis, paste clarity and resistant starch content were also evaluated using standard methods. These results indicate that the flour and starch processed from *A. paeoniifolius* will be useful in selecting this underutilized crop for future applications and various possible uses for development of new acceptable food products and enhance its commercial potential.

**Keywords:** *A. paeoniifolius*, flour, starch, physicochemical properties, resistant starch

**IN-SILICO GENOME-WIDE IDENTIFICATION AND CHARACTERIZATION OF GLUTATHIONE S-TRANSFERASE GENE FAMILY IN CAJANUS CAJAN (L.) MILLSP.**

**Swati Vaish, Divya Gupta and Mahesh Kumar Basantani\***

*Institute of Bioscience and Technology, Shri Ramswaroop Memorial University, Lucknow-Deva Road, Barabanki, 225003, Uttar Pradesh, India  
E-mails: swati.vaish88@gmail.com, guptadivya06@gmail.com, \*Corresponding author: mkbasantani@gmail.com*

Plant glutathione S-transferases (GSTs; EC 2.5.1.1.8) are multifunctional proteins. They are involved in endogenous plant metabolism, normal growth and development, and abiotic and biotic stress tolerance. In the current study, GST gene family was characterized in *Cajanus cajan* using *in-silico* approach. A total of 64 GSTs were identified belonging to seven classes. Of the total 64 GSTs identified, 33 GSTs had their chromosomal locations known. These GSTs were further characterized. The predicted molecular weight of these GSTs fell in the range of 20.95 to 44.13 kDa; and theoretical pIs ranged from 4.95 to 9.69. They were predominantly found to be subcellularly localized in the cytoplasm. The active site amino acid residues were confirmed to be serine in tau, phi, theta and zeta; and cysteine in DHAR and lambda. The domain organization of the GST proteins was confirmed by NCBI batch-CD search. The GST gene architecture followed the canonical pattern of 2-exon/1-intron in tau class, and 3-exon/2-intron in phi class as reported in earlier studies. MEME analysis identified significantly conserved motifs with the width of 11 to 50 amino acids. Serine residue present in one of the motifs was the active site residue of all tau GSTs and was highly conserved. Phylogeny analysis revealed dynamic GST evolution patterns. The characterization of GSTs in the economically important legume *C. cajan* will widen the opportunities for future work such as cloning and characterization of GSTs, and their role in metabolism, growth and development, and stress physiology.

**Keywords:** *Cajanus cajan*, bioinformatics, glutathione S-transferase, legumeinfo, plant stress metabolism, whole-genome sequencing

**CONSERVATION OF RHEUM EMODI THROUGH IN VITRO APPROACHES**

**Ruchi Singh\* and Preeti Chaturvedi**

*Department of Biological Sciences, CBSH, G. B. Pant University of Agriculture & Technology, Pantnagar, Udhampur Singh Nagar. -263145. Uttarakhand, India.*

\*Corresponding author: ruchisingh12apr@gmail.com

*Rheum emodi* Wall ex. Meissn (Family- Polygonaceae) is an important folk medicinal herb of Himalayan Region. Roots and rhizome of *R. emodi* possess anticancer, antifungal, antidiabetic, antiulcer, antioxidant, nephroprotective and hepatoprotective properties due to provenance of number of bioactive compounds. To effectuate the raw material need, the species is collected from the wild, which pose pressure on its availability. Consequently, the species has come under threatened category due to rapidly depleting natural populations. The present study aims to conserve this valuable plant by developing an efficient protocol for micropropagation. Leaf, petiole, roots and nodal part of *in vitro* germinated seedlings were taken as explants for direct and indirect organogenesis using MS medium supplemented with various concentrations of cytokinins (BAP, TDZ, Kn) and auxins (NAA, IBA, IAA) singly and in combinations. Kn + TDZ + 2, 4 -D was found to be most effective for callus induction with 100 % response from petiole explant. Nodal explants produced an average of 19 microshoots per explant after 23 days of inoculation on culture medium supplemented with BAP + TDZ + NAA. Both direct and indirect rhizogenesis was observed from leaf explant in MS medium supplemented with IBA + NAA and BAP + NAA respectively after 23 days of inoculation. Thus, the present study proposed a reliable protocol for the *in vitro* propagation of *R. emodi* for conservation and utilization of the plant for medicinal purpose.

**Keywords:** *Rheum emodi*, conservation, *in vitro* propagation.

## VARIOUS FACETS OF HISTONE MODIFICATIONS

**Madhvi Sharma and Anil Kumar Singh**

*Sher-e-Kashmir University of Agricultural Sciences and Technology, Chatha, Jammu, 180009, India. School of biotechnology  
E-mails: madhvisharma413@gmail.com, aniliivr@gmail.com*

The histone tails provide sites for a variety of post-translational modifications, such as acetylation, phosphorylation, methylation, ubiquitination, and sumoylation. Acetylation of core histones usually induces an 'open' chromatin structure and is associated with gene activation, whereas deacetylation of histone is often correlated with 'closed' chromatin and gene repression. Histone modifications play an important role in the regulation of several biological processes involving DNA dynamics like transcription, DNA repair, and replication. A number of studies have shown that the molecular mechanisms driving plant response to environmental stresses often depend on nucleosome histone posttranslational modifications including histone acetylation, methylation, ubiquitination, and phosphorylation (Liua et al., 2014). The effectiveness of histone deacetylase(HDAC) inhibitors for increasing tolerance to salinity stress has recently been reported (Patanun et al., 2017). In the recent research papers scientists have performed various chromatin modification analyses at selected loci using the standard chromatin immunoprecipitation procedure, and demonstrate that upregulation of these genes is associated with histone H3 lysine 4 tri-methylation (H3K4me3) at the gene body or transcription start sites of these loci (Sato et al., 2016). A number of techniques have also been used to identify the various histone modifications taken place in a cell including ChIP (cross link ChIP, native ChIP), ChIP-seq, ChIP-chip, ChIP qPCR, mass spectrometry, among that ChIP is widely used. A growing number of studies have demonstrated the importance of histone deacetylation/acetylation on genome stability, transcriptional regulation, and development in plants. Hence histone modification factors in stress response may help to engineer plants with increased tolerance to multiple stresses.

**Keywords:** Histone, ubiquitination, ChIP, qPCR, methylation.

## SYNERGETIC EFFECT OF METATOPOLIN AND BENZYADENINE ON AXILLARY SHOOTS BUD INDUCTION AND PROLIFERATION IN *RAUVOLFIA TETRAPHYLLA* (L.) BY USING NODAL EXPLANTS

**Sheikh Altaf Hussain, Naseem Ahmad and Mohammad Anis**

*Plant Biotechnology Laboratory, Department of Botany, Aligarh Muslim University, Aligarh. 202002, India  
E-mails: anism1@rediffmail.com, sheikhaltaf033@gmail.com*

The stimulatory effect of different concentrations (1.0 - 15.0  $\mu$ M) of metatopolin (mT) either alone or in combination with 6-benzyladeninepurine (BA) on *in vitro* shoot bud induction and proliferation were assessed for *Rauvolfia tetraphylla* using mature nodal explants. All tested concentrations facilitated multiple shoot induction on Murashige and Skoog (MS) medium after 1 week of incubation. Maximum (95%) shoot regeneration frequency, mean shoot number ( $19.80 \pm 0.37$ ) with mean shoot length ( $5.16 \pm 0.21$ cm) were obtained on MS medium enriched with 12.5  $\mu$ M mT + 5.0  $\mu$ M BA after 8 weeks of culture. Microshoots  $\leq 4$ cm were excised and were successfully rooted in MS liquid medium supplemented with different concentrations of indole-3-butyric acid (IBA). Best rhizogenesis (90%) was achieved on MS medium augmented with 0.3 $\mu$ M IBA with root mean number ( $9.3 \pm 1.45$ ) and mean length ( $3.3 \pm 0.33$ cm), after 4 weeks of incubation. The regenerated plantlets were transferred to thermocol cups containing soilrite for hardening and acclimatization phase under culture room conditions prior to field transfer. The regenerated plantlets survived best (90%) in pots containing garden soil and manure (3:1) under field conditions. All the regenerated plants were morphologically similar with the mother plant and showed no genotypic variation as was assessed by clonal fidelity using RAPD markers.

**Keywords:** Benzyladenine, Metatoplins, Nodal explant, RAPD Molecular marker.

## GOLD NANOPARTICLES: ONE - POT SYNTHESIS THROUGH GREEN ROUTE AND ANTIBACTERIAL APPLICATION

Lovnish Siyal, Neha Gopal, R. Sahney\*, B. Kumar

*Amity Institute of Biotechnology, Amity University Uttar Pradesh*

\* Corresponding author: rachanasahney@gmail.com;  
rsahney@amity.edu

Ever increasing day-to-day health problems and the cost associated with modern day hospital treatments are forcing to design and develop new materials which can act as antimicrobial agent. Colloidal gold (AuNPs) show unique and considerably distinct physical, chemical, and biological properties due to their high surface-to-volume ratio which can be exploited to develop nano-drug delivery vehicles. Here gold surfaces can be modified with ligands containing functional groups, providing an electrostatic or steric stabilization. Thus AuNPs conjugated with or without antibiotics can be used to improve antibiotic delivery, target specificity, dosage and bioavailability etc. In addition to improving the efficacy of the conjugated antibiotic, AuNPs have been evaluated by many researchers for antibacterial activity against various bacterial strains. There is still an ambiguity regarding the antibacterial activity of naked AuNPs which are not capped with any antibiotics. In this study, we have developed a green method for the synthesis and stabilization of AuNPs by glucose oxidase enzyme. Thus the harsh conditions and conventional usage of toxic reducing agents like NaBH4 and LiAlH4 along with some organic stabilizing agents can be avoided for the synthesis of such inorganic nanomaterials. On the other hand, biomolecules are 'greener' and act as a reducing agent as well as the stabilizing agent during the synthesis of AuNPs. It possesses a very small size exhibit good biocompatibility and a low level of toxicity. The AuNPs were characterized using UV-Vis spectrophotometer, DLS, SEM. The synthesized AuNPs was efficiently capped with active glucose oxidase enzyme which produces peroxide ( $H_2O_2$ ) in presence of glucose. The peroxide acts as a potential antimicrobial agent which was investigated by colony count method and minimum inhibitory concentration measurements.

**Keywords:** Nanoparticles; Gold nanoparticle; Green Synthesis; Anti-microbial.

## PHOTOSYNTHESIS AND GROWTH IN SALINITY EXPOSED MUNGBEAN CULTIVARS -ROLE OF SULHAR, GLUTATHIONE, PROLINE AND GLUCOSE

Sofi Javed Hussain<sup>1\*</sup>, Nafees A. Khan<sup>1</sup>, AsimMasood<sup>1</sup>, and Naser A. Anjum<sup>1</sup>

1. Plant Physiology and Biochemistry Laboratory, Department of Botany, Aligarh Muslim University, Aligarh, 202002, India  
\*Corresponding author: sjavaidjh@gmail.com

In greenhouse pot-culture conditions, the role of sufficient (1.0mM SO<sub>4</sub>) and excess (2.0mM SO<sub>4</sub>) sulfur (S) was studied in the control of photosynthesis and growth of Punt mung (salt tolerant) and Samrat (salt sensitive) cultivars of mungbean (*Vigna radiata*) under 50mM NaCl stress. The modulation of glutathione, proline and glucose was also studied in order to ascertain their control under S nutrition. Both the S-levels Equal promotion in photosynthesis and growth was noted with both S levels in both the cultivars when the plants were not subjected to stress. However, excess-S mediated alleviation in the negative effect of salt was observed that was more prominent in Punt-mung in comparison with the Samrat. In NaCl-treated cultivars, S-application significantly elevated glutathione reductase activity, accumulation of cysteine, GSH and proline, also caused lesser accumulation of glucose in Punt mung as compared to Samrat. Up-regulation of Rubisco activity was thought due to the reduced glucose accumulation with S application that in turn increased the rate of photosynthesis and growth. Overall, S-application in NaCl-fed plants improved photosynthesis and growth through increasing the activity of glutathione reductase, and the production of cysteine, GSH and proline, and decreasing the glucose sensitivity of the studied mungbean cultivars.

**Keywords:** *Vigna radiata*; Salinity; Sulfur; Proline; Glutathione; Cysteine

## HYDROGEN - UREA FUEL: THE DREAM THAT WON'T DIE

Sarita Sachdeva<sup>1</sup> and Sanchit Sood<sup>1\*</sup>

1. Department of Biotechnology, Faculty of Engineering and Technology (FET), Manav Rachna International Institute of Research and Studies, Faridabad, Haryana-121004, India  
 \* Corresponding author: sanchitsoodmru@gmail.com

Human beings live in the kingdom of nature and interact with it constantly. The influence of Nature in the form of the air they breathe, the water they drink, the food they eat, indicates That man is insignificant and nature is supreme, but the irony is that man fails to accept this Harsh truth and has a pseudo belief that HE can control and alter environment. Energy is an Irreplaceable part of our life and it is highly correlated with the environment. The availability of fossil fuels will be increasingly reduced over the years (owing to the depletion of Resources) and to meet the growing demand for energy, new sources will need to be Exploited, especially renewable sources with a smaller environmental impact. One of the Possible alternatives are **HYDROGEN FUEL**. Presently, most of the hydrogen is produced from fossil fuels, which accounts about 98 per cent of its total production. Although they Have the potential for effective H<sub>2</sub> production but it is economically impractical and Unsafe/toxic to the environment. Therefore, among the various technologies, which are used for hydrogen production, biological hydrogen production perhaps exhibits the substantial Prospective to replace the fossil fuels as these technologies are less energy intensive and more Environment-friendly as compared to conventional processes. Here we propose the generation of hydrogen from urea rich water which is the major agricultural waste. By using urea rich Source for generation of energy it will meet dual purpose one, it will make possible the Generation of energy from bio-wastes and second will help in Liquid Waste management.

**Keywords:** Fossil fuels, Biological hydrogen production, Urea rich water, Agricultural waste

## PATHOLOGICAL INTERACTION OF *MELOIDOGYNE INCognITA,* *PECTOBACTERIUM BETAVASCULORUM* AND *RHIZOCTONIA SOLANI* ON GROWTH AND BIOCHEMICAL CHANGES OF BEETROOT (*BETA* *VULGARIS*)

Manzoor R. Khan\* and Zaki A. Siddiqui

Section of Plant Pathology & Nematology Department of Botany  
 Aligarh Muslim University Aligarh-202002(U.P.), India  
 \*Corresponding author: khan11manzoor@gmail.com

Interaction of pathogens have significant influence on disease development, disease severity, etiology of pathogens involved and finally on disease management. Hence, interaction of pathogens is of prime importance for proper management of disease complexes on various crops. In this investigation we studied the interaction of *Meloidogyne incognita*, *Pectobacterium betavasculorum* and *Rhizoctonia solani* on the growth of beetroot (*Betavulgaris*). We also accessed some biochemical changes (Chlorophyll and carotenoids, hydrogen peroxide, malondialdehyde, proline, superoxide dismutase, catalase and ascorbate peroxidase activities) in response to pathogen interactions. Inoculation of plants with individual pathogen reduced plant growth, chlorophyll, and carotenoids while increased H<sub>2</sub>O<sub>2</sub>, MDA, proline, SOD, CAT, APX activities. Inoculation of *R. solani* caused a greater reduction in plant growth, chlorophyll and carotenoid contents and increase in H<sub>2</sub>O<sub>2</sub>, MDA, proline, SOD, CAT, APX activities followed by *M. incognita* and *P. betavasculorum*. Coinoculation of these pathogens caused a greater damage to plant growth, chlorophyll and carotenoids highest increase in H<sub>2</sub>O<sub>2</sub>, MDA, proline, SOD, CAT, APX activities than individual inoculation. Maximum reduction in plant growth, chlorophyll and carotenoids and highest increase in H<sub>2</sub>O<sub>2</sub>, MDA, proline and antioxidative enzyme activities was observed when all the three pathogens were inoculated simultaneously. Number of galls in the root system and nematode population were reduced in the presence of *R. solani* and *P. betavasculorum*. Root rot and soft rot caused by *R. solani* and *P. betavasculorum* were found 3. Disease indices were observed 5 when two or more pathogens were inoculated together.

**Keywords:** interaction, antioxidant, galls, soft rot, root rot.

## **USNEA LONGISSIMA ACH: A PROMISING SOURCE OF NUTRACEUTICAL**

**Vartika Pant\* and P.B. Rao**

*Department of Biological Sciences, CBSH, G. B. Pant University of Agriculture & Technology, Pantnagar-263145, Udhampur Singh Nagar, Uttarakhand, India.*

\*Corresponding author: [vartikapant@gmail.com](mailto:vartikapant@gmail.com)

*Usnea longissima* Ach. (family Parmeliaceae) commonly known as old man's beard, is generally found in the crowns of trees of open or shaded coniferous forest. It is widely used in different traditional systems viz., Homeopathic and Western Medical Herbals (HWMH), Traditional Indian Medicine (TIM), Traditional Chinese Medicine (TCM), etc. It has been used to strengthen hair and in the production of hygienic products for women. In the folk medicine in different countries of the world, it has been used widely as an expectorant, wound dressing and to stanch nose bleeding, as well as in the treatment of ulcers. It has also been used in the treatment of injuries to the legs, bone fractures, and skin eruptions. The present study is made on the investigation of different mineral analysis in *U. longissima* by using Atomic Absorption Spectrophotometer (AAS), antioxidants by 2,2-diphenyl-1-picrylhydrazyl (DPPH) assay, Total antioxidant activity (TAA), Fe<sup>+2</sup> ion chelating activity (FCA), total flavonoid and phenolic content, qualitative phytochemical guesstimation and nutraceutically important bioactive compounds through GC-MS. The results indicated that the higher amount of antioxidants, phytochemicals (cardiac glycosides, flavonoids, tannins, phenols, terpenoids, protein, carbohydrate and alkaloid), minerals (Zinc, Iron, Calcium, etc.) along with the bioactive compounds, were present in the extract and will be discussed in this paper. Being rich in antioxidants, elements and phytochemicals, it can be served as a natural resource and play crucial role in traditional therapeutic applications.

**Keywords:** *Usnea longissima*, nutraceutical, antioxidants, elements, phytochemicals.

## **PROPHYLACTIC DETECTION OF PATHOGENIC BACTERIA USING PCR AND REAL TIME PCR IN MUNICIPAL SUPPLIED DRINKING WATER, JAIPUR, INDIA**

**Tanushree Saxena<sup>1</sup>, Pallavi Kaushik<sup>2\*</sup>,  
Sreemoyee Chatterjee<sup>1</sup> and  
Medicherla Krishna Mohan<sup>3</sup>**

1. Department of Environmental and Life Sciences, The IIS University, S.F.S. Mansarovar, Jaipur-302020, Rajasthan, INDIA. 2\*. Department of Zoology, University of Rajasthan, JLN Marg, Jaipur-302004, Rajasthan, INDIA. 3. Birla Institute of Scientific Research, Statue Circle, Jaipur-302001, Rajasthan, INDIA.  
E-mails: [sreemoyee.chatterjee@iisuniv.ac.in](mailto:sreemoyee.chatterjee@iisuniv.ac.in), [pallavikaushik512@gmail.com](mailto:pallavikaushik512@gmail.com), [mkrishnamohan@gmail.com](mailto:mkrishnamohan@gmail.com), \*Corresponding author: [tanushree.saxena@yahoo.com](mailto:tanushree.saxena@yahoo.com)

Substantial treatment of water is a routine practice in the water supply system but the occasional outbursts of water quality related health issues cannot be overlooked. Microbial contamination of drinking water supply can cause a serious threat to public health therefore, efficient detection methods for pathogens in drinking water supplies are required for the protection of public health and maintaining confidence of consumers. In this study PCR based assay was developed and investigated, for rapid detection and quantification of pathogenic bacteria in municipal supplied drinking water in Jaipur, India. The PCR detects lac Z gene from *Escherichia coli*, oprL gene for *Pseudomonas aeruginosa*, aerolysin gene for *Aeromonas hydrophila* in 6.66%, 56.66% and 26.66% of 60 water samples collected over a period of one year. Random fragment for *Salmonella* sp., ipaH gene for *Shigella* sp. and ctx A gene for *Vibrio cholerae* were not detected in any of the water samples. Quantitative real-time PCR detects *E. coli* ranging from  $4.02 \times 10^2$  to  $2.33 \times 10^3$  copies/ $\mu$ L, *P. aeruginosa* from  $2.13 \times 10^1$  to  $2.08 \times 10^5$  copies/ $\mu$ L and *A. hydrophila* from  $1.48 \times 10^1$  to  $5.26 \times 10^1$  copies/ $\mu$ L in water samples. The study contributes in providing information on drinking water quality and concludes that drinking water supplied in Jaipur city carries pathogenic bacteria in some of the locations which can cause health problems especially to young children, aged and immunocompromised people.

**Keywords:** Drinking water quality, Pathogenic bacteria, Public Health, PCR, Real-time PCR

OP40

ICABB-215

**ABIOTIC PARAMETERS MEDIATED  
TRANSCRIPTIONAL REGULATION OF  
HMG-CoA REDUCTASE IN IN-VITRO  
CULTURE OF BACOPA MONNIERI**

Pragya Bhardwaj<sup>1#</sup>, Chakresh Kumar Jain<sup>1</sup>,  
Ashwani Mathur<sup>1\*</sup>

1. Department of Biotechnology, Jaypee Institute of Information Technology, Noida, A-10, Sector-62, Noida-201307, Uttar Pradesh, India  
E-mails: prgybhardwaj@yahoo.co.in, \*Corresponding author: ashwani.mathur@jiit.ac.in

*Bacopa monnieri*, a well-documented nootropic plant, is extensively used in herbal formulations for neurological disorder. Nootropic properties of the plant are primarily attributed to the presence of triterpenoid glycosides saponins called 'Bacosides' namely Bacoside A, a mixture of four triglycosidic saponins. Triterpenoid saponins are biosynthesized via isoprenoid pathway through farnesyl pyrophosphate by cyclization of 2,3-oxidosqualene, leading to formation of triterpenoid skeletons. The enzyme *HMG-CoA reductase* (HMGR; EC.1.1.1.34), plays a key role in the regulation of the isoprenoid biosynthesis in plants. In present study the role of *in-vitro* culture conditions (abiotic parameter) propagation of *Bacopa monnieri* in MS Agar and MS liquid medium on transcriptional regulation of *HMG-CoA reductase* (HMGR) gene was compared. Plants collected from three different locations (agro-climatic conditions) within India were micropropagated in MS agar and MS liquid medium for 30 days, in plant growth chamber at  $25 \pm 2$  °C with white light illumination of 2450 lux for 12 h followed by 12 h dark period. The plants were compared for their specific growth rate and it was observed that liquid culture enhance specific growth rate of the plant. The total bacoside yield was compared in the methanolic extracts of MS agar and liquid propagated plants. Comparative transcriptional analysis of HMGR gene was also performed using qRT-PCR. Results revealed significant variations in the yield of total bacosides among agar and liquid propagated plants. However relative transcriptional level of *HMG-CoA reductase* was not varied in *in-vitro* culture condition (MS-agar & MS-liquid) compared to field acclimatized plants. The result further provide an impetus to the fact that though a rate limiting step, total bacoside (triterpenoid bacoside) yield may be regulated by cascades of steps involved in bacoside biosynthesis and not only by HMGR. These finding pave the way to explore the role of other intermediates in modulating bacoside biosynthesis.

**Keywords:** *Bacopa monnieri*, bacoside, HMG-CoA reductase, qRT-PCR, transcriptional

OP41

ICABB-230

**MULTISTAGE UNFOLDING DYNAMICS  
OF TDP-43 TO CHARACTERIZE THE  
INTERMEDIATE ENSEMBLES INVOLVED  
IN AMYOTROPHIC LATERAL  
SCLEROSIS**

Amresh Prakash and Andrew. M. Lynn

School of Computational & Integrative Sciences, Jawaharlal Nehru University, New Delhi-110067, India  
E-mails: amreshprakash@jnu.ac.in ,andrew@jnu.ac.in

RNA binding proteins are the central target of various neurodegenerative disorders, as are associated with the intra/extracellular accumulation of protein aggregates which is the hallmark pathological condition of neurodegeneration. Recently, the presence of transactive DNA binding protein 43 (TDP-43) inclusions in patients with tauopathy, ALS and Alzheimer's disease have open new avenues for therapeutic intervention in neurodegenerative diseases. Here, we investigate the folding dynamics of TDP-43, employing long range (5  $\mu$ s) all-atoms molecular dynamic simulation to determine the biophysical behaviour, under the chemical denaturant conditions. Our results from the free-energy landscape (FEL) and hydrophobic distal matrix show the two-state unfolding kinetics, mediated with multiple transition state ensembles, having stable intermediate and metastable states. These results suggested that the characterisation of intermediate ensemble is an essential for the better understanding of the neurodegenerative pathogenic conditions.

**Keywords:** TDP-43; protein dynamics; free-energy landscape; hydrophobic distal matrix

OP42

ICABB-112

**CHEMICAL SYNTHESIS AND TESTING  
OF NOVEL SYNTHETIC  
ANTIMICROBIAL PEPTIDES AGAINST  
MULTI-DRUG RESISTANCE STRAINS  
OF *E. COLI***

**Shailendra Gupta\*, Abhishek, Sameer Shrivastava,  
Rajkumar James Singh, Purnima Gogoi,  
Piyush Kumar Singh, Sonal, Asha Kumari Verma  
and R. K. Agarwal**

\* M.V.Sc., Division of bacteriology and mycology,  
Indian Veterinary Research Institute, Bareilly, U.P

E-mails : abhivbmr@gmail.com, sameer\_vet@rediffmail.com,  
jamesalmighty36@gmail.com, gogoipurnima17@gmail.com,  
rahul.piayush@hotmail.com, sonalvet@gmail.com

ashav223@gmail.com, grace\_bly@yahoo.com,

\*Corresponding author: guptashailendra@gmail.com

The extensive use of antibiotics has led to development of antibiotic resistance which is of increasing global concern. The so called "superbugs" or the multi-drug resistant (MDR) / extensively drug resistant (XDR) strains of bacteria have made the present day antibiotics less effective. Therefore, search for an alternative is the need of the hour, and for which antimicrobial peptides (AMPs) could be promising molecules. The AMPs are relatively short (12 to 100 amino acids), positively charged (net charge of +2 to +9), amphiphilic peptides and have been isolated from a wide range of single-celled microorganisms, plants, invertebrates and even vertebrates. AMPs have several advantages over the conventionally used antibiotics, like most of them are broad-spectrum, have rapid killing action, are selectively toxic against bacterial cell membrane; act synergistically with antibiotics and most importantly have nearly negligible rate of resistance development. Thus, AMPs have all potentials to be developed in a new class of therapeutic agent. Keeping this in view we have designed and synthesized synthetic peptides after analyzing biochemical properties such as hydrophobicity, helicity, net charge, amphipathicity and structural conformations through various available databases. One of the peptides when screened against standard strain of *E. coli* by micro-broth dilution technique, showed a minimum inhibitory concentration (MIC) of 100ug/ml. When tested on two MDR strains of *E. coli* (resistant to ampicillin, nitrofurantoin, trimethoprim and cefotaxime-clavulanic acid), complete growth inhibition was seen at a concentration twice that of MIC. Based on these observations, further study can be planned to test the activity of this peptide on other

bacteria and explore the possibility of using it as a potent therapeutic tool against the MDR strains.

OP43

ICABB-168

**DEVELOPMENT OF QSAR MODEL FOR  
ICL INHIBITORS**

**Nupur S Munjala<sup>§</sup>, Bharti Sharmaa<sup>§</sup>,  
Astha Khanduri, Chittaranjan Routa<sup>\*</sup>**

*Department of Biotechnology and Bioinformatics, Jaypee University of Information Technology, Waknaghat, Solan, Himachal Pradesh, 173234, India*

<sup>§</sup>Contributed equally

\*Correspondence author: chittaranjan.rout@juit.ac.in

*Mycobacterium tuberculosis* causes one of the most deadly disease TB. Persistence is the key to its pathogenesis and prevalence of this disease. Isocitrate lyase (icl), enzyme involved in shunt pathway of the TCA cycle, is the key to persistence. Design and development of inhibitors against this enzyme is computationally challenging due to small active site of this enzyme. Inhibitors with molecular weight < 200 are able to dock properly in the small active site. Quantitative structure activity-relationship (QSAR) model which correlates molecular characteristics with activity reported earlier as an effective tool for designing of novel lead molecules. Diverse groups of molecules were reported active against ICL. In the present work, QSAR model was formed by correlating molecular properties of inhibitors with their *in vitro* activities (IC50) values. Geometry optimization of ICL inhibitors was performed at PM6 basis set using Gaussian software. Thirty groups of descriptors from Dragon7 software are extracted for each inhibitor. On the basis of correlation and variance among the descriptors, each descriptor group was separated into eight independent subgroups: pvhchv, pvhclv, phchv, phclv, pmchv, pmclv, zchv and zclv. Then on each subgroup, AIC and VIF multicollinearity indicators were applied for selection of independent descriptors. Ten descriptors from six descriptor groups (Constitutional indices, Information indices, Burden eigen values, RDF descriptors, 3D-MoRSE descriptors and WHIM) were showing reasonable R2 and Q2 correlation values. The R2 and Q2 values of the model formed are 0.96 and 0.78, respectively. The structural modifications that might improve activity of the molecules could be obtained from this QSAR model.

**Keywords:** TB, QSAR, AIC, VIF, PM6, ICL

OP44

ICABB-187

## RECOMBINANT TPI AND PGAM BASED ELISA FOR DETECTING ANTI-TPI AND PGAM ANTIBODIES IN MAMMARY TUMOURS OF DOG

Richa Arora<sup>1\*</sup>, Sonal Saxena<sup>1\*\*</sup>, Sameer Shrivastava<sup>1</sup>, Shahid Hussain<sup>1</sup>, Subas Chandra Jena<sup>1</sup>, Naveen Kumar<sup>1</sup> and A.K. Sharma<sup>1</sup>

1. Division of Veterinary Biotechnology, Indian Veterinary Research Institute, ICAR- IVRI, Izatnagar

\* Corresponding author: sonalvet@gmail.com

Cancer is one of the leading cause of death in companion animals such as dogs and cats, particularly common in animals that live 10 years or longer. Skin cancers are the most predominant form of cancers in canine species especially in female dogs, with incidence rates of mammary tumours being the highest. As tumours cell metabolism requires high glucose consumption due to a high level of aerobic glycolysis, it has a high demand of energy. The level of glycolytic enzymes such as Triose Phosphate Isomerase (TPI) and Phosphoglycerate Mutase (PGAM) increases in neoplastic cells. The inhibitors to these enzymes can, thus, be used as a novel strategy to target them for anticancer therapy. The present study was undertaken to investigate the presence of circulating antibodies to TPI and PGAM in dogs with tumour of the mammary gland (MGT). An in-house enzyme-linked immunosorbent assay was developed using *E.coli* expressed recombinant TPI and PGAM for detecting anti-TPI and PGAM antibodies, respectively. A total of 81 samples were screened including 22 cases of cancer and 59 healthy cases of dogs. Auto-antibodies for TPI and PGAM were present in 63.3% and 45% of dog cancer sera samples, respectively. The mean OD492nm ± SEM values in dog with MGT for TPI and PGAM ( $1.146 \pm 0.353$  and  $1.203 \pm 0.393$ , respectively) differed significantly ( $p < 0.005$ ) with mean OD492nm ± SEM values in healthy dogs with NCD ( $0.481 \pm 0.262$  and  $0.512 \pm 0.286$  respectively). The auto-antibodies were present in 2.6% of control sera samples for both TPI and PGAM. So, auto-antibodies for both TPI and PGAM were present in highly in cancerous as compared to healthy dogs' serum samples. The assay was apt to distinguish between cancerous dog sera and control sera with sensitivity and specificity of 50-59% and 96.5 -96.6% respectively. This study suggests that circulating TPI and PGAM antibodies can be used as some serum biomarkers for MGT in dogs, but the test should be used with caution, along with a panel of

other biomarkers to increase the specificity. Further studies with a large cohort of well-characterised samples from early cancer patients are required to further confirm the usefulness of TPI and PGAM as biomarkers for early diagnosis of cancer in dogs. Further investigations in this direction may reveal the complicated mechanisms involved in triggering the secretion of anti- TPI and PGAM antibodies, especially in cases of cancer.

**Keywords:** PGAM, TPI, MGT, biomarkers

OP45

ICABB-259

## IN SILICO SCREENING FOR IDENTIFICATION OF NOVEL CYSE INHIBITORS: TARGETING THE B-HELIX CAP OF THE LBH DOMAIN

Deepali Verma and Vibha Gupta\*

Department of Biotechnology, Jaypee Institute of Information Technology, Sector-62, Noida-201309, India

E-mails: deepali.biotechnology@gmail.com, \*Corresponding author: vibha.gupta@jiit.ac.in

The rapid emergence of drug resistant strains of *Shigella* is posing a large threat to human health and necessitates continuous discovery of novel therapeutics. CysE, is an enzyme of *de novo* cysteine biosynthetic pathway that is presents in bacteria but absent in humans, categorizing it as a potential drug target. In recent years, virtual screening (VS) strategy is becoming an essential tool for lead discovery and optimization, hence, this study employs the VS approach for identifying novel CysE inhibitors. A recent study from our group has revealed that a natural substitution of A241V in the  $\beta$ -helix cap of CysE can perturb the distal structural elements leading to subunit dissociation and insignificant enzymatic activity. Based on the premise that this allosterically coupled site may serve as starting point for the rational design of inhibitors against CysE, this research investigation focuses on *in silico* molecular docking of Specs Natural products (NP) database (~1489 compounds) against  $\beta$ -helix cap of CysE with AutoDock Vina. Initially, 14 NPs were short listed based on lowest binding affinities as well as hydrogen bonds/hydrophobic interactions between receptor and these binders. But further analysis of absorption, distribution, metabolism, excretion, and toxicity (ADMET) properties has enabled prioritization to 3 NPs for further studies.

**Keywords:** CysE,  $\beta$ -helix cap, enzymatic activity, *in silico* docking, virtual screening

## FETAL HEART MICRO-RNAs PROFILING AND FUNCTIONAL ANNOTATION: AN INDICATION TOWARDS GENE REPROGRAMMING IN CARDIAC PATHOLOGIES

Sharad Saxena, Vibha Rani\*

*Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sector-62, Noida -201307, U.P, India.  
E-mails: s.a28@hotmail.comv \*Corresponding author:  
vibha.rani@jiit.ac.in*

Cardiogenesis is known to be a complex process, the transcriptomics of which shows striking similarities with failing heart. microRNAs (non-coding RNAs of ~22 nucleotide) are one of the key regulatory elements controlling both heart development and diseases through post-transcriptional modification. However, very little is known about their sequences, expression, molecular pathways they regulate and their target genes in both fetal cardiac development as well as heart diseases. In the present study, 36 differentially expressed known miRNA sequences obtained from next generation sequencing were functionally characterized and validated through in-depth bioinformatics analysis. miRDB custom prediction with prediction score > 80 revealed that 20 miRNAs were targeting more than 100 genes. DAVID, PANTHER and Genemania were used for functional annotation, gene ontology and KEEG analysis. The output from the databases revealed that majority of the potential 1716 target genes were co-expressed, and involved in cell signalling in cardiomyocytes (such as Adrenergic signalling etc), mRNA surveillance pathway, developmental processes, and part of different protein classes (transcription factors and nucleic acid binding proteins). Interestingly, we observed that many of the target genes (such as ADAMTS20, ATP1B1, GPR85, RASGRP1, FBN2, MEF2C etc) expressed during fetal development significantly contributes to severe heart disease progression. The study highlights the gene re-expression pattern between fetal heart development as well as cardiovascular diseases and supports a novel potential therapeutic approach for cardiac pathologies.

## tRNA STRUCTURE ANALYSIS ACROSS WOLBACHIA ENDOSYMBIONTS

Kopal Singhal and Sujata Mohanty\*

*Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sector 62 NOIDA (201309)  
\*Corresponding author: sujata.mohanty@jiit.ac.in*

The advancements in the Omics technology have made it possible to understand the transcription and translational machinery of an organism. Various biological molecules are significant to these processes one of which is the tRNA. tRNA is a type of RNA molecule that assist in the growth of the polypeptide chain by recognizing the sequence at rRNA and attaching the corresponding amino acid to it. In the present study, we have tried to understand the tRNA machinery of seven *Wolbachia* genomes obtained from two dipteran host i.e. *Drosophila melanogaster* and *Drosophila ananassae* (4 Indian: wMel\_AMD, wMel\_KL, wRi\_AMD, wRi\_KL and 3 references: wMel, wRi, wAna). *Wolbachia*, an endosymbiotic bacterium has recently gained importance in control of different vector-borne diseases owing to its ability of host phenotype manipulation. The total number of tRNAs in these genomes ranges from 26 to 37 and length varies from 65 to 91 nucleotides. 19 tRNAs were found to be common to all seven genomes and maximum number of tRNAs were found for leucine. Detailed analysis on the basis of amino acid categories reveal a higher proportion of non-polar aliphatic amino acid tRNAs, however, percentage distribution of each type of tRNAs was found to be more or less conserved throughout the seven genomes. Sequence wide comparison of the different codon specific tRNAs of individual amino acid revealed highly conserved sequences across these endosymbiont genomes. A comparison with the host translational machinery and tRNA structure can enlighten us with the interplay of host-symbiont interactions. Understanding the *Wolbachia* genome and its translational machinery has become crucial to the use of *Wolbachia* as a biocontrol-agent.

**Keywords:** Omics technology, translation machinery, tRNA structure, *Wolbachia* endosymbiont, vector-borne disease control

## CHARACTERISATION OF ANTIMICROBIAL PROTEIN WITH ANTIBIOFILM ACTIVITY FROM THE GOAT MILK ISOLATE

**Garima Sharma, Shweta Dang, Sanjay Gupta and Reema Gabrani**

*Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sector-62, NOIDA, India*

*\*Corresponding author: reema.gabrani@jiit.ac.in*

The aim of the current study was to isolate and identify the bacteriocinogenic strain from milk of Indian goat species and characterization of the antimicrobial substance. Bacterial strains possessing the antimicrobial along with the antibiofilm activity were isolated from the raw milk of Indian goat species Babri and Sirohi (*Capra aegagrus hircus*) from three different areas viz Jodhpur (Rajasthan), Noida and Greater Noida (Uttar Pradesh). The bacterial strain with potential antimicrobial properties was identified by 16S rDNA sequencing. Initially seventy-four isolates were screened for antimicrobial activity against gram positive *Staphylococcus epidermidis* and twelve strains were chosen further analysis. Chosen strains were evaluated for broad spectrum antimicrobial activity against gram positive *Micrococcus luteus* and gram-negative *Pseudomonas fluorescens* and *Escherichia coli*. Antibiofilm activity of screened strains were analysed on the pre-established bacterial biofilm as well as inhibition of biofilm formation of *S. epidermidis*. The potential candidate was selected for the molecular characterization by 16S rDNA sequencing and sequence was deposited to Genbank under accession no. KP671843 and identified as *Pediococcus acidilactici*. The antimicrobial substance produced by bacteriocinogenic strain *P. acidilactici*, isolated from goat milk, was precipitated by 90% of ammonium sulphate followed by ultrafiltration. The molecular weight of partially purified bacteriocin was approximately 3500 Da by tris-tricine SDS-PAGE and showed antibacterial activity against *S. epidermidis* by halo assay. Partially purified bacteriocin showed stability at wide pH and high temperature but the loss of activity was observed after treating with proteolytic enzymes and remained active after the treatment with lipase, amylase, catalase and few detergents/organic solvents. Thus the bacteriocin from *P. acidilactici* showed broad spectrum antibacterial activity and antibiofilm activity.

**Keywords:** Bacteriocin; *Escherichia coli*; *Pediococcus acidilactici*; *Pseudomonas fluorescens*; *Staphylococcus epidermidis*

## STANDARDIZATION STUDIES ON SURFACE STERILIZATION, IN VITRO SHOOT INDUCTION AND MULTIPLICATION OF THYRSOSTACHYS OLIVERI

**Gopinath S M, Ramya R and Yashaswini, Brian Lopez and Sanjay**

*Department of Biotechnology, Acharya Institute of Technology, Bangalore 560 107*

*Thyrsostachys oliveri*, a native species of Myanmar, is a handsome, straight growing, moderate-sized bamboo with persistent culm-sheath and branching nodes. It has multiple uses in various fields ranging from construction and furniture; like making baskets, mat, fishing rods, etc to being used for landscaping and even edible purposes. We have carried out a systematic and detailed study on certain parts (stages) of *in vitro* regeneration technique of *T. oliveri*. For assessing the effect of various sterilisation techniques, random treatments were carried out among which, 1 % Tween 20 for 5 minutes + 0.1 % Bavistin for 10 minutes + 70% alcohol for 1 minutes + 0.04 % Ampicillin for 5 minutes + 1 % mercuric chloride for 5 minutes recorded overall best response. For assessing the effect of various cytokinins on multiple shoot induction, the axillary shoots, containing single axillary bud were inoculated in liquid Murashige and Skoog (MS) medium containing additives and fortified with different combination and concentrations of NAA, TDZ and BAP. Maximum bud break and multiple shoot formation were observed in MS media supplemented with NAA (0.25mg/l), BAP (1.5mg/l) and TDZ (0.25mg/l). To assess of effect of cytokinins in shoot multiplication, initiated shoots were multiplied on MS liquid media fortified with additives and supplemented by various concentrations of NAA, TDZ and BAP. Observations showed medium supplemented with NAA (0.25mg/l), BAP (2mg/l), and TDZ (0.5mg/l) to be optimum. Genotype assessment was also carried out between field and nursery culms; in which, field culms showed superiority.

**Keywords:** *T. oliveri*, axillary shoots, MS media, BAP, TDZ

OP50

ICABB-038

## EXPLORATION OF NOVEL ADHESIVE BANDAGE FOR ACCELERATED AND SCAR-FREE WOUND HEALING

S.M. Gopinath, Karthik G Vaidya and Nilakshi Mazumder

*Dept of Biotechnology, Acharya Institute of Technology, Bangalore, Karnataka.India-560107*

A novel adhesive bandage to accelerate wound healing and also prevent the formation of scars. Wound is an injury to living tissue caused by a cut, blow or other impact, typically one in which the skin is cut or broken.

Scar is a mark left on skin or body tissue where a wound, burn or sore has not healed completely and fibrous tissue has developed. In simpler terms, Scar is a poorly formed extracellular matrix (ECM). There is a necessity of bioactive wound dressing which not only accelerates the healing process but also regulates the extracellular matrix (ECM) deposition to avoid further scarring complications. Herein, we are developing a combination of synthetically extracted ECM functionalized with epidermal growth factors (EGF) and ciprofloxacin HCl based electro-spun nanofiber mats as potential wound dressing.

**Keywords:** Adhesive Bandage, Wound Healing, Scar, Extracellular Matrix (ECM), Electro-spun nanofiber mats

# Poster Presentations

*International Conference on Advances in  
Biosciences and Biotechnology - ICABB-2018*

*(February 01-03, 2018)*

## EFFECTIVE THERAPIES FOR THIRD GENERATION RESISTANT NON-SMALL CELL LUNG CANCER

**Agrani Sinha, Deepak Sharma, Reema Gabrani\***

*Biotechnology Department, Jaypee Institute of Information Technology, A-10, Sector 62, NOIDA*

*E-mails: agranisinha@gmail.com, dk101ggc@gmail.com,*

*\*Corresponding author: reema.gabrani@jiit.ac.in*

Non-small cell lung cancer EGFR-T790M which renders it resistant to first generation drugs can be overcome by Osimertinib. It has been observed that Osimertinib fails to stop the C797S mutation, which impairs the covalent binding between the Cysteine residue at position 797 of EGFR and Osimertinib. Current research is focusing on overcoming resistant to C797S mutation. One of the promising drugs is Brigatinib which can overcome C797S/T790M/activating-mutation (triple-mutation)-mediated EGFR-TKI resistance. Brigatinib fits into the ATP-binding pocket of triple-mutant EGFR. The efficacy of Brigatinib has been shown to be enhanced markedly by combination with anti-EGFR antibody. The mechanism attributed is due to the decrease of surface and total EGFR expression. Thus, the combination therapy of Brigatinib with anti-EGFR antibody is a powerful candidate to overcome triple-mutant EGFR. Immunotherapy and the reviewed use of monoclonal antibodies also carry a hope towards therapy of lung cancer. Based on the data available, active immunization with monoclonal antibodies as anti-idiotype vaccines and antibody targeting with immunoconjugates are the most promising methods. Anti-growth factor monoclonal antibodies are also valuable. Personalized peptide vaccination (PPV) could offer a novel approach to cancer vaccines that can boost anticancer immunity. PPV combined with chemotherapy might be feasible for advanced NSCLC as third line treatment because of the safety, immune responses, and possible clinical benefits. Patients diagnosed as advanced NSCLC patients who failed in at least two chemotherapy regimens were eligible for this study. Overall, we can conclude that new approaches are promising for third generation resistant NSCLC treatment.

**Keywords:** NSCLC, Osimertinib, Brigatinib, PPV, Triple-mutant EGFR.

## LP-23: A POTENTIAL ANTIBACTERIAL LIPOPEPTIDE AGAINST MYCOBACTERIA SMEGMATIS

**Deepika Sharma, Poonam Katoch, Rahul Shrivastava and Gopal Singh Bisht\***

Search for new antibacterial agents having novel mechanism of action has been a major thrust area. Antimicrobial peptides belong to such category of new antibacterial agents that act via their membranolytic action, but suffer from various drawbacks. Synthesis of peptidomimetics based on antimicrobial peptides is one of the approaches to overcome their shortcomings. Therefore, our study was focused on anti-mycobacterial evaluation of LP-23, one of the lead peptidomimetics from our previous study that had shown potent antibacterial activity against various gram-positive and gram-negative bacterial strains (*Escherichia coli* 1.5  $\mu$ g/ml, *Pseudomonas aeruginosa* 1.5  $\mu$ g/ml & *Staphylococcus aureus* 3.1 $\mu$ g/ml). In present work, we have evaluated anti-mycobacterial potential of LP-23 against *Mycobacterium smegmatis*; a commonly used model in anti-mycobacterial studies due to its fast growing and non-pathogenic nature. Results of present study have laid the foundation for additional investigation of LP-23 as potential anti-mycobacterial agent, as it was found to inhibit the visible growth of mycobacteria

## THERAPEUTIC TREATMENT OF LUNG CANCER: MICRO-RNA

**Bhanu Pratap Chauhan, Girisha Maheshwari,  
Dr. Reema Gabrani\***

*Jaypee Institute of Information Technology, A-10, Sector 62, Noida*

*E-mails: bhanuchauhan1907@gmail.com ,*

*girishamaheshwari@gmail.com, \*Corresponding author:*

*reema.gabrani@jiit.ac.in*

Major cause of cancer deaths worldwide is due to lung cancer and 80% of these deaths have been attributed to Non-Small Lung Cancer (NSCLC). One major cause is dysregulation of Micro-RNAs, the non-coding RNAs, ranging in size from 19 to 25 nucleotides. Micro-RNAs are the largest class of the gene regulators. Micro-RNA regulates the translation of protein by binding to target mRNA or degrade the mRNA itself.

miRNAs modulate all gene expression impacting all cellular processes like cell proliferation, cell apoptosis, cell differentiation. The transformation or loss of function of miRNA initiates or contributes to the transformation of normal cell to malignant. The loss of function of miRNA could be due to several mechanisms, including mutation, genomic deletion, miRNA processing alterations or epigenetic silencing. miRNAs can be oncogenic miRNAs by targeting the mRNAs encoding for the tumor suppressor proteins. The let-7 family of miRNAs is downregulated in lung and breast cancer and therefore can act as a tumor suppressor. Let-7 family members inhibit mRNAs of oncogenes like RAS, c-Myc and HMGA2. Many more miRNAs like miR-29 family members (miR29b-1/miR-29a in chromosome 7q32 and miR-29b-2/miR-29c in chromosome 1q23), miR-155 (located in chromosome 21q23) are downregulated in lung cancer. miRNA-21, miR17, miR-18a, mir-19a, miR-20a, mir-19b-1 and miR92-1 are highly expressed in lung cancer. miRNA therapeutic treatment can be achieved by inhibition therapy which covers over expression of the target miRNA and miRNA replacement therapy when the target miRNA is repressed. Hurdles like stability in vivo, potential off-targets effects, issues of delivery and many more challenges need to be addressed. Major challenge is the tissue specific delivery, moreover the rapid advances in systemic drug delivery system and new findings from recent trials provide an optimistic perspective on the progress in this field.

**Keywords:** Micro-RNA, Gene Regulators, cellular processes, oncogenic miRNA, tumor suppressor, inhibition therapy, miRNA replacement therapy

PP4

ICABB-023

## EPIGENETIC THERAPY APPROACHES IN NON-SMALL CELL LUNG CANCER

Girisha Maheshwari, Bhanu Pratap Chauhan and Dr. Reema Gabrani\*

Jaypee Institute of Information Technology, A-10, Sector 62, Noida  
E-mails: girishamaheshwari@gmail.com,  
bhanuchauhan1907@gmail.com, \*Corresponding author:  
reema.gabrani@jiit.ac.in

Epigenetic aberrations offer dynamic and reversible targets for cancer therapy; increasingly, alteration via overexpression, mutation, or rearrangement is found in genes that control the epigenome. Such alterations suggest a fundamental role in carcinogenesis. There are three epigenetic mechanisms: DNA methylation, histone tail modification and non-coding, microRNA

regulation. Epigenetic regulation by DNA methylation and histone modifications modulate chromatin structure and, in turn, either activate or silence gene expression. The involvement of epigenetic alterations in the evolution of different cancers has led to the development of epigenetics-based therapies, mainly targeting DNA methyltransferases (DNMTs) and histone-modifying enzymes. The accumulation of multiple genetic and epigenetic changes, including DNA methylation, has contributed to the development and progression of lung cancer that will provide new insights for identifying biomarkers for diagnosis, prognosis, and treatment of lung cancer. Histone deacetylation and DNA methylation have a central role in the control of gene expression, including transcriptional repression of tumour suppressor genes. Loss of DNA mismatch repair due to methylation of the hMLH1 gene promoter results in resistance to drugs in vitro and in vivo. Treatment with an inhibitor of DNA methyltransferase, DAC (2-deoxy-52 -azacytidine), results in a partial reversal of DNA methylation and sensitization to drug. PXD101, a histone deacetylase inhibitor, shows antitumour activity in vivo and is currently in phase I clinical evaluation. Since the clinical use of DAC may be limited by toxicity and eventual re-methylation of genes, the combination of DAC and PXD101 could have a role in increasing the efficacy of chemotherapy in patients with tumours that lack MLH1 expression due to hMLH1 gene promoter methylation. When epigenetic agents are used in combination with chemotherapy or targeted therapy it is hoped that effective dose and hence toxicity will be reduced with enhanced efficacy.

**Keywords:** DNA methylation; DNA methyltransferases; Epigenome; Histone; histone deacetylase inhibitor

PP5

ICABB-032

## REVIEWING THE INHIBITOR APPROACHES TARGETED AGAINST PLANT VIRUSES

Priyanka Chauhan, Kajal Singla, Mamta Rajbhar, Anjali Singh, Dr. Kapila Kumar\*

Manav Rachna International Institute of Research and Studies Sector-43, Delhi- Surjkund Road, India  
E-mail: pcr3996@gmail.com, kajalsingla1997@gmail.com,  
mamta27496@gmail.com, anjali.singh741996@gmail.com,  
\*Corresponding author: kapila.fet@mriu.edu.in

Viruses are the microscopic pathogens that affect humans, animals, plants and microbes. These

otherwise dead organisms grow and replicate inside host cells and encompass the host's immunity to cause infection. Attention has been paid to human health and massive research work is being conducted on human viruses but there is a dearth of literature for plant viruses which are heavily affecting the plant production and causing economic losses. This highlights the urgent need to study plant viruses, their pathogenesis and to develop and design newer strategies to inhibit these viruses. In the current review, a sincere effort has been made to discuss various viral inhibitor approaches that have been developed in the due course of time to combat plant viral infections. These inhibitor techniques are classified majorly into two categories grouped as traditional (meristem tip culture, cryotherapy, thermotherapy and chemotherapy) and advanced techniques (nucleic acid based approaches like RNA Silencing, cross-protection, transgenic plants, gene pyramiding and protein-protein interaction detection and inhibition). Here, we have elaborated, discussed and compared the principles, methodologies, advantages and disadvantages of each inhibitor technique to study their application in best suited way on various plants to control viral diseases and to improve quality of food crops with increment in production.

**Keywords:** Plant viruses, Inhibitor approaches, PPI, RNAi, Gene Pyramiding, Cross Protection.

PP6

ICABB-033

---

## EMERGING AND RESURGING ENCEPHALITIS VIRUSES: THE INDIAN SCENARIO

Anjali Chandwani, Tejasri Mahija, Shweta Singh,  
Priyanka Chauhan, Kajal Singla, Mamta Rajbhar,  
Anjali Singh, Shivani Khare and

Dr. Kapila Kumar\*

Manav Rachna International Institute of Research and Studies,  
Sector-43, Delhi- Surajkund Road, India

E-mails: chandwani.anjali@gmail.com, tejasri.mahija@gmail.com,  
shweta431994@gmail.com, pcr3996@gmail.com,  
kajalsingla1997@gmail.com, mamta27496@gmail.com,

anjali.singh741996@gmail.com, shivani160995@gmail.com,  
\*Corresponding author: kapila.jet@mriu.edu.in

---

Viral encephalitis has always been a dreaded disease all over the world. It is characterized by acute inflammation in brain potentially leading to permanent brain damage or in worst cases death. Viral encephalitis is mainly caused by a group of arthropod borne vectors and some intermediate host transcending the regional boundaries and making it an epidemic

disease. Five major encephalitis viruses have shown their prevalence in India- Japanese encephalitis virus (JEV), West Nile virus (WNV), Chandipura virus (CHPV), Rabies virus (RABV) and Nipah virus (NV). Although, little is known about the first occurrence of each disease, their outbreak in different parts of the country in the last century has made it a serious scientific case study. In this review we retrospect i) their reason of emergence in the tropical region; ii) resurgence in the area iii) complexity of the factors which have caused their spread and sustained the virus showing its outbreak in fatal mutant forms. The study covers the geographical study of the infected areas and human indulgences in failure of eradicating the viruses- vaccines and curative measures taken by health organizations. Prevalence of arthropod vectors in the tropical region further contributes to the spread of viruses. Outbreaks in the past decade across different parts of the country and lack of systematic study on the causes and surveillance of infected areas have made these viruses epidemic. Despite of the worldwide research in studying the spread of the encephalitis viruses, not much has been done to curb the disease. Through this review we aim to put out the major factors which have made these viruses spread the prominent disease in the Indian subcontinent and measures to be taken to prevent their resurgence.

**Keywords:** Encephalitis, Japanese Encephalitis Virus, Nipah Virus, Chandipura Virus, West Nile Virus, Rabies Virus

PP7

ICABB-070

---

## THE IMPACT OF NEXT-GENERATION SEQUENCING TECHNOLOGY ON HEALTH AND DISEASE

Zara and Sujata Mohanty\*

Department of Biotechnology, Jaypee Institute of Information Technology, Noida, U.P.-201307

\*Corresponding author: sujata.mohanty@jiit.ac.in

---

Next Generation Sequencing (NGS) has wide application in different fields of biological sciences such as disease genomics and proteomics, pharmaceutical sciences, metagenomics, conservation biology, evolutionary biology and many more. NGS technologies have demonstrated the capacity to sequence DNA at high speed with a reduced and affordable cost. The Human genome project completed on 2001 was performed using Sanger sequencing Technology and over a period of 15 years. Completion

of the human genome project provides a platform for various comparative genomics study and is found to be useful in identifying the genetic variations causing diseases like cancer, diabetes, late onset genetic and autoimmune disorders etc. With the advancement of sequencing technology, the NGS, it is proposed to sequence few more human genomes to be used in ecological and evolutionary genomics studies. Although NGS technology can generate massive data within short period of time, handling those data has become a major challenge in these days. Computer based tools are also being developed simultaneously for NGS data storage, analysis and management. NGS along with powerful bioinformatics tools and software is becoming a most promising field in bringing revolution in the field of disease genomics and personalized medicine. In the present review paper, we have highlighted the impact of next-generation sequencing technologies on human health.

**Keywords:** Next-generation sequencing, Application, Revolution, Human health

PP8

ICABB-071

## POTENTIAL EFFECTS OF NICOTINE ON THE HEALTH OF HUMAN FOETUS AND PASSIVE SMOKERS

**Priyansh Srivastava, Pooja Upadhyay, Meghna Singh, Soumya Soni and Dr. Sujata Mohanty\***

*Department of Biotechnology, Jaypee Institute of Information Technology, Noida, U.P.-201307*

\*Corresponding author: sujata.mohanty@jiit.ac.in

Nicotine is an alkaloid present in tobacco plant and is the main content of cigarettes. Numerous studies have been performed to study the effects of nicotine on direct consumers due to its carcinogenic nature. Chromosomal aberrations and DNA damage were observed in case of regular cigarette smokers. Smoking also increases the occurrence of genetic mutations and becomes the possible cause of various diseases like cancer, cardiac arrest and respiratory problems. A population based study conducted on Asian children aged 5 to 18 years, revealed that exposure to tobacco smoke was significantly associated with rhinitis, particularly non-allergic rhinitis. This study adds new evidence that the adverse effect of tobacco smoke exposure is mainly confined to non-allergic rhinitis and more pronounced in teenagers. Studies on the prenatal exposure to tobacco smoke also resulted in the altered brain structure and behaviour problems in the offspring, however, the correlation between the prenatal

tobacco exposure and the behavioural pattern of the new born babies were not established due to insufficient experimental data. In the present paper, we focused on the health hazards of nicotine on fetal cells as well as on the passive smokers.

**Keywords:** Nicotine; Smoking; Chromosomal abberations; non-allergic rhinitis, Teenagers and passive smokers

PP9

ICABB-72

## EGB761 AN ACTIVE COMPONENT OF GINKGO BILOBA: TREATING ALZHEIMER'S DISEASE

**Simran Jamwal, Shubhangi Mathur and Dr. Shalini Mani\***

*Jaypee Institute of Information Technology, A-10, Sector 62, Noida  
E-mails: simran2397@gmail.com,  
mathurshubhangi.2932@gmail.com,\*Corresponding author:  
shalini.mani@jiit.ac.in*

Humans consume a wide range of foods, drugs, and dietary supplements that are derived from plants and which modify the functioning of the central nervous system (CNS). The psychoactive properties of these substances are attributable to the presence of plant secondary metabolites, chemicals that are not required for the immediate survival of the plant but which are synthesized to increase the fitness of the plant to survive by allowing it to interact with its environment, including pathogens and herbivorous and symbiotic insects. In many cases, the effects of these phytochemicals on the human CNS might be linked either to their ecological roles in the life of the plant or to molecular and biochemical similarities in plants and animals. Alzheimer's Disease is a chronic neurodegenerative disease that usually starts slowly and worsens over time. It is the cause of 60% to 70% of cases of dementia. The most common early symptom is difficulty in remembering recent events (short-term memory loss). As the disease advances, symptoms can include problems with language, disorientation (including easily getting lost), mood swings, loss of motivation, not managing self care, and behavioural issues. *Ginkgo biloba* leaf extract labeled EGb761, is one of the most popular herbal supplements. Both flavonoid and ginkgolide constituents are involved in the free radical-scavenging and antioxidant effects of EGb 761 which decrease tissue levels of reactive oxygen species (ROS) and inhibit membrane lipid peroxidation. Regarding EGb 761-induced regulation of cerebral glucose utilization, bilobalide increases the respiratory control ratio of

mitochondria by protecting against uncoupling of oxidative phosphorylation, thereby increasing ATP levels resulting in bilobalide increase. With regard to its "anti-stress" effect, EGb 761 acts via its ginkgolide constituents to decrease the expression of the peripheral benzodiazepine receptor (PBR) of the adrenal cortex. In this review, possible mechanisms underlying neuroprotective actions of EGb761 are described.

PP10

ICABB-074

## **SMOKING CESSATION: AN ANALYSIS OF CURRENTLY AVAILABLE METHODS TO QUIT SMOKING**

**Soumya Soni, Meghna Singh, Pooja Upadhyay, Priyansh Srivastava and Dr. Sujata Mohanty\***

*Department of Biotechnology, Jaypee Institute of Information Technology, Noida, U.P.-201307*

\*Corresponding author: sujata.mohanty@jiit.ac.in

Cigarette smoking is injurious to health and remains a major public health concern in the modern world. Although efforts are being made to sensitize people throughout the world today, against the habit of smoking, many people, still indulge in smoking. The statutory warning: "Smoking is dangerous for health" inscribed on the cigarette packets, actually does not mean anything for smokers. Cigarette smoking is a leading preventable cause of sickness and mortality, killing around 6 million people a year. But surprisingly enough; there are people who still prefer to smoke and every single day nearly 4,400 people start smoking. The pleasurable, reinforcing and addictive properties of smoking are produced mostly by nicotine contained in tobacco. The tobacco-nicotine, inhaled constantly is a sure way of slow-poisoning. In order to strongly deal with this problem, the need of the hour is to inculcate and promote smoking cessation. Smoking cessation (colloquially quitting smoking) is the process of discontinuing tobacco smoking. This paper mainly focuses on the different strategies which are presently used for smoking cessation, including quitting without assistance ("cold turkey" or cut down then quit), medications such as nicotine replacement therapy (NRT), cytisine or varenicline, e-cigarettes and behavioural counselling. In addition, this paper also discusses in detail the importance of smoking cessation and the mechanisms, design strategies, treatment plan, dosage, withdrawal symptoms, advantages, limitations and consumer acceptance of different methods. A comparative analysis of the various methods commonly used for smoking cessation is also made to ascertain the most effective one.

**Keywords:** Smoking cessation; Health hazards; Need of the hour; Cessation strategy; NRT; E-cigarette; Behavioural counselling; Withdrawal symptoms

PP11

ICABB-080

## **miRNA: EPIGENETIC BIOMARKER IN CARDIAC DISEASES**

**Shubhangi Mathur, Simran Jamwal and Dr. Shalini Mani\***

*Jaypee Insititute of Information Technology, A-10, Sector 62, Noida  
E-mails: mathurshubhangi.2932@gmail.com, simran2397@gmail.com,*

\*Corresponding author: shalini.manii@jiit.ac.in

Epigenetics is the study of heritable changes in gene expression that do not involve changes to the underlying DNA sequence *i.e* change in phenotype without a change in genotype which in turn affects how cells read the genes. Epigenetic phenomena are mediated by several molecular mechanisms comprising DNA Methylation, Histone Modification, small non-coding or anti-sense RNAs. MicroRNAs (miRNAs) are short non-coding mRNAs with approximately 18–22 nucleotides in length which bind to target mRNAs, resulting in translational repression and gene silencing and are found in all eukaryotic cells. Over the last few years, the field of micro RNA in cardiovascular biology and diseases has expanded at an incredible pace. Their aberrant expression may be involved in inherited diseases, cardiac diseases, nervous system disorder etc. In the cardiovascular system, miRNAs have been shown to be critical regulators of development and physiology. They control basic functions in virtually all cell types relevant to the cardiovascular system (such as endothelial cells, cardiac muscle, smooth muscle, inflammatory cells, and fibroblasts) and, thus, are directly involved in the pathophysiology of many cardiovascular diseases. miRNAs are regulated in various cardiovascular diseases like hypertension, congestive heart failure, congenital heart defects, coronary artery disease and stroke. Some of these miRNAs also act as potential biomarker of this cardiovascular diseases. This review summarizes the role of miRNAs in myocardial infarction and focuses mainly on their influence on cardiomyocyte regeneration and cell death including apoptosis, necrosis, and autophagy. Authors also highlight the significance of these miRNA from therapeutic point of view.

**Keywords:** miRNA, epigenetics, Cardiomyocyte, Myocardial infarction

---

## CHALLANGES AND STRATEGIES IN THE ERA OF MULTIDRUG RESISTANCE

Hitesh Bhardwaj and Dr. Sujata Mohanty\*

Jaypee Institute of Information Technology, Sector 62, Noida,  
Uttar Pradesh

\*Corresponding author: sujata.mohanty@jiit.ac.in

---

The escalating development of multidrug resistance (MDR) has become one of the major concerns in the medical sciences as it is appeared since the dawn of the antibiotics era. Due to the prevalence of MDR both in case of familiar pathogens (such as *Staphylococcus aureus* and *Mycobacterium tuberculosis*) and emerging pathogens (such as *Acinetobacter baumannii*), it often results in treatment failure, which can have serious consequences, especially in critically ill patients. Although, new strategies to reverse MDR development are being continuously researched and implemented, but almost all of them are proven to be of limited clinical use, failing to demonstrate an improvement in therapeutic efficacy with almost no significant survival benefits observed in clinical trials. An alternative approach that has been applied is to prevent or delay MDR prior or early in its development. Recent investigations have shown that preventing the emergence of MDR at the onset of treatment, rather than reversing MDR once it has developed, may assist in overcoming drug resistance. Newly synthesized antibiotics and new therapeutic strategies are needed to address this challenge. In this review, the main focus is on a number of novel strategies used by small-molecule inhibitors to prevent the development of MDR. These inhibitors hold great promise for prolonging the efficacy of treatment and will be instrumental in improving the clinical outcomes of patients that are susceptible to MDR development.

**Keywords:** Multidrug resistance (MDR); Strategy to reverse MDR; Therapeutic efficacy; Inhibitors; Clinical outcome

---

## RHEUMATIC HEART DISEASE: IMPACT OF SOCIOECONOMIC FACTORS ON DISEASE OUTCOME IN ASSAM, INDIA

Neha Sharma, Devinder Toor and Lokajeet Baro

Amity Institute of Virology and Immunology, Amity University,  
Uttar Pradesh

Assam medical college and hospital, Dibrugarh, Assam  
E-mails: nsharma26@amity.edu, dtoor@amity.edu,  
lokajeet.b@rediffmail.com

---

Rheumatic heart disease (RHD) is a major health concern worldwide and contributes to high morbidity and mortality in India. Pathogenesis of RHD is attributed to various risk factors such as host genetic makeup, socioeconomic factors and aberrant immune response. Previously many studies have reported the association between socio-economic status (SES) and prevalence of RHD in India but no data is available from North-Eastern region. In this study, association between socio-economic factors and prevalence of RHD in Assam, North-East India is studied. A case-control questionnaire based study of 40 RHD cases with age and sex matched healthy controls from Assam medical college and hospital was conducted. So far, a trend has been observed towards increased risk of RHD with respect to various parameters of SES such as education, monthly income, dwelling location and overcrowding. Clinical spectrum of RHD was also found to be associated with low SES. Out of the total patients, 32%, 18% and 12% of RHD patients were diagnosed with mitral stenosis, mitral regurgitation and atrial regurgitation. Out of the severe cases of MS, MR and AR, 65%, 52% and 28% patients were from low SES. Multiple valve involvement was also observed in majority of the patients. Our study suggests compelling contribution of socioeconomic factors in high prevalence of RHD and it also correlates with clinical set-up of the disease. An improved socioeconomic profile of a population can be of great significance to keep a rein on the increased prevalence of RHD.

**Keywords:** Rheumatic heart disease, Prevalence, Socioeconomic factors, Clinical spectrum

## EFFECTS OF AGING AND CAMKII REGULATION ON CARDIOVASCULAR FUNCTIONALITY OF DROSOPHILA MELANOGASTER

Ankit Srivastava and Sujata Mohanty\*

Jaypee Institute of Information Technology, Sector 62, Noida,  
Uttar Pradesh

\*Corresponding author: sujata.mohanty@jiit.ac.in

*Drosophila melanogaster* has been widely accepted as an aging model due to its short life span. Arrhythmicity, reduced contractility of cardiac muscles and decreased heartrate are among various cardiovascular disorders that *Drosophila melanogaster* shares with human beings due to gene similarity and similar aging pattern. The kinase Ca<sup>+2</sup>-calmodulin-dependent protein kinase II (CaMKII) has been seen to play a key role as regulator of Ca<sup>+2</sup> transport in cardiomyocytes and thus regulating cardiovascular functionality. Presence of similar phosphorylation sites in humans for the Ca<sup>+2</sup>-calmodulin-dependent protein kinase II isoform-subunit delta (CaMK2D or CaMK2α) and the CaMKII of *Drosophila melanogaster* was indicated by high degree of alignment found between them. Experiments have been done using flies of two different ages young and old (7 and 60 days) utilizing a genetically-encoded fluorescent Calcium indicator, GCaMP3 that helped to report changes in Ca<sup>+2</sup> handling in cardiomyocytes. It is observed that reduced heartrate and increase in occurrence of arrhythmicity and asystoles occurred due to aging. Furthermore, inhibition of CaMKII by a CaMKII specific inhibitor (KN-93) led to decrease in heartrate whereas overexpression of CaMKII by using a heterozygous strain containing an extra copy of CaMKII gene, a significant increase in heartrate and reduction of arrhythmia was reported. Increase of amplitude of intracellular Ca<sup>+2</sup> transients and decrease of arrhythmogenic index in CaMKII-OE was shown by functional analysis, thus indicating an important role of CaMKII in Excitation-Contraction Coupling (ECC) regulation in *Drosophila melanogaster* heart. As aging and CaMKII plays a crucial role in Ca<sup>+2</sup> handling, contractibility, excitability in human heart, it is of great importance to assess the role of these parameters in the fruit fly heart.

**Keywords:** Aging, Heartrate, Arrhythmia, Ca<sup>+2</sup> handling, Contractibility, Arrhythmogenic Index.

## VIRAL ENCEPHALITIS IN INDIA

Mahima Rawal<sup>1</sup>, Kajal Setia<sup>1</sup>, Smriti Gaur\* and Sanjay Gupta\*

Jaypee Institute of Information Technology, A-10, Sector 62, Noida

E-mails: mahimaraival26197@gmail.com, setiakajal@gmail.com,

\*Corresponding author: smriti.gaur@jiit.ac.in, sanjay.gupta@jiit.ac.in

Viral Encephalitis is an inflammation of the brain, usually caused by a hypersensitivity reaction or a viral infection to a virus. When a virus attacks the CNS directly it is primary encephalitis and when the virus invades other part of the body and travels to the brain it is termed as secondary encephalitis. It is a non-communicable disease. Japanese Encephalitis caused by Japanese Encephalitis Virus (JEV) is recognised as the leading cause of the disease in India. JE belongs to genus Flavivirus of the family Flaviviridae. Most important mosquito vector in Asia is Culex tritaeniorhynchus, it is transmitted through the JEV transmission cycle known as the Zoonotic transmission cycle. Uttar Pradesh contributed more than 75% of cases with an outbreak in Gorakhpur, India. Universal Immunization Programme introduced JE vaccines. Vaccination with SA-14-14-2 vaccine started in 2006. The symptoms of encephalitis can have a number of possible causes, so several tests may be needed to diagnose it like imaging, serological testing, CSF and brain biopsy. Treatment of Japanese encephalitis (JE) consists of supportive care, so a strong surveillance system is developed. Other than Gorakhpur, the epidemic areas in India are: Uttar Pradesh, Bihar, Assam, West Bengal and Tamil Nadu. Bihar has a plan blueprint all set to check encephalitis. Weeks after several children died of encephalitis at Baba Raghav Das (BRD) Medical College, Gorakhpur, the new drug was introduced, traditionally used for acne, to deal with seasonal outbreaks of encephalitis. However, the ultimate objective is detection of early warning signals for any potential JE outbreak and initiate timely effective control measures.

**Keywords:** Hypersensitivity, Zoonotic, Serological Testing, Imaging, CSF, Surveillance

PP16

ICABB-142

## OMEGA 3- FATTY ACIDS AS THERAPY FOR MULTIPLE SCLEROSIS (MS) TREATMENT

**Ashmita Nautiyal<sup>1</sup>, Merin Lawrence<sup>1</sup>,  
Advika Gupta<sup>1</sup>, Sakshi Vashisth<sup>1</sup> and  
Garima Mathur\***

*Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201307, Uttar Pradesh, India  
E-mails: nautiyalashmita96@gmail.com, merinlawrence95@gmail.com,  
advika.gupta27@gmail.com, sakshivashisth95@gmail.com,  
\*Corresponding author: garima.mathur@jiit.ac.in*

Multiple sclerosis (MS) is a complex autoimmune inflammatory neurological disorder of the central nervous system. It is prevalent in Europe and North America, affecting nearly 2.5 million people worldwide. MS can affect people of any age, however it is typically found in adults of 20-45 years of age. MS is more common in females than males. It is a multifactorial disorder, involving various etiological factors such as smoking, vitamin D and genetic susceptibility associated to play a significant role in MS. Interest in exploiting the role of nutrition and diet in MS is rising. The role of diet and nutrition in MS has not been fully elucidated. Studies have shown that population with significantly higher consumption of omega-3 fatty acid rich food such as DHA show lower occurrence of neurological diseases. DHA supplemented diet has shown to reduce the severity of MS in patients and may delay the onset of symptoms. This review summarizes the recent findings on nutrition and diet as an alternative therapy to control the disease progression in MS patients

**Keywords:** Multiple sclerosis, Neurological diseases, Omega-3 fatty acids, Diet, Nutrition

PP17

ICABB-177

## IMMUNOTHERAPY: CANCER TREATMENT

**Avika Chopra\* and Sarika Yadav**

*Sri Venkateswara College, Benito Juarez Road, DaulaKuan,  
New Delhi, Delhi 110021*

*\*Corresponding author: chopraavika@gmail.com*

Immunotherapy, also called biologic therapy, is a type of cancer treatment that boosts the body's natural defenses to fight the cancer. Immunotherapy may stop

or slow the growth of cancer cells, impede cancer from spreading to other parts of the body, boost the immune system to destroy cancer cells. PD-L1 and CTLA-4 pathways are critical to the immune system's ability to control cancer growth. These pathways are often called "immune checkpoints." Many cancers use these pathways to escape the immune system. The immune system responds to the cancer by blocking these pathways with specific antibodies called immune checkpoint inhibitors. Interferons help the immune system fight cancer and may slow the growth of cancer cells. A laboratory made interferon, interferon alpha (Roferon-A, Intron A, Alferon), is the most common type of interferon used in cancer treatment. Interleukins help the immune system produce cells that destroy cancer. Interleukin-2, is used to treat kidney cancer and skin cancer, including melanoma. Immunotherapy can be combined with other therapies like monoclonal antibodies, oncolytic virus therapy, T-cell therapy, cancer vaccines for improved efficacy. Oncolytic virus therapy uses genetically modified viruses to kill cancer cells. The engineered virus enters the cancer cells, replicates and lyses the cell with the release of specific substances called antigens. This triggers the patient's immune system to target the cancer cells and the virus is altered so that it cannot enter healthy cells. Antibodies can now be re-engineered to attach biological beacons or bring together cancer and immune cells with 'bi-specific' antibody. Thus, immunotherapy holds promising future towards the cure of cancer.

**Keywords:** PD-L1: Programmed Death- Ligand 1CTLA-4: cytotoxic T-lymphocyte-associated antigen 4

PP18

ICABB-180

## TRANSFECTION OF EGFP TAGGED RECOMBINANT CHIKV PROTEIN IN MAMMALIAN CELLS

**Ipsita Nandi, Sonakshi Madan, Vijeta Prakash,  
Nikita Sharma, Akanksha Jain, Kushagra  
Bhardwaj, Reema Gabrani\* and Sanjay Gupta\***

*Department of Biotechnology, JIIT, Noida, UP - 201307*

*\*Corresponding authors: sanjay.gupta@jiit.ac.in,  
reema.gabrani@jiit.ac.in*

Chikungunya disease, caused by the Chikungunya virus (CHIKV) continues to be a re-emerging febrile illness, spread via *Aedes* mosquitoes worldwide. While the disease itself is self-limiting and rarely fatal, it results in deteriorated quality of life due to chronic arthralgia. Currently there exist only symptomatic

treatment options for Chikungunya, with no anti-viral vaccine or drugs available. Effective therapeutics could be developed by targeting viral proteins in particular. The CHIKV consists of structural (envelope glycoproteins- E1, E2, E3, K6 and capsid) as well as non-structural proteins (nsP1-4). The nsPs are found to be involved in virus replication cycle but the functions of nsP3 have not yet been studied extensively. Nsp3 contains three domains- Macro, Alphavirus Unique Domain (AUD) and Hypervariable Region (HVR), out of which Macro and AUD are involved in formation of a replicase complex. The present study focuses on transfection of Macro-AUD domain as EGFP recombinant protein in mammalian cell line. The Macro-AUD gene was amplified from Topo-nsp3 vector, where nsp3 gene was isolated from IND-Guj-06 strain of CHIKV and cloned into pEGFP-N2 vector. The recombinants were confirmed with the help of colony PCR, restriction enzyme digestion, migration shift and sequencing. Further, liposome-based transfection was carried out in mammalian cell line. The transfection was completed successfully and green fluorescent protein was observed in cells transfected with the recombinant. This study and its results have the potential to facilitate further CHIKV nsP-3 localization studies in the future.

**Keywords:** Alphavirus; Chikungunya; Macro-AUD; nsP3

PP19

ICABB-186

## MOLECULAR LINK BETWEEN BREAST CANCER AND OBESITY IN MENOPAUSE WOMEN

Kajal Kiran<sup>1</sup>, Misthi Verma<sup>1</sup> and Dr. Shalini Mani<sup>1\*</sup>

1. Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201307, Uttar Pradesh, India  
 \* Corresponding author: mani.shalini@gmail.com

Obesity is a medical condition in which excess body fat has accumulated to the extent that it may have a negative effect on health. Being overweight can cause 13 types of cancer breast cancer being the most prevalent followed by womb, kidney and bowel cancer. Breast cancer(BC) is the most common female cancer worldwide and is the second most commonly diagnosed cancer in Indian women. Global burden of breast cancer will increase to over 2 million new cases/year by 2030. The age-standardized mortality rate for BC in India was found to be 11.1/100,000 where globally it was 12.5/100,000 according to International Agency for Research on Cancer report in 2008. As per

various research obesity is found to be a causal factor for BC in different patients who are in postmenopausal age. There are several factors which links the diet quality and associated risk for BC. Increased use of saturated fats and animal proteins, consequently decreased use of vegetables, legumes and fruit, constituting the so-called Mediterranean diet, are considered responsible for the increased risk of breast cancer. Due to obesity, there are different receptors such as insulin growth hormone receptor and oestrogen receptor which are also known to be over-expressed in case of BC patients too. In the present paper, we summarise the molecular link between obesity and breast cancer in menopausal women. We further suggest the study of these receptors may be helpful in early diagnosis of obese and menopausal women who are susceptible towards breast cancer.

**Keywords:** Breast cancer, obesity, oestrogen, receptors

PP20

ICABB-192

## APPLICATION OF NEXT GENERATION SEQUENCING IN CARDIOVASCULAR DISEASES: A REVOLUTIONIZED APPROACH

Ishita Tiwari<sup>1</sup>, Yashika Rustagi<sup>1</sup>, Drishti Mittal<sup>1</sup>, Isha Gupta<sup>1</sup>, Jasmin Pruthi<sup>1</sup> and Vibha Rani<sup>\*</sup>

1. Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201307, Uttar Pradesh, India  
 E-mails: itiwari233@gmail.com, yashikarustagi@gmail.com, mittaldrishti96.dm@gmail.com, isha123gagan@gmail.com, jasminpruthi09@gmail.com, \*Corresponding author: vibha.rani@jiiit.ac.in

Advancements in genome sequencing technologies propose distinctive opportunities to characterize individual genomic landscapes, making whole-genome sequencing a possible way for obtaining global genomic information and identify mutations relevant for diagnosing and therapy. Ongoing research indicates that NGS will be progressively imperative to study complex and inherited cardiovascular diseases (CVDs). Conversely, NGS technology in genetic studies of CVDs is characterizing a territory which has not been extensively studied till date. Cardiovascular diseases (CVDs) are a group of disorders of the heart and blood vessels and include Coronary heart disease, cerebrovascular disease, Peripheral arterial disease, Rheumatic heart disease, congenital heart disease, etc. CVDs are the main cause of the death worldwide. The identification of mutations can be very important in diagnostic and clinical

practice to cure the diseases and to establish a profile of risk for the heart development. The purpose of advance technology in NGS is to explore the key molecules in several CVDs such as inherited cardiomyopathies, channelopathies, coronary artery disease and aortic aneurysm. There are also many future utilities and challenges related to NGS in studying the genetic basis of CVDs in order to improve diagnosis, prevention, and treatment.

**Keywords:** Next Generation Sequencing, Cardiac Dysfunction, Hypertrophy, Coronary Artery Disease, Genetic Mutations

PP21

ICABB-193

### TOOLS FOR PROCESSING NEXT GENERATION SEQUENCING LARGE DATASET

Jasmine Pruthi<sup>1</sup>, Yashika Rustagi<sup>1</sup>, Drishti Mittal<sup>1</sup>, Isha Gupta<sup>1</sup>, Ishita Tiwari<sup>1</sup> and Vibha Rani<sup>1\*</sup>

1. Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201307, Uttar Pradesh, India

E-mails: [jasminepruthi09@gmail.com](mailto:jasminepruthi09@gmail.com), [yashikarustagi@gmail.com](mailto:yashikarustagi@gmail.com), [mittaldrishti96.dm@gmail.com](mailto:mittaldrishti96.dm@gmail.com), [isha123gagan@gmail.com](mailto:isha123gagan@gmail.com), [itiwari233@gmail.com](mailto:itiwari233@gmail.com), \* Corresponding author: [vibha.rani@jiit.ac.in](mailto:vibha.rani@jiit.ac.in)

Next generation sequencing (NGS) technologies provide a high-throughput means to generate large amount of sequence data which produces hundred times more data in comparison of to the earliest sophisticated Sanger method. This technology is being increasingly used for various genome and transcriptome sequencing related applications due to their speed, cost-effectiveness and high-throughput nature. However, several sequence artefacts, including read errors (base calling errors and small insertions/deletions), poor quality reads and primer/adaptor contamination are quite common in the obtained large dataset in deep sequencing, which can impose significant impact on the downstream sequence processing/analysis. Further, highly efficient and fast processing tools are required to handle the large volume of datasets. Therefore, it is advisable to perform QC and filtering of high-quality (HQ) sequencing data at the end-user level. Most of the programs available for downstream analyses do not provide the utility for quality check and filtering of NGS data before processing. After reads filtration, a set of tool are required in various analysis which includes peak-calling analyses for ChIP-Seq, RNA-Seq, and finding small insertions, deletions, and SNPs using SAM tools. In the present study, we discuss NGS QC

Toolkit, comprised of various easy-to-use tools for quality check and filtering, trimming, generating statistics and conversion between different file formats/variants of NGS data. The toolkit allows automatic and fast parallel processing of large amount of sequence data with user-friendly options. In this study, we also provide an overview of important RNA-Seq analysis tools and demonstrate how they can be used to analyses large dataset.

**Keywords:** Next Generation Sequencing, Base Calling, Adaptor, Quality Control, Trimming

PP22

ICABB-196

### ALTERATIONS OF CELL MEMBRANE INTEGRITY AND EXTRACELLULAR POLYSACCHARIDES MATRIX OF CRYPTOCOCCUS NEOFORMANS BIOFILM ON EXPOSURE TO ESSENTIAL OIL ACTIVE COMPONENTS

Poonam Kumari<sup>1</sup>, Neha Arora<sup>1</sup>, Apurva Chatrath<sup>1</sup>, Rashmi Gangwar<sup>1</sup>, Vikas Pruthi<sup>1</sup> and Ramasare Prasad<sup>1\*</sup>

1. Department of Biotechnology, Indian Institute of Technology, Roorkee, Uttarakhand, India

E-mails: [bpoonam15@gmail.com](mailto:bpoonam15@gmail.com), [nehaarorajiit@gmail.com](mailto:nehaarorajiit@gmail.com), [apurva.chatrath@gmail.com](mailto:apurva.chatrath@gmail.com), [rashmi22gangwar@gmail.com](mailto:rashmi22gangwar@gmail.com), [vikasfbs@iitr.ac.in](mailto:vikasfbs@iitr.ac.in), \* Corresponding author: [rapdyfbs@iitr.ac.in](mailto:rapdyfbs@iitr.ac.in)

Cryptococcosis is a life threatening systemic fungal infection which is further intensified due to the ability of Cryptococcus neoformans to form recalcitrant biofilm resistant to standard antifungal drugs. This has boosted the search for natural therapeutics that is non-toxic and eradicates both planktonic and biofilm cells. Hence, in the present study the anti-biofilm potential of six EO-ACs and membrane permeability alterations of C. neoformans exposed to potent EO-ACs; thymol, carvacrol and citral were evaluated. In order to test the potency of EO-ACs, the minimum inhibitory concentration (MIC) and the biofilm inhibitory/eradicating concentrations (BIC/BEC) were determined. The morphological and physiological changes in response to potent EO-ACs were analysed using biophysical techniques. The deviations in lipid profile and extra-polysaccharide matrix (EPM) were examined by gas chromatography/mass spectrometry (GC/MS) and complemented with FTIR spectroscopy. Further, to realize the true efficacy of the potent EO-ACs in terms of human safety, cytotoxicity assay and co-culture infection model were assessed. Among the tested terpenes, thymol showed the most effective

antifungal and anti-biofilm activity of MIC 16 µg/mL and BIC/BEC 32/128 µg/mL followed by carvacrol and citral. The electron, confocal and atomic force microscopic analysis of EO-ACs treated biofilm revealed absence of EPM, reduction in capsule size and disruption of cell surface. GC/MS analysis showed changes in fatty acid profile in response to EO-ACs with decrease in unsaturated to saturated fatty acid ratio resulting in more efflux of K<sup>+</sup> ions and intracellular content. A substantial reduction in sugars (glucose, mannose, galactose) were observed in treated EPM as compared to untreated. Thymol and carvacrol showed selective killing of cryptococcal cells with minimum effect on keratinocytes suggesting their non-toxic nature. The present work gives new insights into mode of action of EO-ACs and their safety prospect; which could be further explored for development of novel therapeutics against *C. neoformans*.

**Keywords:** Biofilm; *Cryptococcus neoformans*; EO-ACs; Fatty acids; EPM; Keratinocyte

PP23

ICABB-212

## MESENCHYMAL STEM CELL TISSUE ENGINEERING

Shanya Verma<sup>1</sup>, Dr. Vibha Rani\*

Department of Biotechnology, Jaypee Institute of Information Technology, Sector-62, Noida  
Corresponding author: vibha.rani@jiit.ac.in

Mesenchymal stem cells have become one of the most studied stem cells, especially towards the healing of the diseased and damaged tissue and organs. Mesenchymal stem cells capable of self replication to many passages and therefore can potentially be expanded to sufficient numbers for tissue and organ regeneration. MSC's are able to differentiate into multiple cell lineages that resemble osteoblast, chondrocytes, myoblasts, adipocytes and fibroblasts. MSC'S have been used for cell delivery. After so many studies about MSC'S there are still fields to be considered like- determining MSC interaction with host cell signaling molecules, MSC based therapies towards clinically relevant defect models. The ultimate goal of MSC-based therapies has valid biological rationale in that clusters of MSCs differentiate to form virtually all connective tissue during development. MSC-based therapies can only be realized our improved understanding of not only their fundamental properties such as population doubling and differentiation pathways but also translational studies that use MSCs in the de novo formation and/or

regeneration of diseased or damaged tissues and organs. Mesenchymal stem cells (MSCs) are self-renewing, multipotent progenitor cells with multilineage potential to differentiate into cell types of mesodermal origin, such as adipocytes, osteocytes, and chondrocytes. In addition, MSCs can migrate to sites of inflammation and exert potent immunosuppressive and anti-inflammatory effects through interactions between lymphocytes associated with both the innate and adaptive immune system. Along with these unique therapeutic properties, their ease of accessibility and expansion suggest that use of MSCs may be a useful therapeutic approach for various disorders. In the clinical setting, MSCs are being explored in trials of various conditions, including orthopedic injuries, graft versus host disease following bone marrow transplantation, cardiovascular diseases, autoimmune diseases, and liver diseases. Furthermore, genetic modification of MSCs to overexpress antitumor genes has provided prospects for clinical use as anticancer therapy.

**Keywords:** Mesenchymal stem cells, multipotent progenitor cells, multilineage, cardiovascular diseases, orthopedic.

PP24

ICABB-223

## HIGH GRADE BRAIN TUMOUR & DRUG RESISTANCE

Megha Gautam<sup>1</sup>, Shweta Dang<sup>1</sup> and Reema Gabrani<sup>1\*</sup>

<sup>1</sup> Department of Biotechnology, Jaypee Institute of Information Technology, Sector 62, Noida, U.P. India  
E-mails: meghagautam57@gmail.com; shweta.dang@jiit.ac.in  
<sup>1\*</sup> Corresponding author: reema.gabrani@jiit.ac.in

Glioblastoma multiforme (GBM) is accepted as the most common and mortal form of brain tumour with 15 months of median survival rate. Despite anti-cancer therapeutic agents, the median survival of patients with GBM has not significantly increased. Commonly a chemotherapeutic used to treat GBM is Temozolomide orally and paired with radiotherapy. The difficulty in treating this malignant disease is due to its inherent complexity and numerous mechanisms of drug resistance. Drug resistance can generally be categorized as either acquired or intrinsic. The acquired drug resistance occurs when a tumor initially retorted to treatment is no longer sensitive to the anti-cancer agent. Intrinsic drug resistance refers to a tumor that shows insignificant or non-response to the therapy at the beginning of treatment. Current research

indicates that at the molecular level, acquired and intrinsic resistances share several common foundations. The actual causes for drug resistance in glioblastoma include hypoxic areas of tumor cells, cancer stem cells, drug efflux, DNA damage repair, Bcl-2 and miRNA. Other potential mechanisms of resistance and repair include the regulation and control of ABC transporters, which act as efflux pumps for chemotherapeutic agents. Bcl-2 is known as an antiapoptotic protein that is highly expressed in resistant glioblastoma cells which aid in tumor survival. Many studies indicate the role of miR-21 and its upregulation contributes to resistance towards apoptosis upon treatment by drug. The drug resistance in GBM is a cause of poor outcome. Detailed study and understanding of cellular and molecular mechanisms responsible for resistance in glioblastoma can pave the way for new therapeutics and increase the patient survival outcome.

**Keywords:** Bcl2; Glioblastomas Multiforme; miRNA; Temozolomide

the TCDB. phylogenetic analysis of MFS proteins resulted in the clustering of MFS proteins based on function and not evolution. Furthermore, we also performed conservation analysis i.e relative entropy of all the MFS sequences that revealed functionally important residues which are conserved throughout the superfamily. Multigroup sequence harmony calculations that resulted in identification of residues which are conserved in different sub-families. All the deduced functional residues as well as differentially functional residues were mapped on 3D-struct kiure of MFS proteins. In conclusion, apart from functional clustering of all the MFS proteins our study also identifies conserved as well as differentially conserved residues. These residues can be further studied in order to elucidate their role in transport mechanism which can lay a platform for future pharmacological exploitation.

**Keywords:** Sequence Analysis, Phylogenetic Analysis, Relative Entropy, Multigroup sequence harmony, Structural Mapping

PP25

ICABB-224

## PHYLOGENETIC AND CONSERVATION ANALYSIS OF MFS TRANSPORTERS

Poonam Vishwakarma<sup>1,2</sup>, Atanu Banerjee<sup>1</sup>,  
Ritu Pasrija<sup>2</sup>, Rajendra Prasad<sup>3\*</sup>,  
Andrew M Lynn<sup>1\*</sup>

1. School of Computational and Integrative Science, Jawaharlal Nehru University, New Delhi; 2. Department of Biochemistry, Maharshi Dayanand University, Rohtak; India, 3. Amity Institute of Integrative Sciences, Amity University, Gurgaon.

E-mails: poonam.bi01@gmail.com,

\*Corresponding author: andrew@jnu.ac.in

PP26

ICABB-236

## EFFECT OF ANTI-LEISHMANIAL DRUG AMPHOTERICIN B ON TRANSCRIPTION FACTORS STAT3 AND ROR $\alpha$ T IN EXPERIMENTAL VISCERAL LEISHMANIASIS

<sup>a</sup> Khatonier R, <sup>a</sup>Khan AM\*, <sup>a</sup>Sarmah P and

<sup>b</sup>Ahmed Gu

<sup>a</sup> ICMR Regional Medical Research Centre, North-eastern Region, Post Box No-105, Dibrugarh786001 (Assam), India, Department of Biotechnology, <sup>b</sup>Gauhati University, Guwahati (Assam), India  
\* Corresponding author: abdulmaboodkhan@gmail.com

Facilitator Superfamily is one of the largest superfamily of secondary transporters, present across the kingdom of life. These proteins structurally consist of 12 transmembrane helices (TMH) with both the N- and C-terminal usually located on the cytoplasmic side of the membrane. Various studies have suggested the role of MFS transporters as importers as well as exporters, using energy of chemiosmotic ion gradients to transport wide spectrum of substrates including ions, carbohydrates, lipids, amino acids, peptides, and other molecules across the plasma membrane. Some MFS transporters have also been found to be associated with various inherited human diseases like De Vivo disease, Fanconi-Bickel syndrome, and type 2 diabetes mellitus. In the present study, we have performed clustering of 12 sub-families of MFS proteins. All sequences of MFS transporter proteins were taken from

Visceral Leishmaniasis (VL) is a vector borne disease caused by an obligate intracellular protozoon, *Leishmania donovani*. The host immune system requires active signalling of cytokines for induction of microbicidal activity by macrophages against Leishmania parasites. Transcription factors and signal transducers and activator of transcription (STAT) are key factors indispensable for cytokine signalling. STAT3 and ROR $\alpha$ t are two important transcriptional factors involved in Th17 cell differentiation. However, the role of STAT3 signalling in Leishmaniasis is not fully established. Amphotericin B remains the main choice of treatment for visceral leishmaniasis. Therefore we tried to investigate the role of these transcription factors during active *Leishmania donovani* infection in mice and its effect after treatment with

Amphotericin B. We investigated the mRNA expression of STAT3 and ROR $\alpha$ t in mice during active infection and after chemotherapy with Amphotericin B using Real Time Polymerase Chain Reaction (RT-PCR). Amphotericin B was administered intraperitoneally at a dose of 0.5 mg/kg wt. for 15 days. mRNA expression of STAT3 and ROR $\alpha$ t expression was assayed in four groups of mice at days 1, 3, 7, 14, 17, 21, 28, 35, 45 and 60 post infection. We found that ROR $\alpha$ t was significantly up regulated during active phase of infection i.e. day 14-21 post infection and later gradually decreased. Amphotericin B treatment significantly ( $p<0.05$ ) decreased the ROR $\alpha$ t expression both in the uninfected treated and infected drug treated group of mice but was gradually restored after successive treatment doses. *Leishmania donovani* significantly abrogated the STAT3 expression during active infection. However, in infected treated group there is significant down regulation of STAT3 expression contrary to the group i.e. uninfected and treated with Amphotericin B. Our results suggest that Amphotericin B plays a major role in down regulating expression of STAT3 and also have a potent role in modulation of ROR $\alpha$ t during *Leishmania donovani* infection.

**Keywords:** Cytokines, *Leishmania donovani*, Real Time Polymerase Chain Reaction(RT-PCR), Retinoic acid related orphan nuclear receptor (ROR $\alpha$ t), Transducer and activator of Transcription 3 (STAT3) and Visceral Leishmani

PP27

ICABB-237

---

## LEISHMANIA DONOVANI INFECTION IN BALB/C MICE: MODULATION OF KEY INNATE IMMUNITY GENES TLR 2 AND TLR 4 VIA MYD88 SIGNALLING PATHWAY DURING INFECTION AND AFTER TREATMENT WITH AMPHOTERICIN B

Sarmah P, <sup>a</sup>Khan AM, <sup>a</sup>Khatonier R and <sup>b</sup>Bharali R

<sup>a</sup> ICMR-Regional Medical Research Centre, North-eastern Region, Post Box No-105, Dibrugarh786001 (Assam), India, Department of Biotechnology, <sup>b</sup>Gauhati University, Guwahati (Assam), India

\*Corresponding author: abdulmaboodkhan@gmail.com

---

**Back ground:** Visceral Leishmaniasis is a neglected tropical disease caused by *Leishmania donovani* and is the second leading killer globally next to malaria. Among the few drugs currently available, Amphotericin B still remains drug of choice. Innate

immunity has been considered to be the first line of defence against invading pathogens. However, the aetiology of this disease at molecular level has not been yet fully understood.

**Objectives:** To evaluate mRNA profile of MyD88 dependent pathway and its key signalling molecules, TLR 2 and TLR 4 in BALB/C mice during infection and post therapy with Amphotericin B.

**Method:** Animals were grouped as uninfected mice, infected mice, infected, treated with Amphotericin B and uninfected treated with Amphotericin B at 0.75 mg per kg body weight. Mice were sacrificed at different days post infection from day 1 to day 60 and mRNA levels were estimated by Real-Time PCR.

**Results:** During initial days of infection from day 1 to day 17, MyD88 mRNA levels remain up regulated. Up regulation was seen at 21, 28, 35, 45 days post infection. At day 60 post infection, mRNA levels were recorded 6 fold higher compared to control. Treatment with Amphotericin B resulted in decrease in the mRNA levels of MyD88 in both infected treated and uninfected treated groups. The TLR 2 mRNA expression was up regulated in the infected animals and was significantly higher day 7 onwards and maximum increase (8 fold) was recorded at day 35 post infection. Similarly, in the infected treated group, it was up regulated 9 fold at 35 and 45 day compared to controls. In the Amphotericin B treated group of uninfected animals it was down regulated and is similar to mRNA level of controls. The TLR 4 mRNA levels were also up regulated in the infected group and significant increase was seen at during 7- 21 day post infection.

**Conclusion:** The key molecules MyD88, TLR 2 and TLR4 of the innate immunity signalling pathway are significantly up regulated during *L.donovani* infection especially in later phase of infection and may contribute in progression of infection. Amphotericin B due to its potent antileishmanial activity down regulates expression of these key molecules and restores them to control levels. Thus, this study underlines the importance of innate immunity molecules in respect of *Leishmania donovani* infection.

**Keywords:** *Leishmania donovani*, Toll like receptor Pathway, MyD88 pathway, Amphotericin B, Kala azar, Assam.

PP28

ICABB-243

## ANALYSIS OF AEDES AEGYPTI INTERACTOME MEDIATED BY ARBOVIRUSES

Jyoti Rana<sup>a</sup>, Sreejith Rajasekharan<sup>a</sup>, Ipsita Nandi<sup>a</sup>,  
 Amita Gupta<sup>b</sup>, Vijay k. Chaudhary<sup>b</sup>,  
 Vandana Gupta<sup>c</sup> and Sanjay Gupta<sup>a\*</sup>

*a. Center for Emerging Diseases, Department of Biotechnology, Jaypee Institute of Information Technology, Noida, U.P, 201309, India b.*

*Department of Microbiology, University of Delhi South Campus (UDSC), Benito Juarez Marg, New Delhi 110021, India c. Department of Microbiology, Ram Lal Anand College, University of Delhi South Campus (UDSC), Benito Juarez Marg, New Delhi 110021, India*

*\*Corresponding author: sanjay.gupta@jiit.ac.in,  
 sjay1908@gmail.com*

**Keywords:** Arboviruses, structural similarity based computational approach, protein-protein interactions, *Aedes aegypti*, interactome analysis.

PP29

ICABB-245

## ROLE OF INNATE IMMUNITY IN THE PROCESS OF NEURODEGENERATION

Mahima Rawal, Ritik Vaishy, Kajal Setia, Mahima and Manisha Singh\*

*Jaypee Institute of Information Technology, A-10, Sector 62, Noida  
 E-mails: mahimrawal26197@gmail.com, ritikvaishy1996@gmail.com,  
 setiakajal@gmail.com, mahimayadav201998@gmail.com,*

*\*Corresponding author: manisha.singh@jiit.ac.in*

Arboviral diseases are a major public health concern globally. The viruses transmitted by mosquito vector *Aedes* primarily belong to three families namely *Bunyaviridae*, *Flaviviridae* and *Togaviridae*. Most of these viruses play a definitive role in human and/or animal pathology causing important diseases such as dengue, chikungunya, etc., hence imposing a great burden on the society. In this context, information about molecular communication of *Aedes aegypti* with its arboviruses is of great significance. This report describes various pathways, using interactome analysis, involved in the pathogenesis between *Aedes* and the viruses it transmits. A protein structural similarity based computational approach has been employed for identification of the conserved as well as specific *Ae. aegypti* proteins which potentially play important role in the life cycle and infection caused by arboviruses. For seven viruses across the three viral families (La Crosse and California encephalitis virus from *Bunyaviridae*, Dengue, Yellow fever and Japanese encephalitis virus from *Flaviviridae* and River Ross and Chikungunya virus from *Togaviridae*), 447 interactors were recognized computationally among several identified proteins. Gene ontology analysis indicate that, these proteins are primarily implicated in the endocytosis of viruses, regulation of immune responses to viral infection and mRNA decay pathways to control the transcription/replication of viral genomic RNA. This approach provides us with a platform for further investigations to understand the strategies and biochemical pathways used by a virus for replication and the know-how of a mosquito to cope with the infection. Further, with this knowledge advances can be made towards designing common strategy to address majority of infections caused by these arboviruses at the vector level.

The innate immune responses in central nervous system (CNS) are usually conciliated by their resident microglia and astrocytes cells, in isolation to the peripheral immunity. They mostly enlist the T cells infiltration in CNS along with its innate immune system cross talk. The CNS tissues possess immune privilege due to their strong intrathecal inflammatory responses which leads to deterioration of physiological networking in neurons and oligodendrocytes. Additionally, pathogen entry in CNS always includes transit from a peripheral site of entry that will first elicit a response in the draining lymph nodes or spleen. Hence, no adaptive immune responses are elicited. Chronic activation of the innate immune system is now well established as an underlying factor contributing to neurodegeneration process in cerebral cortex. The maintenance of the primary immune cells of brain is critical during the brain homeostasis, but they loose their functionality during the course of aging or any degenerative processes. Now due to the invariable cellular and molecular arrangement of pathogens, known as pathogen-associated patterns, they are identified by the innate immune cells. Moreover, this mechanism along with the extensive framework of immune sensors, it saves the cells from various inside and outside danger. Further, the capacity of these sensors to identify the antigens / pathogens has a developmental initiation in revelation of molecules present on the stressed cells with in its own origin. It was also reported that these immune sensors are expressed by many cells in the body including neuronal ones. In this review we will be discussing the same immune responses in the process and initiation of neurodegeneration at various levels like autonomous immune responses in neurons at cellular level, elicitation of immune reaction inside the extra-neuronal brain tissues, and at systemic level immune responses linked with neurodegeneration. Hence,

failure of immune responses at any of them or all of them may thus, contribute to or result in eliciting neurodegeneration at a progressive scale.

**Keywords:** astrocytes, intrathecal, oligodendrocytes, homeostasis, pathogen-associated patterns

PP30

ICABB-256

## NEXT GENERATION SEQUENCING ANALYSIS PIPELINE

**Madhulika Verma, Anmol J. Hemrom,  
Pankaj Narang, Divya Saxena, Shilpi Singh,  
Ambarish Kumar, Vijaya Brahma and  
Andrew M. Lynn\***

*School of Computational and Integrative Sciences, Jawaharlal Nehru University, New Delhi 110067, India.*

E-mails: madhul27\_sit@jnu.ac.in,

\*Corresponding author: andrew@jnu.ac.in

Whole-transcriptome analysis is of growing importance in understanding how altered expression of genetic variants contributes to complex diseases and measuring genetic response to external stimuli. RNA-Seq (RNA sequencing), or whole transcriptome shotgun sequencing (WTSS), uses next-generation sequencing (NGS) to reveal the presence and quantity of RNA in a biological sample at a given moment in time. Typical analysis protocols include read assembly, transcript annotation, abundance estimation and measurement of differential expression as well as variant detection. We have implemented standardised pipelines for Reference based and De novo analysis of RNA-seq data into a GUI environment, named as NGSAP (Next Generation Sequencing Analysis Pipeline), with user-defined parameters in a single click. Being designed in a Galaxy framework it has features of easy shareability, scalability and reproducibility of the data for analysis. The workflow can be easily downloaded as standard operating protocol in the labs for RNA-seq data analysis.

**Keywords:** Transcriptome, RNA-Seq, Next-generation sequencing (NGS), Galaxy, NGSAP.

PP31

ICABB-262

## SEQUENCING TECHNOLOGIES FOR TRANSCRIPTOMIC ANALYSIS

**Sonakshi Madan, Sonia Purswani, Shreya Deb,  
Nikita Sharma, Chakresh Kumar Jain\***

*Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201307, Uttar Pradesh, India*

\*Corresponding author: ckj522@yahoo.com

Analysis of diseases at molecular levels delivers multiple new insights about their genetics and pathogenesis. Information obtained about abnormal nucleic acid sequences can prove quite beneficial for the discovery of novel conditions, for distinguishing different versions of the same disorder and also for the development of newer, more effective techniques for controlling and curing the disease. The analysis of cellular transcriptomic data has been recognized as a very advantageous approach to the development of predictive biomarkers for diseases like cancer especially. Since its introduction, high-throughput Next Generation Sequencing (NGS) technologies have been gaining increasing popularity throughout the world, which has substantially amplified the speed and reduced the cost of nucleic acid sequencing procedures. It has led to drastic transformation of medical research leading to huge leaps in the area of cancer genomics. Cancer results from a mutation in the genetic code, DNA based alterations and other related factors that lead to uncontrolled cell division can be better understood using NGS. This additionally has better repercussions for clinical oncology since it can help in earlier characterization of tumour type, in heredity risk predictions, in designing of suitable targeted therapies and for more informed, genome based clinical trials and treatments. The challenges faced by NGS however, are the complex procedures and inconvenience caused during handling which necessitate the need for scalable, fast and novel computational framework and methods for efficient data management. These limitations can however be overcome by the use of software tools like TopHat, Cufflinks and CumRbund.

**Keywords:** Bioinformatics; Cancer; Genomic Analysis; NGS

## **IDENTIFICATION OF DRUG TARGET FOR MULTIDRUG RESISTANT BIOFILM FORMING *ACINETOBACTER BAUMANNII***

**Monika Choudhary, Rahul Shrivastava and Jitendraa Vashistt\***

*Department of Biotechnology & Bioinformatics, Jaypee University of Information Technology, Waknaghat, Solan – 173234, Himachal Pradesh, India.*

\*Corresponding author: jitendraa.vashistt@juit.ac.in

*Acinetobacter baumannii* is a gram negative, non motile, aerobic coccobacillus bacterium which is associated with nosocomial infections. This pathogen colonized within host but pathogenicity is relatively low, until infection develops. Among all reported infections caused by *Acinetobacter spp.* about 80% are because of *A. baumannii*. These infections can either be minor tissue infection or severe manifestations like ventilator associated pneumonia and bacteremia. *A. baumannii* has the ability to adhere with biological as well as abiotic surfaces where they are capable of forming biofilms; which makes these bacteria a leading cause of death in hospital patients. Formation of robust biofilms is key characteristic of *A. baumannii* that help its survival under stress conditions such as exposure to antimicrobial agents. Biofilms formation is not opportunistic adhesion of cells but it involves number of tightly regulated molecular mechanisms. Process of biofilm formation complicates pathogen killing and cause latent infections by thriving resilient microbes.

Present study implemented *in silico* subtractive approaches; text mining (PubMed, google scholar) and data mining (STRING 10.5) to explore *A. baumannii* biofilm associated proteins. Among these 323 proteins, nineteen were commonly identified by both approaches that are involved in synthesis of lipid and carbohydrate, associated with outer membrane and required for efflux system. As these proteins like csu, efflux pumps, fimbrial protein, and outer membrane proteins are showing interaction network along with other proteins that may indirectly affect biofilm character of bacteria. These proteins are proposed as potential drug targets to combat multitude of resistance conferred by biofilm phenotype in *A. baumannii* strains.

**Keywords:** *Acinetobacter baumannii*, biofilm associated proteins, *in silico*, multidrug resistant.

## **CLONING, LARGE SCALE PURIFICATION AND CHARACTERIZATION OF CRYSTALLIZATION GRADE CYSK FROM KLEBSIELLA PNEUMONIAE**

**Pallavi Joshi, Deepali Verma, Monika and Vibha Gupta\***

*Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201309, Uttar Pradesh, India  
E-mails: joshi.pallavi5795@gmail.com, \*Corresponding author: vibha.gupta@jiit.ac.in*

The increasing incidences of antibiotic resistance in almost all pathogenic bacteria are causing a major global health concern. Among all multi-drug resistant (MDR) bacteria that cause infection, *Klebsiella pneumonia* (Kpn) is the most dangerous one. It is an opportunistic bacterium that is responsible for nosocomical infections in patients suffering from AIDS or diabetes, elderly people and children. Kpn MDR strains are becoming resistant to every antibiotic available today restricting the treatment options. This calls for urgent identification of novel drug targets for development of new anti-infectives. CysK is one such promising target owing to its varied activities such as in catalysis of last step of *de novo* cysteine biosynthesis in bacteria, as a transcription regulator and in contact-dependent growth inhibition. Elucidation of 3D structure of Kpn CysK will permit structure-based drug design. Here, in this study, we report cloning of Kpn *cysK* in pET21c expression vector and large scale purification of the recombinant CysK using Strep-Tactin affinity chromatography for obtaining crystallization-grade protein.

## **IDENTIFICATION OF BIOFILM ASSOCIATED GENES OF MYCOBACTERIUM SPECIES: A REVIEW OF TECHNIQUES AND STRATEGIES**

**Ayushi Sharma, Jitendraa Vashistt and Rahul Shrivastava\***

*Department of Biotechnology & Bioinformatics, Jaypee University of Information Technology, Waknaghat -173234, Solan (H.P.), India.  
E-mails: ayushisharma3194@gmail.com, jvashist@gmail.com, \*Corresponding author: juit.rahal@gmail.com*

Bacteria have the ability to grow as multicellular aggregates called biofilms that are attached to a

substrate and encapsulated within a matrix. Biofilm formation proceeds through distinct developmental stages that are genetically programmed making the biofilm bacteria phenotypically different from their planktonic counterparts. The biofilm forming cells are tolerant to environmental stresses including antibiotics and disinfectants, thereby contributing to the persistence of microbes in diverse growth conditions. Mycobacteria form biofilm both *in vivo* and *in vitro*. The molecular events occurring during the formation of mycobacterial biofilms have not been explored widely and therefore there is an urgent need to investigate these events. The factors involved in biofilm formation can be identified exploiting genomic sequence of bacteria, through various genome-based approaches coupled with bioinformatic approaches. Most techniques comprise of construction of a library of mutants (random or targeted) followed by screening and analysis, for identification of gene or gene product responsible for the phenotype. Determination of pathogen proteins required for its pathogenicity and related host factors can also be accomplished using selective knockdown or silencing using antisense-mediated, RNA interference (RNAi), or CRISPR interference-based methods. Genes and their products involved in mycobacterial infection and persistence through biofilm formation can serve as potential targets and therefore need to be unveiled for the discovery of new drugs. This will in turn prove beneficial in overcoming the limitation of the existing drugs in the treatment of mycobacterial infections ranging from tuberculosis to nontuberculous mycobacterial infections.

**Keywords:** biofilm, mycobacterium, drug target, mycobacterial persistence, genome-wide screening

PP35

ICABB-097

## TARGETING ACTIVE SITE FLEXIBILITY OF MYCOBACTERIUM TUBERCULOSIS ISOCITRATE LYASE FOR POTENT INHIBITORS

Merin Lawrence and Dr. Vibha Gupta\*

Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sector-62, Noida-201307, Uttar Pradesh, India  
E-mails: merinlawrence95@gmail.com,  
\*Corresponding author: vibha.gupta@jiit.ac.in

Isocitrate lyase (ICL) is the first enzyme involved in the glyoxylate cycle that catalyzes isocitrate into succinate and glyoxylate. *Mycobacterium tuberculosis* (*Mtb*), the causative organism for tuberculosis, relies

on glyoxylate cycle enzymes to survive in its host when the down regulation of tricarboxylic acid takes place and therefore, enables utilization of lipid as the sole carbon source during dormancy. ICL gene is absent in humans, so a drug that will target this essential virulent factor of *Mtb* will be theoretically safe for administration in humans. Till date several natural as well as synthetic compounds have been reported as ICL inhibitors however, these could have not been converted into ideal drugs. The crystal structure of ICL suggests flexibility that is dependent on the nature of ligand present in the active site. This report presents the dynamic details of ICL, thereby providing better insights into the ICL-ligand interaction. This in turn will benefit future works such as identification or designing of improved inhibitors against ICL for TB therapeutic.

**Keywords:** Isocitrate lyase, *Mycobacterium tuberculosis*, Glyoxylate cycle

PP36

ICABB-084

## MINING FOR NOVEL CELLULASES USING METAGENOMICS, METAPROTEOMICS AND METATRANSCRIPTOMICS

Bhumika Gupta, Hari Prasanna Deka Boruah,  
Sanjay Gupta and Indira P. Sarethy\*

Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sector-62, Noida-201309, India  
E-mails: guptabhumika18@gmail.com, dekaboruah@yahoo.com, sanjay.gupta@jiit.ac.in, \*Corresponding author: indirap.sarethy@jiit.ac.in

Cellulose is a linear polymer of D-anhydroglucopyranose units linked by  $\beta$ -1, 4-glucosidic bonds and is the most abundant organic compound in nature (mainly as components of plant cells). The hydrolysis of  $\beta$ -1,4 linkages of cellulose is catalyzed by cellulase. Cellulase is of immense significance and is utilized in various industries (pulp and paper, laundry, food and feed, textile, brewing, wine making, agriculture and biofuel). There are three different classes of cellulase enzymes: endo-(1,4)- $\beta$ -D-glucanase (EC 3.2.1.4) exo-(1,4)- $\beta$ -D-glucanase (EC 3.2.1.91), and  $\beta$ -glucosidases (EC 3.2.1.21) which act synergistically to degrade cellulose. There is a need of novel cellulases with better characteristics for processing under stringent industrial conditions. The primary cellulose producers are microorganisms - fungi and bacteria. Metagenomics - the culture-independent technology which mines the total

microbial genome from natural environment and attempts to discover novel metabolites, including enzymes, from uncultured microorganisms of different habitats, has met with considerable success in recent times. There are other upcoming technologies like metaproteomics (proteins), and metatranscriptomics (RNA) which allow targeted identification of novel enzymes with desired activity from microbial communities. This review discusses in-depth about these strategies and their potential for mining novel cellulases.

**Keywords:** Cellulase, Metagenomics, Metaproteomics, Metatranscriptomics

PP37

ICABB-060

### THE EMERGING ROLE OF DHA IN PARKINSON'S DISEASE

Merin Lawrence<sup>1</sup>, Ashmita Nautiyal<sup>1</sup>,  
Advika Gupta<sup>1</sup>, Sakshi Vashisth<sup>1</sup>, Garima Mathur<sup>1\*</sup>

1. Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201307, Uttar Pradesh, India  
E-mail: merinlawrence95@gmail.com , nautiyalashmita96@gmail.com, advika.gupta27@gmail.com sakshivashisth96@gmail.com,  
\*Corresponding author: garima.mathur@jiit.ac.in

Rising mortality rates due to neurodegenerative diseases across the World has been associated with genetic susceptibility and environmental factors. Parkinson's disease (PD) is the second most prevalent neurodegenerative disease in ageing individuals. Tremor, slowness of movement, rigidity, impaired balance and coordination caused by progressive degeneration of nigrostriatal dopamine-containing neurons results in PD. Despite the presence of several treatments to alleviate PD symptoms, no drug has been effective in preventing the loss of dopaminergic neurons or to regenerate neurons already lost. Clearly, the search for a pharmaceutical tool that could offer neuroprotective or neurorestorative effects is a recent thrust area. Recent studies have established the significant role of nutrition in neuroprotection and prevention of neurodegeneration. Omega-3 fatty acids exhibit the unique property of being able to cross the blood-brain barrier. Docosahexaenoic Acid (DHA), an important omega-3 essential fatty acid, is concentrated in the Central Nervous System (CNS) as a component of cell membranes, especially the synaptic, dendritic and photoreceptors and is known to possess neuroprotective properties. Supplementation of patient with DHA can modify brain functions, suggesting its suitability as a nutraceutical tool for

slowing the disease progression. DHA protects neurons against cytotoxicity by inhibiting nitrogen oxide (NO) production and calcium ( $Ca^{2+}$ ) influx. Short-term administration of DHA reduced levodopa-induced dyskinésias in parkinsonian primates by up to 40%. The anti-inflammatory effect of DHA is due to its ability to inhibit cyclooxygenase-2. More research is warranted to determine if DHA is beneficial for PD patients since studies till date are limited to only animal models. Thus, it is safe to conclude that DHA may represent a new and valuable approach to improve the quality of life of patients with PD.

**Keywords:** Parkinson's disease, Docosahexaenoic acid, Nutrition, Neurodegeneration, Neuroprotection

PP38

ICABB-172

### MOLECULAR DOCKING OF INSULIN RECEPTOR AGAINST NATURAL BIOACTIVE COMPOUNDS AND THEIR DERIVATIVES WITH HYPOGLYCEMIC EFFECT

Beant Kaur and Manpreet Kaur Paintal

Guru Nanak Girls College (Affiliated to Panjab University), Model Town, Ludhiana Punjab Pin 141002  
E-mail: pearl4aug@gmail.com

In Type 2 Diabetes, either body doesn't produce enough insulin, or the cells in the body don't recognise the insulin that is present. As a result elevated blood sugar levels have many fatal consequences. There are some natural bioactive compounds found in herbs and spices that are used against the treatment of Type 2 diabetes because of their hypoglycemic effect. Present study is an computational based docking method to evaluate the role of these bioactive compounds/ ligands and their derivatives, present in namely three herbs: Ginger, Garlic and Fenugreek as hypoglycemic agents targeted against Insulin receptor using molecular docking approach against using HEX . All the compounds were screened through ZINC which is a free database of commercially available potential drug like candidates for virtual screening and evaluated on basis of their total energies, on complex formation between the receptor and the ligand. The aim of the present study was to find best fit of these ligands bind with insulin receptor and can serve as potent insulin receptor binder in absence of normal insulin mechanism. According to the present study binding energies of the best docked pose are in order of cinnamon >funugreek> garlic.

**Keywords:** Insulin Receptor, HEX , ZINC database, LAZAR, LIGPLOT

PP39

ICABB-173

## COMPARATIVE ANALYSIS OF ALKALOIDS AND ITS DERIVATIVES AS BINDING LIGANDS OF B-DNA: A COMPUTATIONAL APPROACH

Preeti Vyas and Manpreet Kaur Paintal\*

Guru Nanak Girls College, Model Town, (Affiliated to Panjab University), Ludhiana Punjab Pin 141002  
E-mail: pearl4aug@gmail.com.

B-DNA is the most naturally occurring nucleic acid and has a role in replication and transcription and therefore has been interesting target for developing novel anticancer agents against B-DNA capable of inhibiting replication/ transcription process. Alkaloids are important chemical compounds that serve as a rich reservoir of drug discovery. Alkaloids are among the most active components in natural herbs and some compounds have already been successfully developed into chemotherapeutic drugs. Present study is computational based docking method to evaluate the role of naturally derived alkaloids and their structural analogues targeted against B-DNA using computational approach. The sequence of target dodecamer B-DNA sequence for docking was selected from Protein Data Bank. Drug library was generated for structural analogues of three classes of naturally occurring alkaloids compounds, namely, Berberine, Evodamine and Erybraedin C using ZINC which is a free database of commercially available potential drug like candidates for virtual screening. Docking calculations were performed using AutoDock suite of programs. The results were evaluated primarily on the basis of binding energy, hydrogen bond formation, hydrophobic interactions, inhibition constants ( $K_i$ ). Maximum human recommended dose for the screened compounds was evaluated through online insilico toxicity screening using LAZAR and the values were correlated with the inhibition constant ( $K_i$ ). The interactions between the receptor and ligand were analysed through LIGPLOT. The aim of this study was to screen a potential natural alkaloid based drug against B-DNA. The minimum binding energies of the structural analogues of Evodiamine and Berberine were comparable with the reference compounds of Erybraedin C. The values of the inhibition constant  $K_i$  and maximum dose reflected that these analogues are very good candidates for oral mode of drug delivery

as  $K_i >>>$  maximum recommended dose. Further evaluation and validation of results can be confirmed through molecular simulations as well as drug kinetics and other wet lab studies.

**Keywords:** Alkaloids, Berberine, Erybraedin C, Evodamine, AutoDock, ZINC database, LAZAR, LIGPLOT

PP40

ICABB-239

## UNFOLDING DYNAMICS OF THE TDP-43 RRM-1 DOMAIN INVOLVED IN FRONTEMPORAL LOBAR DEGENERATION REVEALED BY ATOMISTIC SIMULATIONS

Gunjan Dixit, Amresh Prakash and Andrew M. Lynn\*

School of Computational and Integrative Sciences, Jawaharlal Nehru University, New Delhi 110067, India.  
E-mails: gunjan.dikshit@gmail.com,  
\* Corresponding author : andrew@jnu.ac.in

The accumulation of misfolded and aggregated proteins is the major pathological condition of various neurodegenerative disorders. TDP-43 (TAR DNA-binding protein) is a DNA and RNA binding protein, usually involved in mRNA splicing, translational regulation, and transport. Mutations in human TDP-43 are known to be associated with Amyotrophic lateral sclerosis (ALS) and frontotemporal lobar degeneration (FTLD). Here, we employed all-atoms MD simulation to illustrate the folding pathway of the RRM1 domain of TDP-43 involved in ALS and FTLD. Multiple runs of thermal unfolding simulation were carried at high temperature (500K) for 20 ns, for the both WT and mutant (D169G) to capture the conformational transition. We repeated simulations 100 times to achieve the cumulative (2is) multiple trajectories for each protein to ensemble all the possible conformations during the unfolding simulation. The obtained trajectories were concatenated to construct the Free Energy Landscape (FEL). Results show the formation of an intermediate state in the unfolding process of the mutant. The obtained trajectories were also analyzed with MSMBuilder to cluster the unfolded state ensemble. The time structure based independent component analysis (tICA) was conducted for 100 trajectories of each protein which revealed the existence of multiple transition states ensemble as intermediate and metastable states in mutant as compared to WT.

**Keywords:** TDP-43, Protein unfolding, MD Simulation, Free energy landscape, MSMBuilder.

PP41

ICABB-049

## ENHANCED LIPID PRODUCTION USING FED-BATCH FERMENTATION OF OLEAGINOUS YEAST ISOLATES FOR FUTURE BIODIESEL

**Gunjan<sup>1</sup>, Kumari Sweta<sup>1</sup>, K.K. Bandyopadhyay<sup>1</sup>  
and Debarati Paul<sup>1\*</sup>**

1. Amity Institute of Biotechnology, Amity University, Noida, U.P.  
E-mails: gunjan.sngh15@gmail.com , swetariteshsinha@gmail.com ,  
kkbandyopadhyay@amity.edu , \*Corresponding author:  
dpaul@amity.edu

This study investigated the potential of different oleaginous yeast utilizing agricultural waste as cultivation media for the sustainable production of microbial lipids as biodiesel feedstock. Oleaginous yeast has been reported to accumulate substantial amounts of lipids that can be converted to biodiesel via transesterification. In our study three oleaginous yeast strains were isolated; FLP from flower, CS1 from soil and WEP from peels of fruits. All three oleaginous yeast strains were grown along with R. toruloides using batch and fed-batch fermentation. The culture medium used was waste "extract" derived from vegetable 'mandi' waste containing various carbon sources such as glucose, xylose, glycerol etc and other growth factors. Batch fermentation resulted in production of 66% lipid of dry cell biomass in case of R. toruloides, while 59%, 62.5% and 65% were extracted from FLP, WEP and CS1 respectively. Fed-batch fermentation was performed using glucose as feed for medium to increase final biomass and lipid production in which R. toruloides resulted highest lipid content of 76% followed by 70%, 68% and 66% of lipid in strains namely FLP, WEP and CS1 respectively. Fatty acid methyl esters (FAMEs) analysis of R. toruloides showed that this strain produced higher proportions of 22.5% saturated fatty acid (palmitic acid C16:0), 42% of unsaturated fatty acid such as (C18-oleic acid; C18:2; and C18:3 ± linoleic acid) and also 11.28% of monounsaturated fatty acid (Nonadecyclic acid C19:1) when grown on waste medium via fedbatch fermentation. Considering the yield and cost, lipids extracted from R. toruloides using waste medium in fedbatch fermentation would be a promising alternative source for biodiesel production in the near future. Properties of different fatty acids were analyzed and the results indicated that apart from

biodiesel production the fatty acids may be used for production of soaps, cosmetics, natural additive, finishing agents, lubricants, surface active agents etc.

**Keywords:** Waste extract, oleaginous yeast, lipid, biodiesel, fed batch, batch, fermentation.

PP42

ICABB-052

## 3D- BIOPRINTING: THE PROMISING FUTURE OF MEDICINE

**Raina Jana<sup>1</sup>, Akash Yadav<sup>1</sup>, Abha Singh<sup>1</sup> and  
Neeraj Wadhwa<sup>1\*</sup>**

1. Department of Biotechnology, Jaypee Institute of Information  
Technology, Noida, Uttar Pradesh, India  
\*Corresponding author: neeraj.wadhwa@jiit.ac.in

The three-dimensional bioprinting is one of the most recent and promising invention in the field of medicine and pharmacology. It combines the cells, growth factors and biomaterials to fabricate the biomedical parts that maximally replicate tissue characteristics. This field is mainly being applied to the regenerative medicine so that the need of the tissues and organs for the transplantation surgery can be addressed. However as compared to the non-biological printing, the 3D bioprinting is much complex due to its choice of materials, growth factors and the technical challenges related to it. Hence, addressing these complexities requires the integration from other fields of engineering, biomaterial science, physics and medicine. Skin tissue grafts, Vascularized heterogenous tissue constructs, aortic valves, tracheal splints, early stage kidney prototype have been developed. This technique has already been started being used for the transplantation, grafting and for vascular tissues. However the future applications are being focussed in this paper for the development of 3D- bio printed tissue models for the research, drug discovery and toxicology.

PP43

ICABB-054

## ORGANIC LEATHER AS A STARTUP

**Abha Singh<sup>1</sup>, Divya Batra<sup>1</sup>, Raina Jana<sup>1</sup> and  
Neeraj Wadhwa<sup>1\*</sup>**

1. Department of Biotechnology, Jaypee Institute of Information  
Technology, Noida, Uttar Pradesh, India  
\*Corresponding author: neeraj.wadhwa@jiit.ac.in

Mushrooms have been closely linked with human culture Many species of mushroom can be consumed

and have many health, hair and skin benefits. Some species are very poisonous and are known as toadstools. Mushroom also has other applications like in production of cosmetics, treatment for various disorders like diabetes and may also be used for curing heart disorders. Mushrooms also have found industrial application in leather industry and it is reported that the fruiting bodies and mycelium of some mushroom can be utilized to make leather. Fruiting bodies of *Phellinus ellipsoideus* are very large and its cap is being used for leather production. Muskin is one such leather. Process for creating muskin is fully natural and free of toxins so even if the muskin comes in contact with skin it causes no harm to the individual. Muskin is much smoother and cheaper than animal leather. MuSkin startup can give huge profits within few weeks and that too by investing a small amount of money. Mycoworks is another company that is working towards the production of leather utilizing mycelia of *Ganoderma lucidum*, also known as the reishi mushroom, a popular fungi in Asia that's commonly used in natural remedies and teas. In this paper natural alternatives to leather and their benefits, like being animal-free, sustainable, and cost-competitive is being discussed.

PP44

ICABB-059

## MYCOREMEDIAION: AN APPROACH TO REMEDIATE HEAVY METALS

Pooja Upadhyay<sup>1</sup>, Saloni Sachdeva<sup>1</sup> and Dr. Pammi Gauba<sup>1\*</sup>

1. Department of Biotechnology, Jaypee Institute of Information Technology, Sector-62, Noida, UP, India - 201307  
 \*Corresponding author: pammi.gauba@jiit.ac.in

Mycoremediation is a term that is applied to the use of fungi to clear the environment from contaminating substances. Metal pollutants are released into the environment anthropologically at potentially harmful levels. Fungi develop an effective strategy to cope with the harmful consequence of metal and metalloid exposures. The metal remediation is a complex process that depends on the chemistry of metal ions, physiology of the organism, and physicochemical factors like pH, temperature, ionic strength, and metal concentration. All of the three types of fungi-saprophytic, parasitic and mycorrhizal species participate in bioremediation process. Fungi are considered as important decomposers in the ecosystem, which can significantly reduce and degrade persistent and highly toxic pollutant. Fungal morphology involves mycelia that play an important

role in apical growth and secretes useful enzymes at the time of high metal stress condition which is helpful in remediation procedure. Mycoremediation is environmentally friendly, requires less space, has a low cost, and can be practically implemented. The success of the mycoremediation technology is based on large-scale mushroom availability, soil contaminants within the mycelium range to be absorbed, and favourable environmental. Benefit is that contaminated land which is unfit for agriculture could be both restored and made to yield a nutritious crop. There is a need of even more extensive research and its implementation in this field, because mycoremediation is that tool which can give pollution control an all new face to sequester or degrade contaminants.

**Keywords:** Mycoremediation, Metal Remediation, Metal Stress, Mycelium.

PP45

ICABB-061

## GREEN FOOD PROCESSING TECHNIQUES

Sakshi Awasthi<sup>1</sup>, Megha<sup>2</sup> and Dr. Vibha Rani<sup>1\*</sup>

Jaypee Institute of Information Technology, Sector 62, Noida, UP, 201309

\*Corresponding author: vibha.rani@jiit.ac.in

The best way to improve the sustainability of human food interaction through the food life cycle, is simply and fundamentally to consume less. There are many points within the food cycle where we can consume less. From the past several years, the food industry demand for minimal processed food leads to significant alterations in the processing methods as some processing techniques applied under critical conditions lower their nutrient level and bioavailability by inducing physical and chemical changes, thereby reducing their acceptability. Growing consumer demand for better soil practices to consume less energy/resource, understanding food provenance to reduce transport costs, reducing food packaging, making efficient and recyclable food packaging and increasing composting of food waste are examples of socio-political interventions that "green up" sustainable food practices, reducing consumption of associated resource at each stage of the food cycle. Green Food Processing could be a new concept to meet the challenges of the 21st century, to protect both environment and consumers, meanwhile increasing the competition of industries to be more ecologic, economic and innovative. This green approach should be the result of a whole chain of values in both senses

i.e. economic and responsible, starting from the production and harvesting of food raw materials, to process of preservation, transformation, and extraction together with formulation and finally to marketing. Green food technology is the basic finding to balance between food supply and demand in a manner that is sustainable and also insures the long-term survival of population. This study presents current knowledge on green food processing techniques for education at industrial scale and their role in promoting sustainable food industry. The different techniques like pulse electric field, instant controlled pressure drop, ultrasound assisted food processing, supercritical fluid extraction are also discussed.

**Keywords:** Green food processing, pulse electric field, instant controlled pressure drop, ultrasound assisted food processing, supercritical fluid extraction

PP46

ICABB-079

## MICROALGAE IN COMMERCIAL MARKET

**Pooja Upadhyay, Saloni Sachdeva and Dr. Pammi Gauba\***

*Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sector-62, NOIDA-201309  
\*Corresponding author: pammi.gauba@jiit.ac.in*

Microalgae are pivotal for the global food chain, as they act as a major part of phytoplankton. Also, their exceptional ability for CO<sub>2</sub> fixation makes them more significant in earth's ecosystem. Further, they play an underestimated role in eliminating contaminants from environment. Along with ecological benefits, microalgae can act as green cell-factories for the manufacture of high value, products with straightforward applicability and increasing market demand and via processes that are environment-friendly and essentially safe. The idea of producing various co-products came into existence after the limitation in bioenergy production by algae was realized; improving the economics of a microalgae bio refinery. Microalgae have found commercial applications as natural sources of valuable macromolecules, including carotenoids, long-chain polyunsaturated fatty acids, and phycocolloids. As photoautotrophs, their simple growth requirements make them attractive for bioprocesses aimed at producing high added-value compounds that are in large demand by the pharmaceutical market. A few compounds synthesized by microalgae have indeed proven to possess anti-inflammatory, antiviral,

antimicrobial, and antitumoral features. Example includes pigments, proteins, lipids, carbohydrates, vitamins and anti-oxidants. This paper briefly reviews the main existing and potential high-value products which can be derived from microalgae and considers their commercial development.

**Keywords:** Microalgae, Green Cell-Factories, High-Value Products, Commercial Applications.

PP47

ICABB-086

## LATEST TRENDS IN COSMECEUTICALS

**Paramveer Yadav, Nisha Sharma, Pratiksha Rajput, Prakhar Srivastava, Neeraj Wadhwa\***

*Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sector 62, Noida, India  
E-mails: param.3nov@gmail.com, \*Corresponding author: neeraj.wadhwa@jiit.ac.in*

In the recent years the fastest growing segment in cosmetic industry is 'Cosmeceuticals' and also the use of cosmeceuticals has drastically risen. Cosmeceuticals are the advances made in the dermatological products which are the future generation skin care products. All the cosmeceutical products claim to have the active ingredients that have the properties of either disease fighting or therapeutic. These are topically applied hybrids of cosmetics and pharmaceuticals which are intended to enhance the beauty and also maintains the youthful and vibrant appearance. They too have ingredients which have health related functions or benefits. Being hybrids of cosmetics and pharmaceuticals, they are applied topically as cosmetics but also contains the ingredients with pharmaceutical properties that influences the biological functions of the skin. Hence, today cosmeceuticals are serving as the connecting link between pharmaceuticals and personal care products. This paper explains the antioxidant activity of some of the ingredients present in the cosmeceuticals to maintain the skin younger and beautiful. The ingredients with antioxidant activity include vitamin C, vitamin E, Superoxide Dismutase, Ferulic acid, etc. And this property of these ingredients is profoundly utilised by the leading cosmeceutical brands to combat the various skin aging problems like fine lines and wrinkles. Some of the well-known cosmeceutical brands like Ultraceuticals®, Reviva labs®, Skinceuticals® and Elizabeth Arden® are also discussed further in this paper. All these brands follow up some of the procedures regarding safety,

toxicity and efficacy of the products manufactured by them.

**Keywords:** Cosmeceuticals, cosmetics, pharmaceuticals, antioxidant, regulatory aspects

PP48

ICABB-095

## ALGAE - BIOFUEL PRODUCTION

Anirudh Bhatia, Jasveen Bhasin,  
Jatin Aggarwal and Vibha Gupta\*

Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201307, Uttar Pradesh, India  
E-mails: anirudhbhatia25@gmail.com, jasveenbhasin1998@gmail.com, jatinaggarwal120@gmail.com, \*Corresponding author: vibha.gupta@jiit.ac.in

The world has been confronted with an energy crisis due to depletion of finite non-renewable fossil fuel resources. The use of fossil fuels like coal petroleum is now considered unsustainable due to depleting resources and accumulation of greenhouse gases in the atmosphere. Whereas a biofuel is produced through contemporary biological processes, such as homeostasis, growth etc. rather than a fuel produced by geological processes such as those involved in the formation of fossil fuel, from prehistoric biological matter. Renewable biofuels generally involve contemporary carbon fixation through the process of photosynthesis. Algal species grow in a wide range of aquatic environments, from freshwater through saturated saline. They can grow almost anywhere even on sewage or salt water. More than 40% of the global carbon fixation is done by algae. Large amounts of lipids, proteins and carbohydrates are produced by microalgae over short period of time. *Cladophorafracta* and *Chlorellaprotothecoid* were studied for biofuel production. About 60-70% of their total biomass can produce biofuel thus reducing the environment pollution. It was found recently that the only source of renewable biodiesel that is capable of meeting the global demand for transport fuel comes majorly from microalgae. Microalgae have additional advantages over terrestrial plants. Since they are single-celled organisms that duplicate by division, high-throughput technologies can be used to rapidly evolve strains. This can reduce processes that take years in crop plants, down to a few months in algae. Algae will reduce the burden from the terrestrial plants which are currently used for biofuels and will increase the biofuel production. They can be grown on land that would not be used for traditional agricultural, and are very efficient at removing nutrients from water. Thus, not only would production of algaebiofuels minimize land

use compared with biofuels produced from terrestrial plants but, in the process of culturing these microalgae, waste streams can be remediated. Algae production strains also have the potential to be bioengineered, allowing improvement of specific traits and production of valuable co-products, which may allow algal biofuels to compete economically with petroleum. These characteristics make algae a platform with a high potential to produce cost-competitive biofuels.

**Keywords:** Fossil Fuel, Microalgae, Biofuel, Pollution, Oil, *Cladophorafracta* and *Chlorellaprotothecoid*

PP49

ICABB-103

## OPTIMIZATION STRATEGIES FOR MAXIMAL BACTERIOCIN PRODUCTION FROM LACTIC ACID BACTERIA

Priyanka Joshi<sup>1</sup> and Reema Gabrani<sup>1\*</sup>

<sup>1</sup> Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201309, Uttar Pradesh, India  
E-mails: priyankaj5795@gmail.com \*Corresponding author: reema.gabrani@jiit.ac.in

The capability of bacteria to produce anti-bacterial peptides has captured the curiosity of scientists around the globe. These peptides, commonly regarded as bacteriocins, hold diverse applications in food and health industry. Especially, Lactic acid producing bacteria have garnered special interest because of their GRAS status and their bacteriocins being stable in wide temperature; and pH range, colorless, odorless and tasteless, non-toxic, and active in even nanomolar concentrations. For instance, Nisin, a widely studied bacteriocin of *L. lactis* is now approved as a food preservative to prevent food spoilage from *Listeria monocytogenes* and *Clostridium botulinum*. Interventions are also taking place to assess their significance in combating multi-drug resistance and possible anti-cancer properties. Since, they offer multitude of potential applications its essential to maximize their production and activity. Optimization of media composition and environmental conditions entail a collective group of effective strategies aimed at maximizing bacteriocin production and activity. Optimization of media encompasses careful selection of a set potential carbon sources, nitrogen sources, and other additives in varying concentrations. Then, through exhaustive experiments, these sets are narrowed down to one choice, which delivers the maximum bacteriocin production and activity. As evident by the media optimization for *Lactobacillus*

*plantarum* AA135, addition of Vitamin DL-6,8-thioctic acid almost doubled the bacteriocin activity. Temperature and pH are the key environmental conditions which play significant role in bacteriocin production, hence need thorough optimization as well. This review aims at providing a comprehensive guide of media composition and environmental condition optimization yet achieved, for the bacteriocins produced by Lactic acid bacteria.

**Keywords:** carbon source; nitrogen source; pH; surfactant; temperature

PP50

ICABB-158

## ACTIVE COSMETIC INGREDIENTS OBTAINED THROUGH BIOTECHNOLOGY FOR SKIN CARE

**Sakshi Tyagi<sup>1</sup>, Monika<sup>1</sup> and Dr. Vibha Gupta<sup>1\*</sup>**

*1. Department of Biotechnology, Jaypee Institute of Information Technology, Noida, UP- 201309 India*

E-mails: sakshityagi2398@gmail.com, monikaantil60@gmail.com

\*Corresponding author: vibha.gupta@jiit.ac.in

Humans have always trying to modify or alter the natural processes for faster results and easy lifestyle. Biotechnology is one of the fields that contributes to understand and manipulate the biological systems for their use in medical, agriculture and industrial sectors. Due to high demand and better results in cosmetics, scientists are going through a phase where they are merging biotechnology, pharmaceutics and cosmetics industry. A combination of these three fields results in an emerging field, *Cosmeceuticals* which deals in cosmetics products, functional cosmetics and drugs. As an outcome, cosmetic industries are using different fields of biotechnology such as genomics, proteomics and molecular biology to develop the active cosmetic ingredients which are safer, cost effective and more promising than traditional skin care products. Skin aging, skin scars, marks, uneven skin tone and dehydrated skin are the common problems which are being addressed with the help of active ingredients obtained through biotechnology. Some of the active ingredients such as ethylbisiminomethylguaiacol manganese chloride (EUK-134 TM), sugars like xylitylglucoside and matrikines which are being synthesized to resolve some of the skin related issues. As the demand of biotechnological products is increasing rapidly, companies like L'Oréal, P&G etc. are capturing the forefront position in the cosmeceuticals field. This study focused on the role of biotechnology to develop

safer and more efficacious products to fulfill the demand of mankind.

**Keywords:** Biotechnology, cosmeceuticals, active ingredients, skin aging

PP51

ICABB-178

## BIOFABRICATION TECHNOLOGIES FOR PRODUCT DEVELOPMENT

**Sonakshi Madan, Reema Gabrani\* and  
Sanjay Gupta\***

*Department of Biotechnology, JIIT, Noida, UP- 201307*

\*Corresponding authors: sanjay.gupta@jiit.ac.in,  
reema.gabrani@jiit.ac.in

Biofabrication refers to the use of biological or biologically derived raw materials for the development of useful products. It encompasses a wide range of products- from antibiotics to artificial leather to biofuels and organs for transplantation. Ever since the inception of this concept, great strides have been made in this field, with the aid of advances in tissue culture, bio-material sciences and mechanical engineering. Not only does biofabrication provide useful biological products, it does so in an environment friendly, pollution free manner. The production of artificial leather and animal free meat products resolves quite many ethical issues associated with the use of animals for human benefit. The finest applications of biofabrication can be observed in the medical and pharmaceutical industry, in the form of safer artificial organs and prosthetics as well as better and more reliable biomimetic models for drug testing. Advances in computer assisted design and manufacturing technology and the development of more efficient tools has made possible 3D printing of a variety of tissues and organs. This review aims to list various technologies involved in the process of biofabrication, including cell sheet, solid scaffold, embedding and moulding technology, and their potential applications in various industries.

**Keywords:** Animal free; Bioengineering; Organ transplant; Tissue engineering

## DESIGNING PRINCIPLES FOR PHOTOBIOREACTORS: AN APPROACH FOR MASS MICROALGAL CULTIVATION

**Sakshi Khanna<sup>1</sup>, Ritika Kamthan<sup>1</sup>, Riya Sharma<sup>1</sup> and Garima Mathur<sup>1\*</sup>**

1. Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201307, Uttar Pradesh, India  
E-mails: khannasakshi54@gmail.com, kamthan.ritika247@gmail.com, sharmariya697@gmail.com, \* Corresponding author: garima.mathur@jiit.ac.in

In the recent times, a significant escalation in microalgal based biofuels production has resulted in technological advancements associated with mass cultivation of microalgae. Photobioreactors (PBRs) are closed cultivation systems with different categories such as tubular, flat-plate, vertical, annular, fermenter-type and internally illuminated. PBRs are a preferred mode of algal cultivation due to associated advantages such as less availability of utilizable lands, reduced processing cost and auxiliary energy demand. For large scale production of biofuels, microalgae need to grow in massive quantities either in open pond (raceway type) systems or in PBRs. PBRs help in achieving high productivity per unit area and provide optimum environmental conditions required for the microalgal growth mimicking its natural habitats. Though open pond systems are the most inexpensive option, it is difficult to regulate the process conditions necessary for the growth. Less chances of contamination, high biomass productivity per unit area and controlled environment for growth are some of the advantages of using PBRs over open pond systems. Extensive research is going on modification and design advancements of PBRs for increasing the productivity. Recently, the effect of various light filters has been investigated to enhance the fatty acid yield in algal biomass. This review addresses general design considerations pertaining to reactors that use natural light and photosynthetic growth mechanisms, with an emphasis on commercial large-scale reactors for microalgal cultivation.

**Keywords:** Photobioreactors, Open pond, Biofuels, Microalgae, Large-scale reactors

## THE GLYCEROL BIOREFINERY FOR INDUSTRIALLY IMPORTANT CHEMICALS

**Riya Sharma, Ritika Kamthan, Sakshi Khanna, Garima Mathur\***

Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201307, Uttar Pradesh, India  
Emails: sharmariya697@gmail.com, kamthan.ritika247@gmail.com, khannasakshi54@gmail.com, \*Corresponding author: Email: garima.mathur@jiit.ac.in.

According to International Energy Agency, the global energy consumption is expected to increase nearly 33% by 2035. The additional requirement of energy sources would be greatly depending on renewable sources. Biofuels remain a preferred choice for their low carbon emissions and being reliable and cleaner technology. The idea of biorefinery has been observed as the most sustainable way to produce useful products of industrial importance, derived from waste. Glycerol is produced as a major by-product of biofuels industry which constitutes to 70-75% of total waste. Glycerol is a preferred raw material for biorefinery due to its low cost, high abundance and high degree of reduction. Conversion of glycerol to industrially important metabolites is essential to increase the economics of biofuel industry. Various studies have been conducted to compare the efficiency of the wild-type and the genetically engineered strains of yeasts and bacteria (mostly *E. coli*) for microbial fermentation of glycerol. It has been observed that genetically modified strains of several yeasts and bacteria show higher productivity as compared to the wild strains. Here, we illustrate the approaches and strategies employed for genetic and metabolic engineering for biotransformation of waste products to value added products such as industrial grade alcohols, ketones, organic acids, biopolymers etc.

**Keywords:** Biorefinery, Biofuel, Biotransformation, Metabolic Engineering, Glycerol

## OPTIMIZATION OF PVA GEL TECHNOLOGY FOR NON-SEGREGATED MSW LEACHATE TREATMENT.

Himanshu Chaturvedi, Gyan Prakash Misra, and Priyanka Kaushal\*

*Dept. of Energy & Environment, TERI University, 10 Institutional Area, Vasant Kunj, New Delhi-110070 India)*

\*Corresponding author: priyanka.kaushal@teriuniversity.ac.in

In developing country like India, where Municipal Solid Waste (MSW) Management is at its beginning, open dumpsites lead to negative impact on the health and environment. Leachate generated from non-segregated MSW leachate has been a major concern. Biological treatment like PVA gel technology has been proved to be effectual for treating the MSW leachate. The current study was designed for the optimization of the conditions for efficient treatment of MSW leachate by PVA gel. Current study was conducted out at Municipal Solid Waste based 12 MW Waste-to-Energy Plant in Ghazipur, eastern part of Delhi, India. Physio- chemically and anaerobically treated leachate samples were subjected to PVA gel reactor. Parameters like BOD COD, Hydrolic retention time (HRT) and temperature were changed to get the optimized the treatment efficiency of PVA gel on non-segregated MSW leachate. Number of samples were analyzed to get the optimum strength of PVA gel while reducing BOD, COD, and with varying time of HRT and different temperature range. Observation concluded that partially treated leachate having BOD nearly 600mg/L, COD nearly 1500mg/L, HRT of 5hr or more and temperature range of 30-40°C have shown maximum treatment efficiency of PVA gel.

**Keywords:** BOD, COD, HRT Polyvinyl Alcohol (PVA) Gel, Municipal Solid Waste

## PRE-BLEACHING OF UNBLEACHED BAMBOO PULP WITH LACCASE ENZYME PRODUCED BY PSEUDOMONAS SP. PBS-2 FROM NORTH-EAST INDIAN BIO-RESOURCE

a,b Boruah P and aGoswami T\*

*<sup>a</sup> Cellulose Pulp & Paper Group, Material Science and Technology Division, CSIR-NEIST, Jorhat, Assam <sup>b</sup> Academy of Scientific and Innovative Research, CSIR, Chennai, India*

E-mail: paranjoli.boruah7@gmail.com,

\*Corresponding author: goswamit@neist.res.in

The enzymatic pre-bleaching of unbleached bamboo pulp using a potential lignolytic bacterium *Pseudomonas* sp. PBS-2 isolated from decayed bamboo collected from Hindustan Paper Corporation Ltd, Jagiroad, Assam, India has been studied with an objective to minimise the use of harmful bleaching agents e.g. chlorine, calcium hypo-chloride, chlorine dioxide etc. which are conventionally used in pulp bleaching process. The highest laccase enzyme production by this strain was 2118.84 U/mL at 30 C, pH 10 and incubation time of 96 h. Initially the unbleached bamboo pulp was treated with laccase enzyme followed by bleaching with a few eco friendly agents such as hydrogen peroxide (H<sub>2</sub>O<sub>2</sub>), ozone etc. in order to see the efficacy of bleaching after enzymatic pre-treatment. Laccase pre-treatment effectively decreases the lignin content of unbleached bamboo pulp by 5% compared to control pulp. However, laccase pre-treatment followed by hydrogen peroxide and ozone bleaching further decreases lignin content to 3.25 percent. Enzymatic pre-treatment enhances the pulp brightness significantly from 16.07 % in control pulp to 68.2%. Pulp brightness increases further up to 80.62% following hydrogen peroxide and ozone treatment of the laccase pre-treated pulp. The scanning electron micrographs of laccase pre-treated pulp reveals clear conserved cellulosic fibres with mild cracks and pores on the surface. The enzyme pre-treated pulp after hydrogen peroxide and ozone treatment shows clearly visible fibrils, linearly arranged on the surface. Longitudinal cracks and occasional grooves are also visible on the surface along with an increase in whitish appearance. The findings of the present study are encouraging which may lead to the development of cleaner bio-formulations as an alternative to chlorine based bleaching in pulp and paper industry.

**Keywords:** *Pseudomonas* sp. PBS-2, north-east, laccase, bio-bleaching, bamboo pulp, lignin

## EFFECTS OF PROBIOTICS ON GUT-BRAIN AXIS

**Shubhanshu Upadhyay, Ritika Kamthan and Smriti Gaur\***

*Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201307, Uttar Pradesh, India  
E-mails: shubhanshu19999@gmail.com, kamthan.ritika247@gmail.com \*Corresponding author: smriti.gaur@jiit.ac.in*

In the last few decades, there has been a surge in studies on health benefits of probiotics. They not only help in maintaining gut metabolism, but these microbes are beneficial in other ways too. Gut microbiota helps in conversion of dietary nutrients into metabolites that acts as biologically active compound, affecting immunity and neurobiology. These microbes have been known to induce hormones and neurotransmitters equivalent to those found in humans. Studies over Zebrafish (*Danio rerio*) have proven that microbiota modulates different neuro-active molecules such as Brain-derived Neurotrophic factor (BDNF) and Serotonin Signaling. Probiotics are observed to produce many neurotransmitters acting as novel anti-depressants, which helps against anxiety and cognitive symptoms. The modus operandi of Gut bacteria is that they directly trigger afferent neurons of the intrinsic nervous system through vagus nerve which sends signals to the brain. Through varied mechanisms, gut microbes maintain the framework of sleep and stress reactivity of the neuro-endocrine axis. This study helps in better understanding of bi-directional relation between gut-brain axis, by emphasizing on probiotics and their applications, for clinical treatments of infectious diseases including those of viral or bacterial origin, antibiotic induced diarrhea, decreased risk of colon cancer, improved lactose digestion; without the harmful side effects of medicinal drug usage.

**Keywords:** gut-brain axis, immunity, microbiome, neuro-active molecules, neuroendocrine axis probiotics.

## DEVELOPMENT OF AN ANTI-FUNGAL DRUG LOADED NANOEMULGEL FOR THE TREATMENT OF ORAL CANDIDIASIS

**R. S. Narang<sup>1</sup>, Anmol Dogra<sup>2</sup>, Javed Ali<sup>3</sup> and Jasjeet Kaur Narang<sup>2\*</sup>**

*1. Department of Oral and Maxillofacial Pathology, Sri Guru Ram Das Institute of Dental Sciences and Research, Amritsar, Punjab; 2. Department of Pharmaceutics, Khalsa College of Pharmacy, Amritsar, Punjab 3. Department of Pharmaceutics, Jamia Hamdard, Hamdard University, New Delhi-110062;  
E-mails: narangraman@yahoo.com, javedaali@yahoo.com,  
\*Corresponding author: jasjeet2975@yahoo.com*

Fluconazole, a potent antifungal drug has potential for the treatment of oral candidiasis. However, it suffers from the problem of poor aqueous solubility and low permeation, which inturn limits its application. The objective of the present investigation was to formulate a fluconazole based nanoemulgel which is thermodynamically stable, has improved aqueous solubility and exhibits improved mucosal penetration. The aqueous titration method was used for the formulation of the nanoemulgel. For the formulation, the solubility of fluconazole in various oils, surfactants, and cosurfactants was determined. Further the miscibility of the various solvents and cosolvents used was also evaluated. Based on the results of the study, the oil, surfactant, cosurfactant which exhibited maximum solubility of fluconazole were selected and aqueous titration method was used to formulate emulsions which were further sonicated using a probe sonicator to reduce the globule size to nanometer range. An optimized quantity of the gelling agent was incorporated in the optimized nanoemulsion to yield a Transparent nanoemulgel. The nanoemulgel formulated was evaluated for optical clarity, homogeneity, viscosity, grittiness and spreadability. The results of the evaluation study revealed that the formulated Fluconazole loaded nanoemulgel was optically transparent, homogeneous, free from grittiness and having optimised viscosity and spreadability. The results of the study clearly indicated successful formulation of a nanoemulgel of fluconazole with its potential for the treatment of oral candidiasis.

**Keywords:** Aqueous titration method, Fluconazole, nanoemulgel, oral Candidiasis

---

## THE FAULT IN OUR GUT: OBESITY, DIABETES AND GUT MICROBIOTA

Avishi Aggarwal, Diksha Rathore,  
Twinkle Wahi, and Smriti Gaur\*

*Department of Biotechnology, Jaypee institute of Information Technology, Noida, Sector 62, Uttar Pradesh, India*  
E-mails: avishiaggarwal18@gmail.com,  
\*Corresponding author: smriti.gaur@jiit.ac.in

---

Obesity and Type 2 diabetes are two metabolic diseases which have reached epidemic proportions worldwide. Though their etiology is complex, but both are suggested to occur due to interplay between the behavior, environment and genetic factors. The gut microbiota plays a crucial role in gastro-intestinal mucosa permeability, regulates the fermentation and absorption of dietary polyssacharides, which may explain its importance in the regulation of fat accumulation and the resultant development of obesity-related diseases. Since the time of birth to adulthood, the variations in the gut microflora occurs due to various reasons such as diet, immune response, which lead to the shift in the population of the bacteria. Such a shift in the bacterial population may cause adverse effects such as G-protein coupled receptor activation, fermentation of energy source which may further contribute to the development of obesity and other metabolic disorders like type 2 diabetes. The recent findings also suggest that calorie restriction and physical activity have an impact on gut microbiota composition related to body weight loss, which also seem to be influenced by the individual's microbiota. Although no *in vivo* evidence is present but these studies state that specific phyla, classes or species of bacteria, or bacterial metabolic activities could be beneficial or detrimental to patients with obesity. The gut microbiota is, therefore, a potential nutritional and pharmacological target in the management of obesity and obesity-related disorders.

**Keywords:** obesity, type 2 diabetes, gut microbiota, G-protein

---

## A FACILE COMPOSITE COMPRISING OF ENCAPSULATED CITROBACTER FREUNDII LCJ 002 AND IRON OXIDE NANOPARTICLES FOR THE REMOVAL OF TOXIC DIAZO DYE CONGO RED

Naveen Kumar\*, Surbhi Sinha, Tithi Mehrotra and Rachana Singh

*Amity Institute of Biotechnology, Amity University, Noida, Uttar Pradesh*  
E-mails: ssinha2@amity.edu; tithimehrotra\_6@yahoo.com; rsingh2@amity.edu, \*Corresponding author: naveen.amityib@gmail.com

---

Releasing of textile dyes into water bodies is a major environmental issue. Colour removal, in particular, has recently become one of major scientific interest, as indicated by the multitude of related research reports. We report a facile method to synthesize a composite of bacterial biomass *Citrobacter freundii* LCJ 002 - iron oxide nanoparticles immobilized in calcium alginate to monitor its decolourization performance in Congo Red dye removal from aqueous solution. Iron oxide nanoparticles (10 -20 nm) were prepared chemically using a co- precipitation method and were characterized using Dynamic Light Scattering (DLS) and Fourier Transform Infrared Spectroscopy (FTIR). The composite encapsulated in calcium alginate beads at 200 rpm and 37 °C showed 92.76% decolourization of dye Congo Red at pH 8. The incredible decolourization capability of the immobilized composite of *Citrobacter freundii* LCJ 002 - iron oxide nanoparticles render it practically useful for the treatment of wastewater containing dyes.

**Keywords:** Microbial isolation, Immobilization, Biosorbent, Iron oxide nanoparticles, *Citrobacter freundii*, CR removal

## THE EMERGING TREND: BIOREMEDIATION OF ORGANIC AND INORGANIC AIR POLLUTANTS

**Parul Chauhan, Mahender Singh Rawat,  
Richa Verma, Sakshi Bhadouria and  
Pammi Gauba\***

*Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sector-62, Noida, Uttar Pradesh-201307*

\*Corresponding Author: pammi.gauba@jiit.ac.in

The challenge of increasing economy in developing countries has decreased the quality of life tremendously on the earth. Increasing level of pollution, therefore increases the concern among the authority and people at global level. To overcome this a very effective and ecofriendly technique Bioremediation is emerging among the scientist in recent years. Bioremediation is an option that offers the possibility to destroy or reduce harmful contaminant in air, soil and water using natural biological activity of plants and microbes. Soil and water remediation through this technique has shown the effective results thus now used in various contaminated sites and also in wastewater treatment plants. In the field of air pollution this technique is not that much studied but has shown a great hope in air remediation. So, this review paper focuses upon the remediation of air pollutants (sulfur dioxide, nitrogen oxide, formaldehyde and other organic-inorganics compounds) through plants and their mechanism. Limitation of this technique is that it is slow and also depends upon the tolerance power of plants. To enhance the remediation of pollutants and to increase capability of plant uptake two methods are adopted: - plants with combination of soil microbes and use of transgenic plants by genetic engineering. The rate at which urbanization and industrialization is increasing the only way to protect planet is this approach of bioremediation.

**Keywords:** Bioremediation, Transgenic plants, Microbes, Air pollutants.

## BIODEGRADATION OF DIMETHOATE RESIDUES BY NATIVE RHIZOBACTERIAL ISOLATES

**Pratibha Yadav<sup>1</sup>, S Krishna Sundari<sup>1\*</sup>**

*1. Jaypee Institute of Information Technology, A-10, Sector-62, Noida, Uttar Pradesh 201309*

E-mails: skrishnasundari@gmail.com,

\*Corresponding author: krishna.sundari@jiit.ac.in

Microbe assisted biodegradation of pesticide is amongst vastly explored techniques, for effective degradation of xenobiotic compounds. Dimethoate is a known broad spectrum organophosphate pesticide, and as a consequence, it enjoys enormous application around the world. Dimethoate is reportedly toxic (in a systemic mode) for non-target organism, upon contact and ingestion. Excess application of dimethoate to control crop pests leads to its accumulation in environment. Thus there is a need to explore microorganisms with ability to tolerate and degrade dimethoate present at higher concentrations in agriculture soils. Another challenging aspect would be to explore microbes that not only degrade pesticide residues but also promote plant growth providing a two-way benefit to environment and society. Keeping this in mind in our study we have isolated rhizobacterial isolates from agriculture soil sprayed with organophosphate pesticides. Four potential native isolates were studied further and they showed survival at 500 ppm of dimethoate, with MIC ranging between 2000 to 3200 ppm. Isolates were found to utilize dimethoate as sole source of nutrients i.e. C/N/P on minimal media proving acclimatization of isolates to stress and enhanced remediation ability. Degradation of dimethoate was then confirmed by analytical techniques like FTIR spectrophotometry where shift in major standard dimethoate peak was observed in microbe treated samples, followed by GC-MS and HPLC analysis of one representative isolate proving complete degradation (100%) of dimethoate in 48hrs. Plant growth promoting ability of native isolates was also recorded that showed increase in biomass of host plant (moong) under dimethoate stress, as compared to unchallenged control. The study provides a solution to address accumulation of toxic pesticide residues in environment.

**Keywords:** Dimethoate, PGPR, FTIR, HPLC, GC-MS, degradation etc

## **STUDIES ON OPTIMIZATION OF SIDEROPHORE PRODUCTION BY MICROBIAL ISOLATE OBTAINED FROM AQUATIC SOIL AND ITS ANTIBACTERIAL ACTIVITY**

**Alazhar Colombowala<sup>1</sup>and Aruna K.<sup>1</sup>**

*Department of Microbiology, Wilson College, Mumbai- 400007*

*E-mails: colombowala49@gmail.com*

Siderophores are small low molecular iron chelating molecules produced by many bacteria to meet the iron requirements for multiple metabolic functions, iron serves as a cofactor in many enzymes and cellular processes. In the present study, Soil obtained from aquatic environment was used for screening and isolation. 35 bacterial cultures were isolated and subjected for siderophore production using CAS-agar assay method. Orange haloes were measured and expressed as CAS-reaction rate (mm per day). 6 isolates showed positive CAS reaction. The highest CAS-reaction rate was observed in these isolates i.e. Sid 33, Sid 34, Sid 29, Sid 35, Sid 10 and Sid 14. Quantification for siderophore production was estimated using above six isolates out of which Sid 10 showed maximum production i.e. (34.69%) so was selected for further studies. The bacterial isolate was subjected to check effect of different physicochemical parameters and showed highest siderophore production on King B media at a pH of 7 at 37°C under shaker conditions, other parameters showed effective production in media supplemented with maltose, glycerol and ammonium nitrate and at 0.05%, 0.45% and 0.1% concentrations respectively. Antibacterial activity was performed against clinical pathogens, ESBL and MBL cultures; high frequency of antibacterial activity was seen against (*Salmonella spp.*, *Shigella*, *E. coli*, ESBL 73b and MBL 234) by Sid 10. The culture was checked for IAA and exopolysaccharide production. The isolate was also checked for the effect of salinity as well as effect of heavy metal ions on siderophore production. Identification of the bacterial isolate was done using biochemical and 16S rRNA and was found to be *Pseudomonas aeruginosa*. The Isolate will be further subjected to molecule identification for determining siderophore nature and checked for field trials for enhancing the fertility of the soil and help the plantlets grow well by increasing the Fe content of the soil.

## **OPTIMIZATION OF INDOLE ACETIC ACID PRODUCED BY BACTERIUM ISOLATED FROM RHIZOSPHERIC REGION OF TRITICUM AESTIVUM (WHEAT PLANT)**

**Abhilasha Upadhyay, Radhika Birmole and  
K. Aruna**

*Department of Microbiology, Wilson College, Mumbai-07*

*E-mail: abhilasha2482@gmail.com*

Interactions between plants and microbes have been known for a very long time. The microbiota are an intimate part of plant ecosystem and study of these organisms will lead to better management of plant yields. Rhizosphere bacteria stimulate plant growth in multiple ways like fixing atmospheric nitrogen, synthesizing phytohormones, reducing toxic compounds or by suppressing pathogenic organisms. Indole acetic acid (IAA) is one of the most physiologically active auxins and is a major property of rhizosphere bacteria. Indole acetic acid is a product of L-tryptophan metabolism by several microorganisms including Plant Growth Promoting Rhizobacteria (PGPR). The present study focuses on isolation of indole acetic acid producing organisms from rhizospheric region of soil samples collected from wheat fields in North India. Out of the 16 isolates obtained after enrichment, 10 cultures were tested positive for IAA production using Salkowski's reagent, of which one potential isolate was used for further study. The isolate was also screened in vitro for other plant growth promoting characteristics like production of ammonia, hydrogen cyanide, siderophore, nitrogen fixation and phosphate solubilization. The bacterial isolate was tested and found to be positive for exopolysaccharide production. The culture was identified using Bergey's Manual of Determinative Microbiology 8<sup>th</sup> edition and confirmed using 16S rRNA technique. Study of media for maximum IAA production was carried out using different media and optimization of the physico-chemical conditions (pH, temperature, Optical density, carbon, nitrogen and tryptophan concentration). The findings of this work suggest the use of IAA producing bacteria as efficient bio fertilizer. These symbiotic relationships are in fact beneficial in global context because they act to promote plant growth.

## USING SYNTHETIC BIOLOGY TO INCREASE THE BIOFUEL PRODUCTION

Ritika Kamthan, Riya Sharma, Sakshi Khanna,  
Garima Mathur\*

*Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201307, Uttar Pradesh, India  
E-mails: kamthan.ritika247@gmail.com, sharmariya697@gmail.com, khannasakshi54@gmail.com, \*Corresponding author: garima.mathur@jiit.ac.in*

The global biofuel production has increased to approximately 137 billion liters in 2016 and is expected to provide nearly 27% of world's transport fuel by 2050. Biofuels is a substantial way to shift to low carbon fuel, replacing liquid fossil fuels, increased energy security, reduced oil price volatility and dependence on oil imports. The economics of production of various generations of biofuels includes production costs and total investment to meet the future demand. Synthetic biology is the catalyst needed to engineer algal or microbial cells which forms the basis for fourth generation biofuel production. Algal biofuels, having high lipid content of the algal cell would be a perfect candidate for high energy density transportation fuels. Ability to replace fossil fuel consumption rests on developing the technology to produce biofuel economically whilst reducing any negative environmental impacts. We aim to illustrate the current challenges and possibilities to sustainably increase the biomass production using genetic and metabolic engineering aspects of synthetic biology. It is concluded that fourth generation biofuel production has introduced the "cell factory" notion in this sphere, hence brought a paradigm shift in filling the gaping hole between research and reality.

**Keywords:** Synthetic biology, Biofuel, Microalgae, Economics, Sustainable

Glucomannan is considered to be a dietary fibre which is actually present in some plant species in the form of hemicelluloses component in the cell wall. Its structure consists of linear chain of mixed residues of  $\alpha$ -1, 4 linked D-mannose and D-glucose monomers arranged in blocks. The molecular weight of native GM lies between  $1 \times 10^4$ – $2 \times 10^6$  low molecular weight GM could be obtained by the de-polymerization. The average molecular weight of KGM is 500,000–2,000,000 varies with species, growing area, storage time and processing methods. The glucomannan from different sources varies in their mannose to glucose ratio: Konjac tubers have a molar ratio of 1.6:1 or 1.4:1 (ratio differ with konjac breeds), Orchid tubers and Scotch pine and have molar ratios of 3.6:1 and 2.1:1 respectively. Diversity of glucomannan also depends on degree of acetylation in GM chain. Acetylation degree values are 5 to 10% or of the every 19th sugar residue (attached randomly at C-6 position in KGM), actually responsible to facilitate dispersion and solubility by inhibiting the intra-molecular hydrogen bonds. This solubility function is attractive for multiple pharmaceutical applications. However increase in acetylation degree in GM slowed the gelation process. The intrinsic viscosity of KGM (solution was highest among the polysaccharides that facilitate swelling behavior and hence gel formation finding application in food industry. Gels have good stability, films, hydrogel, beads, micro and nanoparticles of Glucomannan may have potential usage for drug delivery systems without causing toxicity, treatment of chronic constipation, decreases serum cholesterol, increase insulin sensitivity, its supplement could play role in significant weight loss, carboxymethylated glucomannan improves the paper properties like burst index, dry tensile index, wet tensile index of paper. These diverse applications make Glucomannan a most sought after biomolecule.

## APPLICATION OF GLUCOMANNAN

Sonia Sharma and Neeraj Wadhwa

*Department of Biotechnology, Jaypee Institute of Information Technology, Noida, Uttar Pradesh, India  
\*Corresponding author: neeraj.wadhwa@jiit.ac.in*

Glucomannan (GM) a water-soluble polysaccharide possesses mannose residues which are extracted from tubers, bulbs, softwoods and roots of many plants.

## IRRADIATED CHITOSAN MEDIATED CHANGES ON GROWTH, BIOCHEMICAL PROCESSES AND MENTHOL PRODUCTION IN *MENTHA ARVENIS L.* IN NORTHERN HIMALAYAS. \*

<sup>1</sup>Mohammad Afaan Fazili, <sup>2</sup>Abdul Hamid Wani,  
<sup>3</sup>Tariq A. Wani

1. Department of Botany, Genetics, Cytogenetics and Plant Breeding Laboratory, Aligarh Muslim University, Aligarh, Uttar Pradesh 202002. 2. Professor, Department of Botany, Section of Mycology and Plant Pathology, University of Kashmir, Hazratbal, Srinagar 190006.<sup>3</sup>Associate Professor, Department of Botany, Government Degree College, Sopore, Baramullah, 193201.  
E-mail: afaanfazili@gmail.com

There is an urgent need of enhancing the content and yield of active constituents of medicinally important plants, keeping in view of their increasing demand worldwide. Application of radiation to degrade natural bioactive agents, such as chitosan and then using them as growth promoting substances is a novel emerging technology to explore full genetic potential of crops in terms of growth, yield, and quality. In the present study, chitosan, irradiated by Co- 60 gamma -rays was used to study the influence on the growth attributes, physiological and biochemical processes as well as menthol production in *Mentha arvensis L.* Of the various applied doses IC<sub>80</sub> (80 mg L<sup>-1</sup>) proved to be the optimal for almost all the parameters studied. Interestingly, the increase in menthol content was about 72.21% at 90 days after plantation at this treatment.

**Keywords:** Chitosan, gamma irradiation, menthol content, *Mentha arvensis L.*

## ECO-FRIENDLY WASTEWATER TREATMENT- USE OF A MICROALGAE Dr. Shailesh Solanki\*

Associate Professor, Department of Environment, Noida International University, Greater Noida

\*Corresponding author: shailesh.solanki@niu.edu.in

Earth have only 2.5% of fresh water for several consumptions, but due to human's negative practices towards water resources are contaminating and

resulting in rise of waste water which are further unusable for human's activities. Organic and inorganic substances which were released into the environment as a result of domestic, agricultural and industrial water activities lead to organic and inorganic pollution. Algae based technology are great option for treating waste water and also in revert as production of useful products with low cost and high efficiency. Micro algae bacteria use to provide good quality treated water by removing organic matters, BOD removal, nutrients (including nitrogen and phosphorus) and heavy metals responsible for the main cause of eutrophication in water bodies and some hazardous contaminants and pathogens. One of the other major contribution of algae as product is utilization of the CO<sub>2</sub> from the atmosphere during the treatment process and release of O<sub>2</sub> as output which result in fixing the global warming problems and avoiding use of chemicals to treat water impurities too. Although, the entire process is safe, environment cooperative, and reliable as per aspect. In single step, when algae are provided with untreated waste water, sunlight and CO<sub>2</sub>, green algae and microbes rapidly convert nutrients and organic carbon from waste water to renewable source. As the process achieve stringent nitrogen and phosphorus removal, BOD removal standard with no need for aeration or added chemicals, due to the oxygen produce during photosynthesis and the energy stored in the resulting biomass and enable positive waste water treatment turning waste water in clean source. Waste water treatment by microalgae is economical, green and environmental friendly process.

**Keywords:** Micro algae, Waste water, water treatment, nutrient removal, treatment systems, stages

## HANDMADE PAPER MAKING BY ECO-FRIENDLY PROCESSES: PRODUCTION OF ACID FREE, CHLORINE FREE AND AZO FREE PAPER

Arshia Bhat<sup>1</sup>, Bhavya Sirohi<sup>1</sup>, Avni Gupta<sup>1</sup>,  
Sukriti Mishra<sup>2</sup>, Vrinda Beria<sup>2</sup>, Rimjhim<sup>2</sup>,  
Ojasvi Verma<sup>2</sup>, Nishtha<sup>1</sup>, Jyoti Rani<sup>3</sup>, Aashna  
Gupta<sup>3</sup>, Jyoti Arora<sup>1\*</sup>, Mallika Pathak<sup>2</sup>,  
Bani Roy<sup>2</sup>, Amrita T. Sheikh<sup>2</sup> and Pratibha Jolly<sup>3</sup>

1. Department of Zoology, 2. Department of Chemistry, 3. Department of Physics, Miranda House, University of Delhi, Delhi -110007, India

\*Corresponding author: jyoti.arora@mirandahouse.ac.in

The production of paper and paper products ranks among the world's largest industries which puts a

pressure on environment as this process requires a lot of trees to be cut down. Cutting down of trees poses a serious problem to our wildlife and environment, so we need to make our approach eco-friendly. Synthetic dyes employed for imparting colour in handmade paper industry contain *azo* group which produces carcinogenic or harmful amines on reduction. These dyes have certain properties, such as, solubility, economical and exhibiting good light fastness. In this study, eco-friendly processes were used for making handmade paper. Organic dyes were extracted from a variety of plants sources (such as rhizomes of turmeric, *Curcuma longa*; leaves of indigo, *Indigofera tinctoria*, leaves of neem, *Azadirachta indica* etc.) using standardized procedures. Paper waste collected from different departments and administrative office of Miranda House was shredded and mixed with white cotton rags (waste from a textile mill) followed by pulp production in Hollander Beater. Pulp was treated with mordant (alum) to fix the colour of organic dye followed by sodium bicarbonate prior to addition of natural dyes thus making it acid-free. Paper sheets were then prepared from dyed pulp by spreading it onto the Univat, and Screw Press was used to remove excess water from the formed sheets. Paper sheets were also made using plant fibres (e.g. bamboo pulp) instead of cotton rags for providing greater tensile strength and rose petals, marigold petals were also used to provide a texture to the paper. Finally, sheets were dried under sun followed by calendering and cutting of sheets. Papers of varied shades and patterns were obtained, which were used for making different products such as envelopes, paper bags, folders, etc. The paper generated by implementing eco-friendly processes is acid-free, chlorine-free and *azo*-free, and also conforms to the stringent regulations imposed by regulating agencies world-wide.

PP69

ICABB-249

### **IRRITABLE BOWEL SYNDROME: A GUT- BRAIN AXIS DISORDER?**

**Akanksha Jain, Tanya Gupta and Garima Mathur\***

*Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201307, India*

*E-mails: akanksha21096@gmail.com, tanyagupta9697@gmail.com,*

*\*Corresponding author: garima.mathur@jiit.ac.in*

The past decade has seen a surge in the knowledge pool associated with extensive microbial community that resides within our intestine- the gut microbiota. The gut microbiota is subjected to variation due to diverse factors including type of delivery, diet,

antibiotic usage, exposure to chemicals, infection, lifestyle and stress. These factors led to dysbiosis and can have serious negative consequences on behavioral and mental health of an individual. This review summarized the possible role of gut microbiota in irritable bowel syndrome (IBS). IBS is the most common gastrointestinal disorder affecting people of all ages worldwide. The most affected risk groups include females, younger age children along with preceding GI infections. It is a prototypic condition, associated with gut- brain axis and bio-psychosocial etiology. Few clinical studies have investigated the role of dysbiosis in IBS. This condition can be improved using probiotics, which restores the normal microbial balance. This review summarizes the possible correlation of gut microbial composition and IBS.

**Keywords:** Gut-brain axis, Microbiota, Dysbiosis, Irritable bowel syndrome, Probiotics

PP70

ICABB-085

---

### **DHA SUPPLEMENTATION AND ALZHEIMER'S DISEASE**

**Advika Gupta, Sakshi Vashisth, Merin Lawrence,  
Ashmita Nautiyal, Garima Mathur\***

*Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201307, Uttar Pradesh, India*

*E-mails: advika.gupta27@gmail.com, sakshivashisth96@gmail.com,*

*merinlawrence95@gmail.com, nautiyalashmita96@gmail.com*

*\*Corresponding author: garima.mathur@jiit.ac.in*

---

Alzheimer's disease (AD) covers series of events ranging from initial pathological changes in the brain before onset of symptoms, leading to dementia due to accumulation of  $\alpha$ -amyloid protein in the brain. AD, a progressive neurodegenerative disorder, is the most common form of dementia contributing to 60-70% of the cases. WHO estimates nearly 44 million people worldwide either have AD or associated dementia. Global cost of Alzheimer care is estimated to be approximately \$605 billion, equivalent to 1% of world GDP. Currently, there is no cure or accepted preventive treatment for AD. Considering the growing elderly population and high prevalence of AD patients, there is an urgent need of a cost-effective treatment for prevention of AD. There are growing evidences supporting the role of omega-3 fatty acids such as Docosahexaenoic acid (DHA) in prevention and treatment of AD. It plays a major role in neuroprotection and reduced neuroinflammation. Evidences basically stem from importance of omega-3 fatty acids in early brain development and

maintenance of brain functions and vision. *In vivo* studies proved that supplementation of diet with omega-3 fatty acids results in reduced oxidative damage, improved neurotransmission and neuronal membrane excitability. Furthermore, the decreased levels of DHA in the phosphatidylcholine of neuronal plasma membranes of elderly patients are predictive of the development of AD. Possible mechanisms regulating the blood brain barrier transport of DHA in healthy population is still not currently deciphered. The purpose of this review is to investigate the possible role of nutrition in AD, with major emphasis on omega-3 fatty acids.

**Keywords:** Omega-3 fatty acids, Docosahexaenoic acid, Alzheimer's disease, Nutrition, Neurodegenerative disorder

PP71

ICABB-233

### MORPHINE AND ITS SIMILARS: OVERCOMING THE SIDE EFFECTS

\* Saumya Yadav<sup>1</sup>, Tanya Gupta<sup>1</sup>, Manisha Singh<sup>1</sup> and Rachana<sup>1</sup>

<sup>1</sup> Department of Biotechnology, JIIT Noida, Sector - 62,  
Noida 201309, India,

\*Presenting author: saumyaydv@gmail.com

Opioids, a term, that has been derived from opium and gained popularity as a means to manage pain, during mid 19<sup>th</sup> century, had morphine as a major ingredient. Opioid receptors identification in 1973 helped us to understand the pharmacological effects and side effects of these opioids in a better way. Major problem using morphine is its addiction many semi-synthetic and synthetic opioids are being synthesized to avoid addictive property of morphine and morphine like opioids. In 2016-17, various new opioid analgesics were discovered, BU08028 was one of them. It has antinociceptive and antiallodynic properties and also shows structurally similar to orvinol but has binding similarities with buprenorphine. It is used as a replacement for morphine (but no addiction) treats respiratory depression, caused by opioids. Other structure based opioids like: PZM21, NFEPP, and ST034307 etc. have also been designed. PZM21 is a biased agonist, which target the opioid receptors only in the parts, affected by pain while NFEPP is the agonist which best binds to the receptors in acidic environment i.e. pH sensitive. All of these compounds show minimal side effects shown by morphine such as: respiratory regression, sedation, constipation, addictiveness and opioid dependence. Though these

are still in trials, in future, they can be a great alternative to the conventional opioid drugs. The present study depicts the story of journey by opioids, till date.

**Keywords:** Morphine, Opioids, BU08028, PZM21, NFEPP, Addiction

PP72

ICABB-013

### ANTIUROLITHIATIC PROPERTIES OF *BRYOPHYLLUM PINNATUM*

Akanksha Krishnan, Priyadarshini\*

Department of Biotechnology, Jaypee Institute of Information Technology, Noida

\*Corresponding author: priyadarshini@jiit.ac.in

*Bryophyllum pinnatum* commonly known as Pattharcamma is a perennial herb which grows 3-5 feet in height and has tall hollow stems with fleshy dark green leaves that are distinctively scalloped and trimmed in red, and bell-like pendulous flowers. *Bryophyllum pinnatum* is widely distributed throughout India and cultivated in gardens as well as on the hills of North-Western India, Deccan and Bengal. In Ayurveda the leaves are bitter poisonous to insects, whereas in Unani the bark is bitter and poisonous, tonic, astringent to bowels and analgesic. The leaves of *Bryophyllum pinnatum* are rich in phytochemical compounds such as alkaloids, triterpenes, glycosides, flavonoids, cardenolides, steroids, bufadienolides and lipids. The plant is known as a PâcâGabheda in the Ayurvedic system, which means the "dissolver of stones". *Bryophyllum pinnatum* has been traditionally used in ethnomedicinal practices for the treatment of urinary calculi, the leaves are also known to possess wound healing, antimicrobial and anti-inflammatory activities. Urolithiasis is the formation and retention of urinary calculi. Traditionally leaf juice along with powder of 2-3 peppers was used to expel kidney stone. Since it is widely used in traditional medicine it is a vital component in many polyherbal formulations aimed to treat urolithiasis. Many studies have been performed to evaluate the efficacy of *Bryophyllum pinnatum*, showing in-vitro inhibitory activity on calcium oxalate crystallization. The effects of alcoholic and hydro-alcoholic extracts of *Bryophyllum pinnatum* leaves on the formation of urinary calculi (urolithiasis) in ethylene glycol induced lithiasis in rats showed inhibitory effect. The mechanism of action of leaf extract is not known but the antilithiatic effect of it may be through dissolution of preformed stones and/or prevention of the formation of CaOx crystals. Several

research reports also confirmed its antioxidant activity. The mechanism of action of the plant in urolithiasis is yet not known, therefore detailed study on it's action on the process of kidney stone formation will help clinicians to manage the disease successfully.

**Keywords:** *Bryophyllum pinnatum*; P $\beta$ c $\beta$ Gabherda; enthanomedicine; urinary calculi; urolithiasis.

PP73

ICABB-014

## MACROTYLOMA UNIFLORUM AND ITS MEDICINAL PROPERTIES

**Bhavya Lamba and Priyadarshini\***

Department of Biotechnology, Jaypee Institute of Information Technology, Noida

\*Corresponding author: priyadarshini@jiit.ac.in

*Macrotyloma uniflorum* (Horse gram) is a rich source of protein, minerals, and vitamins. It is an underutilized pulse crop grown in wide range of adverse climatic conditions. *Macrotyloma uniflorum* is an erect, sub-erect or trailing, densely hairy, annual climbing herb up to 60 cm tall with a perennial fibrous rhizome stem densely covered with whitish hairs. The tap root produces a branched root system with smooth, rounded nodules containing nitrogen fixing bacteria. Besides nutritional importance, horse gram was well recognized by the folk and traditional medicine as a potential therapeutic agent to treat kidney stones, urinary diseases, piles, common cold, throat infection, fever, intestinal diseases, diabetes etc. In recent years due to inception of nutraceutical concept and increasing health consciousness, the demand of functional food has increased leading to isolation and utilization of potential phytocompounds from legumes including horse gram as it decreases the risk of many diseases. Horse gram, previously known as *Dolichos biflorus* is an unexplored food legume, tolerant to drought salinity and heavy metal stresses. Horse gram is mainly grown in India, Africa, Australia, Burma, Malaysia, Mauritius, and West Indies. It is adapted to wide range of temperature regimes where other crops invariably fail to survive. In India, it is generally sown late in the rainy season by resource-poor farmers in marginal and drought-prone condition. One of the reasons of kidney stone disease is hypercalcemia and seeds of *M. uniflorum* contain more insoluble dietary fiber, which may help to reduce calcium in the urine. It combines with calcium in the intestines, so the calcium is excreted with the stool instead of through the kidneys. Insoluble fiber also speeds up movement of substances through the intestine, so there will be

less time for calcium to be absorbed. *Macrotyloma uniflorum* has the greatest potential for further utilization as a herbal medicine in urolithiasis.

**Keywords:** *Macrotyloma uniflorum*, nutraceutical, hypercalcemia, kidney stone.

PP74

ICABB-016

## MICRO-RNAs AS BIOMARKERS FOR DIAGNOSIS OF CANCER

**Aarushi Singh and Shalini Mani\***

Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sector 62, Noida, India

E-mails: aarugzb@gmail.com, \*Corresponding author: shalini.mani@jiit.ac.in

One of the major challenges in cancer research is to identify a stable biomarker, which can be routinely measured. During the past several years it has become clear that alterations in the expression of microRNA genes contribute to the pathogenesis of most, perhaps all, human malignancies. MicroRNAs (miRNAs) the small non-coding RNAs are involved in regulating a range of developmental and physiological processes such as gene expression, their dysregulation has been associated with development of diseases including cancer. These microRNAs can be used as non-invasive biomarkers for diagnosis of cancer and other infectious diseases like HIV and hepatitis. Human serum and other body fluids are rich sources of novel biomarkers. Physiological and pathological changes are reflected in the circulating miRNAs. Several preclinical and clinical trials have made their way to miRNA therapeutics. miRNA expression profiles have known to be related to tumor classification, diagnosis and disease progression. We summarize the knowledge of mechanism of miRNA in gene expression and the functions of these circulating microRNAs and also the analytical challenges in using miRNAs as biomarkers. Herein, we give an overview of recent researches related to this and the future of miRNAs as biomarkers for diagnosis.

**Keywords:** Cancer, Biomarker, miRNA, Diagnosis

## EFFECT OF INHIBITORS AND STIMULATORS IN NEPHROLITHIASIS

Fpratishthika Singh and Priyadarshini\*

*Department of Biotechnology, Jaypee Institute of Information Technology, Noida*

\*Corresponding author: priyadarshini@jiit.ac.in

Nephrolithiasis commonly known as kidney stone disease is a common disorder characterized by presence of stones in the urinary tract. Super saturation of stone-forming salts in urine is essential; however the abundance of the salts does not always result in stone formation. The mechanism of calcium oxalate stone formation includes nucleation, crystal growth, crystal aggregation and crystal retention. The stone formation does not occur in urine of healthy individuals despite frequent CaOx super saturation, because of the presence of several urinary inhibitory molecules. In healthy individuals there is equilibrium between stimulators and inhibitors of crystallization. Hence lack of inhibitors and/or an excess of stimulators which are also known as modulators play a vital role in the stone formation. Molecular modulators are basically of two types - stimulators and Inhibitors. Stimulators are the components that aids in the promotion of the stone formation, while inhibitors are the components that inhibit the process of stone formation. Most of the inhibitory molecules are macromolecules such as glycoproteins (Nephrocalcin, Tamm-Horsfall protein, Osteopontin, Urinary prothrombin fragment 1 and Bikunin) and glycosaminoglycans (Chondroitin Sulfate(CS), Heparan Sulfate (HS) and Hyaluronic acid). Many inorganic compounds (e.g. citrate, magnesium, pyrophosphate) are also known to inhibit the stone formation. Low urine volume, low urine pH, calcium, sodium oxalate and urate are known to promote stone formation. Calgranulin, Albumin, CD44, model peptides also acts as modulator in kidney stone formation. Albumin and Tamm-Horsfall protein act as both stimulator and inhibitor. In the process of kidney stone formation both stimulator and inhibitor are involved, imbalance between them leads to nephrolithiasis.

**Keywords:** Nephrolithiasis; supersaturation; osteopontin; glycosaminoglycans; sodiumoxalate; CaOx

## PHYTOTHERAPY: EMERGING TREND FOR ROS INDUCED UROLITHIASIS

Chetna Faujdar and Priyadarshini\*

*Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sector- 62, Noida-201307, Uttar Pradesh, India*

E-mails: malikchetna26@gmail.com, \*Corresponding author:

Email: priyadarshini@jiit.ac.in

Reactive oxygen species are by products of natural cellular metabolism which when produced in excess may trigger significant cellular damage and pathogenesis. Reactive oxygen species play a significant role in the formation of kidney stones also. Exposure of crystals to renal epithelial cells induces formation of reactive oxygen species which further support the formation of renal calculi. Calcium phosphate and calcium oxalate crystals activate the enzyme NADPH oxidase and leads to the production of reactive oxygen species. As a result other factors like phospholipase A2 and neutral sphingomyelinase are also activated which further increase the production of cyt-C in the mitochondria. All such factors eventually increase NF- $\kappa$ B, activated protein-1 and TGF- $\beta$  which ultimately leads to activation of caspases and damage to renal cells. Injury and damage to renal cells favors the crystal nucleation even at lower supersaturation level. Significant decrease in nitrite, alpha tocopherol, superoxide dismutase activity along with an increase in lipid peroxides has been observed in patients with urolithiasis. Some of the allopathic drugs which are used to treat such diseases have also been reported to produce free radicals and cause even more tissue damage. Applicability of antioxidants to mop up free radicals is of great therapeutic importance in such a situation. Variety of phytoconstituents have been listed in literature for their amazing antioxidant properties including alkaloids, tannins, isoflavanones, flavanoids, phytosterols, volatile and essential oils. Plant based antioxidants have been shown to suppress the activity of factors like phospholipase A2 and reduce the production of renal malondialdehyde and urinary 8-isoprostanate, oxidative damage and inflammation. Therefore different phytoconstituents can be used to scavenge free radicals and reduce reactive oxidative species which may ultimately inhibit different stages of urolithiasis.

**Keywords:** Reactive oxygen species, Malondialdehyde, Urolithiasis, Phytoconstituents, Caspases

## **PREPARATION OF OIL IN WATER NANOEMULSIONS OF DONEPEZIL FOR THE TREATMENT OF ALZHEIMER'S**

**Ishita Bhatnagar, Himanshu Sukhpal,  
Stuti Awasthi, Shivanika Shankar, Mayank Pareek,  
Attinderpal Kaur and Shweta Dang\***

*Novel Drug Delivery Systems Lab, Department of Biotechnology,  
Jaypee Institute of Information Technology, Sector 62, Noida,  
UP, 201309*

*E-mails: ishitabhatnagar02@gmail.com, himanshusukhpal@gmail.com,  
stutiawasthy@gmail.com, shivanikashankar@gmail.com,  
mayankrpareek5@gmail.com, attinderkahlon9@gmail.com,*

*\*Corresponding author: Shweta.dang@jiit.ac.in*

Alzheimer's disease is a chronic neurodegenerative disease, which is the cause of about 70% cases of dementia and lead to about 1.9 million deaths worldwide in 2015. The current medication for the same include NMDA receptor antagonists and acetylcholinesterase inhibitors. The aim of the present study is to develop and characterize nanoemulsions loaded with donepezil hydrochloride. Donepezil hydrochloride is an acetylcholinesterase inhibitor drug and has been widely used for the treatment of Alzheimer due to its longer plasma half life and minimal peripheral anticholinesterase activity. We hypothesize that preparing nanoemulsions of donepezil will improve its bioavailability to the brain. On the basis of solubility studies and transparency of the formulation different excipients were chosen. Labrasol was selected as the oil phase, 1% cetylpyridinium chloride as surfactant and glycerol as co-surfactant and the final formulation was prepared by homogenization followed by ultrasonication. The developed and optimized formulation showed average particle size of 62nm and polydispersity index of 0.21. The findings suggested that the developed nanoemulsion was in nano range and particles were homogenous in nature.

**Keywords:** Alzheimer's disease, Donepezil Hydrochloride, Drug Delivery, Nanotechnology, nanoemulsions.

## **EVIDENCE BASED VALIDATION OF HERBAL MEDICINES**

**Sonia Purswani, Bhavya Lamba, Sonakshi Madan,  
Shreya Deb, Ashwani Mathur\***

*Department of Biotechnology, Jaypee Institute of Information  
Technology, A-10, Sec-62, Noida-201307, Uttar Pradesh, India  
E-mails: soniapurswani37@gmail.com, lamba.bhavya08@gmail.com,  
madan.sona@gmail.com, shreyadeb0408@yahoo.in, \*Corresponding  
author: Email: ashwani.mathur@jiit.ac.in, Tel: +91-9810540276*

Growing demand of herbal medicines had seen a sudden surge throughout the world due to minimum side effect and there is a call for ensuring the quality and safety of herbal drugs in order to increase its acceptance in global market. This can be achieved by validation through several modern analytical techniques. Herbal medicines are medicines derived from plant extracts and are primarily consortia of phytocompounds of therapeutic importance. Validation of herbal medicines refers to the process of establishing evidence showing that the procedure, process or activity carried out in testing and production, maintains the required level of compliance at all stages. In other words, it refers to evaluating and verifying the presence of active phytocompounds in traditional medicine and testing its efficacy by clinical trials. Most of the developing nations are hub of such herbal products but lacking in pre-existing guidelines required for validating the final formulation. The outcome could be poor efficacy of many herbal formulation due to low or insignificant amount of active phytopharmaceutical ingredient. Therefore it is important to determine the phytochemical constituents of herbal products in order to ensure the reliability and reproducibility of pharmacological and clinical research to understand their bioactivities and possible side effects in order to enhance the quality of herbal medicines. The presentation will highlight existing methodologies for the research and development, manufacturing, and quality control of the herbal formulations in traditional medicines and strategic investigations of the therapeutic potentials of plants for developing stringent validation guidelines in developing countries.

**Keywords:** Validation, Phytocompounds, Herbal Medicines, Analytical Techniques

## **ANTIBODY DRUG CONJUGATE - A TARGETED APPROACH TO CANCER**

**Vani Shree<sup>1\*</sup>, Taru Jain<sup>1\*</sup> and Dr. Shweta Dang<sup>1\*</sup>**

*1.Jaypee Institute of Information Technology, Sector-62, Noida,  
201301*

*E-mails:vani26shree@gmail.com , tarujain28@gmail.com,*

*\*Corresponding author: shweta.a3@gmail.com*

Targeted therapies attack diseased cells while leaving healthy ones alone. Antibody Drug Conjugates (ADCs) is an innovative approach that could result in more effective treatments for cancer (or other diseases) with fewer toxic side effects than traditional chemotherapies. It consists of three components - Monoclonal antibody (mAb), linker and cytotoxic drug. Monoclonal antibodies are attached to cytotoxic drugs via stable linkers which attack on the targeted cancer cells. There are two marketed ADCs, Brentuximab vedotin and Trastuzumab emtansine. Brentuximab vedotin, Adcetris®, is composed of an anti-CD30 mAb connected with a cleavable peptide to the highly potent tubulin inhibitor MMAE. CD30 is a member of the tumour necrosis factor (TNF) family identified on Reed-Sternberg cells of classical Hodgkin lymphoma (HL). Binding of BV to the cell surface will lead to internalisation and lysosomal proteolytic cleavage of the linker releasing the MMAE. Trastuzumab emtansine (T-DM1), Kadcyla®, the antibody used is the well-known trastuzumab, a humanised IgG1 anti-HER-2 Ab linked with a stable non-cleavable linker to the maytansinoid DM1. There remain major hurdles that ADCs need to overcome: low delivery efficiency, target antigens expressed in normal tissues, the heterogeneity of target antigen expression in the tumour and more. The future of ADCs seems promising as the combination of new linker technologies and more powerful cytotoxic payloads leads to the emergence of more stable and effective ADCs.

**Keywords:** Monoclonal antibody, linker, cytotoxic drug, brentuximab vedotin and trastuzumab emtansine.

## **ANTIMICROBIAL AND CYTOTOXICITY EVALUATION OF POLYPHENON 60 AND CIPROFLOXACIN LOADED NANO EMULSION AGAINST UROPATHOGENIC STRAINS**

**Atinderpal Kaur<sup>1</sup>, Sonal Jain<sup>1</sup>, Reema Gabrani<sup>1</sup> and  
Shweta Dang<sup>1\*</sup>**

*1. Department of Biotechnology, Jaypee Institute of Information  
Technology, Sector 62, Noida, UP.*

*E-mails: atinderkahlon9@gmail.com , jain.sonal0208@gmail.com ,  
reema.gabrani@jiit.ac.in , \*Corresponding author:  
Shweta.dang@jiit.ac.in*

Ciprofloxacin is a broad spectrum synthetic antibiotic that can be used to treat many bacterial infections. But the rising antibiotic resistance has limited its use. Combining it with a natural antimicrobial compound (Polyphenon 60) can enhance the therapeutic value, as non-specific action of natural compounds does not allow bacteria to become resistant. The preliminary antibacterial activity of both Polyphenon 60 (P60) and ciprofloxacin (Cipro) was evaluated against *E. coli* and it was found that P60 when combined with Cipro showed synergistic behaviour with FIC index value of 0.424. With the aim to enhance stability and antibacterial action P60 and Cipro were encapsulated in a single nanoemulsion. In the present work, microtiter dish assay was performed to study the antibacterial potential of P60+Cipro loaded nanoemulsion(NE). The % cell viability was also studied via 3-(4,5-Dimethylthiazol-2-Yl)-2,5-Diphenyltetrazolium Bromide (MTT assay). Adhesion assay was performed to explore the mechanism of antibacterial action. In addition growth curve analysis of *E. coli* in the presence of NE was performed. To further understand the mechanism of action of NE against *E.coli*, Confocal Laser Scanning Microscopy was performed. The antibacterial study via microtiter dish assay showed that the nanoemulsion formulation could inhibit the growth more effectively (Avg. % inhibition ~89%) as compared to corresponding aqueous formulation (Avg. % inhibition ~67%) and placebo (Avg. % inhibition ~76%) at their MIC values. The cytotoxicity analysis also showed that the optimized formulation was nontoxic to Vero Cells with % viability (~78%) as compared to aqueous form (~61%) and placebo (~37%) at their respective MIC values. Moreover, it was observed that the Nanoemulsion was able to inhibit bacterial adhesion to mammalian cells as compared to aqueous formulation. Growth curve of *E. coli* indicated the

inhibitory action of NE at the 5th h of inoculation Confocal Laser Scanning Microscopy showed that the formulation exerts its antibacterial activity by disrupting the bacterial cell membrane. Hence, from the results it was concluded that the developed nanoemulsion loaded with P60 and curcumin had enhanced antibacterial activity and also active against resistant uropathogenic strains when compared with aqueous form of drugs and could further be explored for the treatment of urinary tract infection caused by *E.coli*.

**Keywords:** Adhesion assay; Biofilm; Ciprofloxacin; Confocal laser microscopy; Polyphenon 60; Uropathogens

PP81

ICABB-047

### TREATMENT OF ALZHEIMER: NATURAL REMEDIES VERSUS SYNTHETIC DRUGS

Sukriti Srivastava<sup>1</sup>, Atinderpal Kaur<sup>1</sup> and  
Shweta Dang<sup>1\*</sup>

<sup>1</sup>Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201307, Uttar Pradesh, India  
E-mail: Sukriti15gemini@gmail.com, Atinderkahlon9@gmail.com,

\*Corresponding author: shweta.dang@jiit.ac.in

Alzheimer's disease is a chronic neurodegenerative disease which starts slowly and gets worse over time causing dementia in 60% to 70% of cases. Treatments have been found to improve the symptoms temporarily but none that could reverse or stop the progression of the disease. Long-term usage of NSAIDs is associated with a reduced likelihood of developing AD. There is tentative evidence that caffeine may be protective. Five medications are currently used to treat the cognitive problems of AD: four are acetylcholinesterase inhibitors (tacrine, rivastigmine, galantamine and donepezil) and the other (memantine) is an NMDA receptor antagonist. Reduction in the activity of the cholinergic neurons is a well-known cause of Alzheimer's disease. Acetylcholinesterase inhibitors are employed to reduce the rate at which acetylcholine (ACh) is broken down, thereby increasing the concentration of ACh in the brain and combating the loss of ACh caused by the death of cholinergic neurons. Other than these synthetic drugs there are many natural remedies available with lesser side effects for treating Alzheimer. Drinking herbal teas which have egcg, hormone therapies with testosterone and DHEA may help but there are risks. Muira puama, a Brazilian plant may have acetylcholinesterase inhibiting activity.

Studies indicate that the alpha-tocopherol and tetrahydrocannabinol may slow cognitive decline. Scyllo-Inositol has been studied in recent years. A high concentration of silica in drinking water seems to protect against Alzheimer's disease, blue green algae have a cholinesterase inhibitor. Curcumin has effective antioxidant and anti-inflammatory activities and can control cognitive deficits, inflammation, amyloid accumulation and oxidative damage. Researches have shown that people on high DHA and Acetyl L-carnitine intake showed less beta-amyloid built up in brain. Carnosine and alpha lipoic acid are potent antioxidants and brain booster. Therapy with Vitamin B lowers homocysteine levels in the brain, preventing neuronal damage.

**Keywords:** Acetylcholinesterase inhibitor; Alzheimer; Dementia; Neurodegenerative; NSAIDS.

PP82

ICABB-067

### BIOMEDICAL AND PHARMACEUTICAL APPLICATIONS OF CHITOSAN BASED MATERIALS

Himanshu Mishra, Sakshi Vashisth,  
Siddhant Khandelwal and Garima Mathur\*

Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201307, Uttar Pradesh, India  
Emails: himanshumishra@gmail.com, sakshivashisth96@gmail.com, siddhant.jaypee@gmail.com, \*Corresponding author: garima.mathur@jiit.ac.in

Chitosan is biopolymer derived from seafood waste and several strains of fungus including *Mucor rouxii*, *Absidia coerulea*, *Rhizopus oryzae*, *Penicillium funiculosum*. Commercially it is derived as deacetylated form of chitin. Excellent physicochemical properties conferred by this polymer such as biocompatibility, biodegradability, bioactivity, bioresorptivity, non-toxicity and good adsorption properties suggest the suitability of this polymer as biomaterial. Chitosan appeals a great deal of industrial consideration in contrast to synthetic polymers due to some of its fundamental properties including degree of deacetylation, molecular weight, bonding nature, antifungal, antibacterial properties and permeability to oxygen. Chitosan based matrices and gels are extensively used in biomedical field as scaffold material and adhesive based chitosan for wound healing. Chitosan-based nanoparticles and nanogels are promising as a delivery tool for tumor therapy and as various diagnostic purposes. Modification of chitosan by blending is an attractive method for

improving its properties and diversifies its applications. Recently, the potential of chitosan as additive for modification and improvement of existing dental material has been investigated, where it has been successfully utilized in modifications of dentifrices, enamel repair, adhesion and dentine bonding, as dental restorative materials and stem-based regenerative therapeutics. This abstract highlights the application of chitosan based materials in biomedical and pharmaceutical field.

**Keywords:** Chitosan, Biopolymer, Tissue engineering, Dental implant, Drug delivery

PP83

ICABB-087

### THERAPEUTIC POTENTIAL OF CANNABIS

<sup>1</sup>Shivanika Shankar,<sup>1</sup>Ishita Bhatnagar,<sup>1</sup>Stuti Awasthi,<sup>1</sup>Mayank Pareek  
<sup>1</sup>Kuldeep Nigam,<sup>1</sup>Atinderpal Kaur,<sup>1</sup>Shweta Dang\*

<sup>1</sup>Department of Biotechnology, Jaypee Institute of Information Technology, Sector 62, Noida, UP, 201309  
E-mails: shivanikashankar@gmail.com, ishitabhatnagar02@gmail.com, stutiaawasthy@gmail.com, mayankrpareek5@gmail.com, kuldeepnigam1604@gmail.com, atinderkahlon9@gmail.com, \*Corresponding author: Shweta.dang@jiit.ac.in

**Background:** Cannabis term is used for plants *Cannabis sativa*, *Cannabis indica*, and *Cannabis ruderalis*. It induces mental and physical effects of psychoactive, mildly euphoric, relaxing intoxication or "high" and change in perception. Cannabis also induces an increase in heart rate, a lowering of blood pressure due to vasodilatation. Other effects of cannabis are appetite stimulation, dry mouth, and dizziness etc. However, there is an up rise in the use of cannabis among the young population as an alternate of synthetic drugs, to cure symptoms of many disorders like Parkinson's disease, multiple sclerosis, and Alzheimer's disease.

**Aim:** To review and highlight the recent mechanism of action, effects on psychomotor and cognitive performance and health risk of cannabis consumption.

**Result and Conclusion:** The *cannabis* plant (*Cannabis sativa*) contains many compounds (cannabinoids), but (delta) 9 -tetrahydrocannabinol (THC) is the main psychoactive ingredient. THC breaks down to produce cannabinol and was identified—along with cannabidiol (CBD, the main non-psychoactive component). THC is concentrated in the flowering head of the female plant and selective

growing in the past 5–10 years has substantially increased THC content from 1–3% to 6–13% and above. Endocannabinoids are important for regulation of pleasure, body movement, memory, thinking, concentration, appetite, and pain. It is also important for brain development and directs neural cell survival, proliferation, and differentiation. Unlike many active molecules which are stored, these are produced "on demand" from membranous fatty-acid precursors. The release of active endocannabinoids is due to cellular stimulations like neuronal depolarization. These endocannabinoids bind to cannabinoid receptors (CB1 and CB2). CB1 endocannabinoid system regulates synaptic neurotransmission of excitatory and inhibitory circuits. CB2 receptors regulate the control of "inflammatory" pain. Some patients with symptoms of neuropathic pain, insomnia, seizures of various disorders like Parkinson's disease, multiple sclerosis and Alzheimer's lack these endocannabinoids. Hence, on cannabis intake THC and CBD binds to cannabinoid receptors and gives relief from the above-mentioned symptoms.

**Keywords:** Cannabis; Endocannabinoid; Cannabinoid receptors

PP84

ICABB-091

### GUT MICROBIOTA AND METABOLIC SYNDROME

Ishika Verma, Rika Semalty, Garima Mathur\*

Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201307, Uttar Pradesh, India  
E-mails: ishikaverma6504@gmail.com, rikasemalty@gmail.com, \*Corresponding author: garima.mathur@jiit.ac.in

Metabolic Syndrome (MetS) is a complex condition involving hypertension, central obesity, hyperglycemia and hyperlipidemia, primarily arising due to defects in metabolic processes in the body. It is reported to be associated with increased risk of cardiovascular disease and type 2 diabetes, resulting in morbidity and mortality. MetS manifests due to environmental, behavioral, physiological and genetical factors. The prevalence of metabolic syndrome is increasing worldwide, with adults comprising 20–25%. Sedentary lifestyle, high calorie intake and increased life expectancy are several factors responsible for the increase in severity and occurrence of MetS. Since MetS is a cluster of complex conditions, it is challenging to treat it with pharmaceutical drugs. Moreover, these drugs have limited effectiveness and also have serious side-effects in the long run. Recent studies have shown

that maintaining a healthy gut microbiota can help in treatment of MetS. Gut Microbiota are microorganisms, inhabiting the gut, which are acquired during birth and are known to modulate host physiology and metabolism. Gut microbiota composition and function is strongly influenced by diet. Recently, studies have shown that unbalanced gut microbiota composition and its activity affect fat accumulation and associated metabolic processes. Therefore, gut microbiota may serve as an effective therapeutic target for prevention and management of MetS.

**Keywords:** Metabolic syndrome, Gut microbiota, Cardiovascular disease, Type 2 diabetes, Obesity

PP85

ICABB-094

## CURRENT CANCER VACCINES

**Sidhi Mishra, Simrat Kaur, Utsav Bhardwaj and Priyadarshini\***

*Department of Biotechnology, Jaypee Institute of Information Technology, Noida*

\*Corresponding author: priyadarshini@jiit.ac.in

With cancer being one of the leading causes of deaths, there's an urgent need of therapies that kill cancer cells and spare the host's normal cells. Therapeutic cancer vaccines specifically target cancer cells and leave the normal cells intact and enhance the response. There is minimal or no side effects of therapeutic vaccines which makes them safe to use. Thus, these vaccines may be utilized to inhibit further growth of advanced cancers that are refractory to other therapies. These vaccines are different from prophylactic vaccine as these are used to cure the disease and prevent from any reoccurrence by inducing the formation of memory cells in the body. Mainly there are three types of therapeutic cancer vaccine and most of the vaccines are produced either based on these types or with their combinations: - 1) Tumor cell vaccine- This type of vaccine uses the tumor cells either from the patient itself or from well-established cell lines. 2) Protein/peptide-based vaccine- these tumors associated antigen are weak in eliciting an immune response so they are combined with adjuvants or an immune modulator. 3) Genetic vaccine- a new strategy to deliver antigens or tumor associated antigens/fragments in vivo by plasmid, viral vector, DNA vectors, etc. These are further divided into three types mainly DNA vaccine, RNA vaccine, viral-based vaccine. Many therapeutic cancer vaccines are in phase trials whereas some have cleared all the Phase trials and are used in hospitals to cure the related diseases.

**Keywords:** Cancer, Vaccine, Tumor, Antigen, Prophylactic

PP86

ICABB-110

## ASSESSMENT OF VITAMIN D IN TYPE 2 DIABETIC PATIENTS

**Rizwana Parveen<sup>1</sup>, Nidhi. B. Agarwal<sup>2\*</sup> and Prem Kapur<sup>3</sup>**

*1. Department of Pharmaceutical Medicine, School of Pharmaceutical Education and Research, Jamia Hamdard, Hamdard Nagar, New Delhi 110062, India 2\*. Centre for Translational & Clinical Research, School of Chemical and Life Sciences, Jamia Hamdard, Hamdard Nagar, New Delhi 110062, India 3.Hamdard Institute of Medical Sciences and Research, Jamia Hamdard, Hamdard Nagar, New Delhi 110062, India*

The global prevalence of diabetes has substantially increased over time. Evidences suggest that 90% cases of type 2 diabetes (T2DM) could be attributed to modifiable habits. On the basis of evidence from animal and human studies, vitamin D (VD) has emerged as a potential risk modifier for T2DM. Thus, based on the previous data, the aim of the study was to assess serum VD levels in T2DM patients. A case-control study was conducted, including 44 subjects in each group. Blood samples for estimation of VD were collected. Serum VD levels were found to be significantly lower in diabetics as compared to the controls. Additionally, the overall prevalence of hypovitaminosis D among T2DM participants was higher than in controls. Thus, the present study concludes that T2DM patients are at higher risk of hypovitaminosis D. Therefore, supplementation of VD in T2DM patients is suggested to prevent further behavioral complications.

PP87

ICABB-116

## MEDIA OPTIMIZATION FOR BACTERIOCIN PRODUCTION

**Saumya Singh, Mehak Aggarwal, Niharika Tiwary, Sahil Srivastava, Manu Choudhary and Reema Gabrani\***

*Biotechnology Department, Jaypee Institute of Information Technology, A-10, Sector 62, Noida*

\*Corresponding author: reema.gabrani@jiit.ac.in

Bacteriocins are basically known as peptides produced by mostly all the bacteria to kill or inhibit the growth of similar or closely related bacterial strains. They are structurally, functionally, and ecologically diverse. In

order to assess their application as narrow-spectrum antibiotics they are being tested continuously. Bacteriocins are categorized in several ways, including producing strain, common resistance mechanisms, and mechanism of killing. There are several large categories of bacteriocin which are only phenomenologically related. These include the bacteriocins from gram-negative bacteria, the colicins, the microcins, and the bacteriocins from Archaea. Recently the spotlight has been on bacteriocins for their role as alternatives for antibiotics against the antibiotic resistant strains of pathogens. But the production of bacteriocins has been a major obstacle which makes further researches related to bacteriocins difficult to pursue. Since it is produced by bacteria, the extraction mechanisms are quite costly and the amount obtained is usually not enough. Various techniques are being constantly implored to overcome this issue. One such solution is optimization of media to increase the production of bacteriocins. The media used for optimization is MRS (Man, Rogosa and Sharpe), the strain used for bacteriocin production is *Bacillus subtilis* (GAS101). *Escherichia coli* and *Staphylococcus epidermidis* are the strains against which the optimization is checked. The optimization is carried out by complimenting the MRS media with certain components like carbohydrates, protein sources, inorganic salts and other such compounds in different concentrations either individually or in a certain combination in a manner that the yield of bacteriocin is increased. The poster discusses the various components that could be used for media optimization and techniques used for the same.

**Keywords:** Bacteriocin, optimization, media, strains, MRS

PP88

ICABB-120

---

### METHOD VALIDATION OF CDC BIOASSAY FOR ASSURING EFFICACY OF ANTI- CD20 MONOCLONAL ANTIBODY BIOSIMILARS

Utpreksha Vaish<sup>1</sup>, Nripendra N. Mishra<sup>1</sup>,  
Richi V. Mahajan<sup>1</sup>and Anu Prakash<sup>1</sup>,  
Subhash Chand\*#, Surinder Singh\*

1. National Institute of Biologicals, (Ministry of Health and Family Welfare) Sector-62, Institutional Area, Noida, Uttar Pradesh 201309  
\*Corresponding author

---

Anti-CD20 monoclonal antibodies represent one of the important advances in mAb therapy which target malignant and auto-immune B-lymphocytes and thus

indicated for the treatment of non-Hodgkin lymphomas, chronic lymphocytic leukemia and autoimmune diseases such as rheumatoid arthritis. Besides the first therapeutic anti CD20 mAb i.e. Rituximab, a number of biosimilars have been launched or in the pipeline which requires regulatory approval. Bioassay, a critical attribute, is the estimation of potency of a test agent by comparing its response to a known standard and is employed in assuring the quality of Bio-therapeutics. The objective of this study was to validate and establish the assay suitability criteria and sample acceptance criteria for complement dependent cytotoxicity (CDC) bioassay for anti- CD20 biosimilars. A validated bioassay over the six simulated potencies was found specific for anti-CD20 Biosimilar. The %GCV for precision (repeatability and intermediate precision) and accuracy was less than 20% over more than 40 individual performances using internal reference standard (IRS) and test samples. System suitability criteria was determined from the result of performances are Slope from 4PL fit > 1.3, EC50 ( $\mu$ g/ml) range of 0.08 - 0.32, Fold Response of > 5, A/D (Max. /min.) value of > 3. Sample acceptance criteria were determined by factors such as Test for regression; 95 % (F-test), Test for Linearity; 95% (F-test) and Test for parallelism; 95% (F-test) as compared to the IRS with 95% confidence interval and estimated relative potency of 80-120% of the IRS. The reported method is the first of its kind wherein a detailed set of assay suitability criteria and sample acceptance criteria have been established to aid to the regulatory bodies and to assure the quality of anti-CD20 "Biosimilars" which are targeting the market.

PP89

ICABB-126

---

### MOLECULAR CHARACTERIZATION OF GLYCOPROTEIN D (GD) OF BOVINE HERPESVIRUS-1 AS A POTENTIAL DIAGNOSTIC ANTIGEN

Barkha Ratta, Ajay Kumar, Meeta Saxena and Swagatika Priyadarsini\*

Division of Biochemistry, IVRI, Izatnagar-243122, India.  
E-mails: 1ajayivri@gmail.com, 2visheshmeeta@gmail.com,  
3drswagatika.vet@gmail.com,\*Corresponding author:  
barkhaivri@gmail.com

---

Bovine herpesvirus-1 (BoHV-1) causes infectious bovine rhinotrachetitis and Pustular Vulvovaginitis in cattle. BoHV-1 causes significant reduction in milk yield leading to huge economic loss to dairy industry. Glycoproteins gB, gC and gD of BoHV-1 are highly

immunogenic and induces protective immunity in cattle. One of the hallmarks of herpesviruses is the ability to become latent in the host and after reactivation of latent infection, bulls can shed virus in semen. Glycoprotein D (gD) is present in the viral envelope, involved in virus penetration and has been considered the major target in vaccine development and can be exploited for serological diagnosis of BoHV-1. In the present study, gD encoding gene was expressed in prokaryotic cell system to be used for diagnostic purpose. Viral genomic DNA extracted from BoHV-1 grown on Madin-Darby Bovine Kidney (MDBK) cell monolayer was used as a template for PCR amplification of gD gene (1255bp). Gel purified gD gene was cloned into T/A cloning vector ptz57R/T and further subcloned into pET-32a, prokaryotic expression vector. Recombinant plasmids were screened by restriction enzyme (RE) digestion and PCR for gD insert. For the expression of gD protein, the pET32a recombinant vector was transformed in BL21 strain of *E.coli* competent cells using IPTG as inducer. Expression of recombinant gD protein was seen in SDS-PAGE at 4 hours of induction and further confirmed with Ni-Probe HRPO conjugate. This expressed gD protein can further be exploited for the development of a field-based diagnostic tool for easy detection of *BoHV-1* infection.

**Keywords:** Bovine herpesvirus-1 (BoHV-1), Madin-Darby Bovine Kidney (MDBK), SDSPAGE

PP90

ICABB-128

---

### EXPRESSION OF METHIONINE SULFOXIDE REDUCTASE A: PROTEIN REPAIR ENZYME IN PROKARYOTIC SYSTEM

Indhu M.S, Shruthi N, Upmanyu V and Bhure S.K.

Division of Animal Biochemistry, ICAR-IVRI, Izatnagar, Bareilly-243122 Division of Biological standardization, ICAR-IVRI, Bareilly-243122  
E-mails: indhuvet@gmail.com, shruthi936@rediff.com, sdbhure@rediffmail.com.

---

Oxygen plays a vital role for survival of all aerobic organisms at the same time it is the source of reactive oxygen species (ROS). The level of ROS may be increase due to imbalance in free radical production and antioxidant defense system. ROS induce oxidative damage to lipids, proteins and nucleic acids. Cells protect against oxidative damage by (1) destroying ROS before damage can occur through antioxidant enzymes, (2) repairing the damage to the

macromolecules after it occurs. Recently, considerable interest directed towards repair of protein damage due to oxidation. The methionine sulfoxide reductase A (MsrA) is one of the enzyme that restore the protein damage by catalyzing the reduction of free and protein bound oxidized methionine to methionine using thioredoxin. Under the study, we expressed MsrA in prokaryotic system. The msrA gene was amplified from buffalo testis, subsequently cloned, sequenced and expressed in pET-28c (+) vector. The recombinant protein expression was carried out in T7 Express lysY cells using 1mM IPTG induction at 37°C for 4h. The expressed MsrA was purified under denaturing condition and dialyzed against the buffer containing 25mM Tris-Cl, 10mM MgCl<sub>2</sub>, and 30mM KCl (pH 8). The expressed recombinant MsrA was confirmed by Western blot using His probe. The hyperimmune serum had been raised in chicken against the recombinant MsrA and was used to localize the MsrA in testis/epididymis. Since buffalo sperms are more prone to oxidative stress during cryopreservation, the further studies are aimed to evaluate the effect of supplementation of MsrA on the sperm functionality of frozen-thawed semen.

**Keywords:** ROS, Protein repair, MsrA, Cryodamage, Sperm

PP91

ICABB-130

---

### MEDICINAL PLANTS FOR PREVENTION AND TREATMENT OF PARKINSON'S DISEASE

Rika Semalty, Ishika Verma and Garima Mathur\*

Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201307, Uttar Pradesh, India  
E-mails: rikasemalty@gmail.com, ishikaverma6504@gmail.com,  
\*Corresponding author: garima.mathur@jiit.ac.in

---

Worldwide population growth has been associated with subsequent rise in the aged people afflicted with neurodegenerative disorders. Neurodegenerative diseases represent an enormous burden in terms of human suffering and economic cost associated with the treatment. Parkinson's disease (PD), an age related neurodegenerative disorder, ranked as the second most common disorder with more than 10 million people affected worldwide. Classic symptoms of PD includes bradykinesia, distinctive shuffling walk known as Parkinsonian gait, muscle stiffness, tremors, depression and dementia. The pathogenesis of PD is not well explored. Levodopa remains currently the most potent drug for slowing down the PD

progression, but includes lots of side effects and wearing off effect. Extensive research has been performed to screen the role of naturally isolated compounds for their antioxidant and neuroprotective potential. The approach can be extended to the development of novel therapeutic targets for PD therapy. The natural occurrence of anti-parkinsonian drug levodopa in plants such as Mucuna pruriens and Vicia faba, dopamine agonist activity in Banisteria caapi and anti-cholinergics in Datura stramonium have been well documented. Traditional Chinese medicine system based on Ginkgo biloba is popular in many Asian countries. Recently, small bioactive compounds have been isolated from Cannabis sativa for cannabinoid-based PD therapy has been investigated. The current review summarizes the potential of existing medicinal plants, their ingredients and formulations in treatment and prevention of PD.

**Keywords:** Parkinson disease, Levodopa, Neurodegenerative disorder, Antioxidant, Neuroprotection

PP92

ICABB-152

### EXPLORING MECHANISM OF ACTION OF OPIOIDS

Vatsal Jain<sup>1</sup>, Vandana Joshi<sup>1</sup>, Yashi Singh<sup>1</sup>, Vinakay Agarwal<sup>1</sup>, Manisha Singh<sup>1</sup> and Rachana<sup>1\*</sup>

<sup>1</sup> Department of Biotechnology, JIIT Noida, Sector - 62, Noida 201309, India

\* Corresponding author: rachana.dr@gmail.com

Opioids are substances that are used for treating moderate to acute and chronic pain. These can be either natural or synthetic in nature. Peripheral and central nervous system and the gastrointestinal tract are some sites where most of the opioid receptors are found and these receptors are the site for opioid binding. Action of opioids on opioid receptors increases the threshold to the pain, leading to the decrease in perception of pain. Pharmacologists understand that due to allelic variations patients differ in their response to specific opioids and other opioid analgesics. This lead to several trials of different opioids and other drugs on patients before finding an agent that gives effective analgesic effect. Opioids may act on Non Opioid receptors as well but then they act as antagonists, agonists or partial agonists. Opioid binds to 7 transmembrane G-protein linked receptors to cause efflux of potassium ions and influx of calcium ions, this lead to cellular hyperpolarization. The effect on  $\mu$  receptor is considered the most important effect with

its activation directly linked on both analgesics and other effects. Most opioid antagonists or analgesics bind to MOR ( $\mu$  Opioid Receptors) in the peripheral and central nervous system in an agonist manner to provide analgesia. The history, structure and effects of opioids binding to different receptors:  $\mu$ ,  $\alpha$  and  $\delta$  opioid receptors will be discussed in this study.

**Keywords:** Opioids, Pain,  $\mu$  receptors, Analgesics

PP93

ICABB-157

### SCREENING OF CAROTENOID PRODUCING BACTERIA FROM VARIOUS SOURCES

Darshana Raut<sup>1</sup> and K. Aruna<sup>1</sup>

Department of Microbiology, Wilson College, Mumbai- 400007  
E-mails: rautdarshana9@gmail.com

Carotenoids are a group of bioactive compounds and are responsible for bright yellow, orange, red pigments of various plants, microorganisms and animals. In this study, microorganisms from different environment capable of producing carotenoids were isolated. 65 samples were collected from different sources such as soil in and around Mumbai, floral petals, pond water and agro waste. 84 cultures of orange and yellow colour were selected. The colony characteristics of each organism were determined. All the isolates were further tested for production of carotenoids using UV-Vis spectrophotometer. It revealed that out of 84 isolates, 18 cultures showed the presence of three peaks (340nm, 470nm and 540nm) which is a characteristic feature of carotenoids. The presence of carotenoids was also further qualitatively confirmed by appearance of blue ring on addition of 85% sulphuric acid in the extract. The three isolates were chosen which showed maximum carotenoid production. The organisms were subjected to 16s rRNA sequencing and were identified to be *Microbacterium arborescens* and *Microbacterium plaudicola*. Among these isolates, *Microbacterium arborescens* AruD 915 showed maximum production and was selected for further studies.

## RESISTANCE TO 'WONDER DRUGS'- ANTIBIOTICS: A REVIEW

Srishti Mitta<sup>1</sup>, Vanshika Singh<sup>1</sup> and  
Dr. Shalini Mani<sup>1\*</sup>

1. Department of Biotechnology, Jaypee Institute of Information Technology, Noida, UP- 201309 India

\*Corresponding author: shalini.mani@jiit.ac.in

Antibiotics have been a major source for combating disease since its discovery in the 20th century. But with the cure also came the resistance against it and now it has become a major concern for the world. We aim to summarize the introduction and analysis of some life-threatening pathogens like *Staphylococcus aureus*, *Pseudomonas aeruginosa* and *Neisseria gonorrhoea*. Here we also highlight various antibiotics against which these micro-organisms have developed resistance and their detailed mechanism of action. As per literature, there has been an emergence of a new strain VRSA(Vancomycin resistant *S.aureus*) from an already prevailing strain MRSA(Methicillin resistant *S. aureus*) which carries transposon Tn1546, acquired from *Enterococcus faecalis*, a vancomycin resistant strain known to alter cell wall structure and metabolism. In the case of *P.aeruginosa*, antimicrobial susceptibility pattern showed that Carbapenems and Aminoglycosides were the most effective classes of drugs but on the other side it shows resistance against Cefoperazone+Sulbactam, piperacillin/tazobactam and cefipime. Additionally, *N.gonorrhoea* which causes gonorrhoea, the most common sexually transmitted infection(STI) has recently accelerated its resistance against wide spectrum cephalosporin. But recently, there has been extensive research going on as a result of which 3 new drugs which are in the various stages of their clinical development have been designed and being studied. By reviewing the available literature, it has been found that various next-generation techniques like CRISPR can be used to sensitize bacteria to antibiotics and further kill the resistant strains.

**Keywords:** antibiotics resistance, *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Neisseria gonorrhoea*

## TARGETING OF NATURAL COMPOUNDS AS POTENTIAL ANTICANCER AGENTS AGAINST G-QUADRUPLEX STRUCTURE

Neha Arora and Manpreet Kaur Paintal

Guru Nanak Girls College, Model Town, (Affiliated to Punjab University), Ludhiana Punjab Pin 141002

E-mail: pearl4aug@yahoo.com, nehaa01994@gmail.com

G-quadruplexes are four-stranded DNA secondary structures that deviate from the normal duplex form of DNA are over-represented in gene promoter region and are viewed as emerging therapeutic targets in oncology, as transcriptional repression of oncogenes through stabilization of these structures provide a novel platform for anticancer strategy. Present study is a computational based docking method to evaluate the role of naturally occurring compounds targeted against G-quadruplex using insilico approach. The sequence of target chimeric G-quadruplex for docking was selected from Protein Data Bank. Drug library was generated for structural analogues of for three classes of natural compounds, namely, Curcumins, Isoflavaones and Distamycin A using ZINC, a free database of commercially available potential drug like candidates for virtual screening. Docking calculations were performed using AutoDock suite of programs. The results were evaluated primarily on the basis of minimum binding energy, hydrogen bond formation, hydrophobic interactions and inhibition constants. Maximum human recommended dose for the screened compounds was evaluated through online insilico toxicity screening tool LAZAR and the values were correlated with the inhibition constant (Ki) evaluated from AUTODOCK. The interactions between the receptor and ligand were analysed through LIGPLOT. The main aim of this study was to screen a potent natural potential anticancerous compounds against G-quadruplex under study. Maximum human recommended dose for the screened compounds was evaluated through online insilico toxicity screening tool LAZAR and the values were correlated with the inhibition constant(ki) evaluated from the AutoDock. The interaction between the receptor and the ligand were ananlysed LIGPLOT. Structural analogs of Isoflavonones and Curcumins have shown comparable free binding energy consistent with their inhibition constant and ideal candidates for oral drug delivery system. These results can be further evaluated and validated through molecular stimulation and pharmacokinetic studies.

**Keywords:** G-quadruplex, Curcumin, Isoflavanones, Distamycin, AutoDock, ZINC database, LAZAR.

PP96

ICABB-182

## RECENT APPLICATIONS OF BACTERIAL CELLULOSE AND ITS COMPOSITES

**Shubham Rajput<sup>1</sup>, Manya Singh<sup>1</sup> and Garima Mathur<sup>1\*</sup>**

1. Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201307, Uttar Pradesh, India  
E-mails: sr9999146261@gmail.com, \*Corresponding author: garima.mathur@jiit.ac.in

Bacterial cellulose (BC) is a biodegradable polysaccharide of bacterial origin, mainly produced by *Acetobacter sp.*, gram negative bacteria. The unique physio-chemical properties possessed by BC over plant cellulose are high water holding capacity, high degree of crystallinity, in situ foldability and moulding, ultrafine fibre network, improved tensile properties, biocompatible, ability to be shaped into three-dimensional (3D) structures during synthesis. Intense researches on BC mainly focus on biosynthetic process to achieve high cellulose production at low-cost. Due to excellent structural and physicochemical properties, BC and its composites finds vast application in food, cosmetics, pharmaceutical, pulp and paper industry, environmental and biomedical fields. BC is extensively used in food industry as a traditional dessert (*nata de coco*), vegetarian meat, food additive, nutraceutical and as preservative membrane in food wrapping. Potential applications of BC have been extended to cosmetic sector as facial mask, facial scrub, cleansing formulations and contact lenses. Biomedical and pharmaceutical applications of BC include targeted drug delivery, dental implants and prosthetic dentistry, scaffolds in tissue engineering, artificial blood vessels, vascular grafts and wound healing. Studies have reported the use of BC as a binding agent in paper industry to add strength and durability to the pulp. The present review summarizes the recent applications of BC and its composites in the various industrial and biomedical fields.

**Keywords:** Bacterial cellulose, Composites, Tissue engineering, *Acetobacter*, Nutraceutical, Prosthetic dentistry

PP97

ICABB-198

## ADVANCEMENT IN THE OVARY FREEZING TECHNIQUE FOR THE TREATMENT OF OVARIAN DISEASES

**Maria Ishaque<sup>1</sup>, Amita Tiwari<sup>1</sup>, Manisha Singh<sup>1\*</sup>, and Rachana<sup>1</sup>**

1. Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201307, Uttar Pradesh, India

Cryopreservative techniques have been very useful for the women/couple facing fertility problems. These techniques are helpful for the patients undergoing gonadotrophic treatment for cancer, facing endometriosis, bone marrow transplantation, transgender operation and some other autoimmune diseases etc. Various cryopreservation options available under these techniques are: embryo freezing, egg freezing and ovary auto-transplantation etc. Ovary freezing is now being popular among the people as it has led to increase in higher live births. In this technique ovarian tissues are extracted from the cortical portion and then preserved. After the recovery of the patient these tissues are transplanted back into the patient's body. There are two standard methods for cryopreservation of human ovary and embryo (a) slow freezing and (b) vitrification. Both the methods carry very low risk for intracellular crystallization. Vitrification has a little risk of cellular toxicity and osmotic trauma. Earlier slow freezing was reported to be superior for preserving ovarian tissue. But now the vitrification techniques are improved and have got the good results. However, experimental results are still conflicted as there is no significant difference in the follicles after thawing/warming (72.7% in slow freezing and 66.7% in vitrification). More researches and experiments are being performed to get more improved techniques. The present study describes basics and the advancement in the ovary freezing technique in detail.

**Keywords:** Cryopreservation, Vitrification, Slow-freezing, Ovarian autotransplantation, Oopherectomy

## GENITAL AND URINARY TRACT INFECTIONS IN DIABETES

**Mohini Yadav<sup>1</sup>, Dr. Vibha Rani\***

*Department of Biotechnology, Jaypee Institute of Information Technology, Sector-62, Noida  
Corresponding author: vibha.rani@jiit.ac.in*

Type 2 Diabetes Mellitus is a divergent group of disorder characterized by varying degrees of insulin resistance, impaired insulin secretion and increased glucose production. It is known that diabetes doubles the risk of various vascular diseases and is commonest amongst them are the genitourinary infections. There is approximately 60% increased risk of urinary tract infections (UTI) and about two to four-fold increase in genital infections. Various dysfunction in the immune system, poor metabolic control and incomplete emptying of the urinary bladder contribute in the foretelling of UTI in diabetes patients. Clinically these are characterized as complicated UTI and uncomplicated UTIs. Uncomplicated typically affect those individuals that are healthy and don't have any prior urinary tract abnormalities. These are further differentiated into lower UTI including cystitis and upper UTI including pyelonephritis. Whereas complicated UTI are those that affect the urinary tract like urinary obstruction, urine retention, renal failure and transplantation. They are a significant cause of morbidity amongst infant boys, older men and females of all ages. Individuals suffering from diabetes are also at a higher risk of getting affected with UTI's. These are caused by a number of pathogens, but most commonly are caused by *Escherichia coli*, *Klebsiella pneumoniae*, *Proteus mirabilis*, *Enterococcus faecalis* and *Staphylococcus saprophyticus*. The epidemiology of urinary tract infections (UTIs) among men and women with diabetes is similar to the epidemiology of those without. Women have greater risk than men, and frequency of sexual activity is a risk factor. The bacteriology and antibiotic susceptibility patterns also do not, in general, differ from those without diabetes. Although persons with diabetes are more likely to have asymptomatic bacteriuria, asymptomatic bacteriuria does not lead to increased risk of symptomatic infection. However, diabetes doubles the risk of UTI. The source of this increase is not well understood, although bladder dysfunction, which increases with duration of diabetes, and glycosuria are hypothesized mechanisms.

**Keywords:** Type 2 Diabetes Mellitus, genitourinary infections, cystitis, pyelonephritis, glycosuria

## COMPARATIVE TOXICITY ANALYSIS OF ANTI-DIABETIC DRUGS IN CARDIAC CELL LINE

**Megha<sup>1</sup>, Tanya Suneja<sup>2</sup>, Sakshi Awasthi<sup>3</sup>,  
Mohini Yadav<sup>4</sup>, Shanya Verma<sup>5</sup>, Dr. Vibha Rani\***

*Department of Biotechnology Jaypee Institute of Information Technology, Sector-62, Noida  
Corresponding author: vibha.rani@jiit.ac.in*

Diabetes mellitus is one of the most common non-communicable diseases globally. It is the fourth leading cause of death in the most developed countries and there is substantial evidence that it is an epidemic in many developing and industrialized nations. This is posing a serious threat to be met in the 21<sup>st</sup> century. Diabetes mellitus is caused by the abnormality of carbohydrate metabolism which is linked to low blood insulin level or insensitivity of target organs to insulin. Both the number of cases and the prevalence of diabetes have been steadily increasing over the past few decades. Globally, an estimated 422 million adults were living with diabetes in 2014, compared to 108 million in 1980. The classification of diabetes mellitus and the tests used for its diagnosis were brought into order by the National Diabetes Data Group of the USA. Cardiovascular disease (coronary heart disease, stroke, peripheral vascular disease) is the most important cause of mortality and morbidity among patients with type 2 diabetes. Type 2 diabetes is a syndrome characterized by relative insulin deficiency, insulin resistance and increased hepatic glucose output. Over the past several years, there have been a significant number of anti-diabetic agents developed for the treatment of type 2 diabetes. Currently available oral agents for the treatment of type 2 diabetes mellitus include a variety of compounds with differing mechanisms of action, adverse effect profiles, and toxicities. The oral anti-diabetic drugs can be classified as either hypoglycemic agents (sulphonylureas) or anti-hyperglycemic agents (biguanides and thiazolidinediones). The experimental analysis provided by the MTT(3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyl tetrazolium bromide) assay has demonstrated that the antidiabetic drug containing biguanides showed comparatively less toxicity as compared to drug consisting of sulphonylureas. Similarly, giemsa staining and morphology analysis have convincingly indicated that sulphonylureas containing drugs (Gliclazide®) contribute to more cardiovascular complications in contrast to drugs substituted with biguanides (Metformin®). Oral

hypoglycemic agents like sulphonylureas and biguanides are still the major players in the management of the disease but there is growing interest in herbal remedies due to the side effects associated with the oral hypoglycemic agents.

**Keywords:** Diabetes, Cardiovascular disease, MTT assay, giemsa staining, hypoglycemic agents.

PP100

ICABB-217

## IMPROVED YEILD ATTRIBUTING TRAITS AND QUINONIC COMPOUNDS IN *NIGELLA SATIVA L.*- A PHYOTHERAPEUTIC HERB OF INDIA

Ambreen Asif<sup>1\*</sup> and MYK Ansari<sup>2</sup>

1. Research Scholar, 2. Professor, Cell Molecular Biology and Genetic Section, Department of Botany, Aligarh Muslim University, Aligarh-202002, UP, India

\*Corresponding author: ambreenasif1@gmail.com

The usage of synthetic chemicals in medicines has been questioned in recent years due to alarming side effects. This has burgeoned the scientific interest in phytotherapeutics. Increased efficiency of medicinal plants for the production of phytochemicals and derived drugs pave the way for wide pharmacological applications. A large number of medicinal plants and their purified constituents have been shown to have potential therapeutic benefits. *Nigella sativa L.* is also among such medicinal plants which possess a rich pool of chemical diversity. *Nigella* oil revealed the presence of both a fixed and volatile oil. Alkaloid, flavanoids, tannins and coumarins are also present as other important bioactive compounds. Because of the presence of such chemical compounds, it has antibacterial, anticarcinogenic, antioxidant, anticonvulsant and anti-allergic properties. Under the pin head of phytotherapeutic importance of *N. sativa*, present study was carried out to evaluate the effect of Ethyl methane sulfonate (EMS) on yield traits and phytochemistry of this medicinal herb. The existing germplasm (seeds) were treated with 0.10%, 0.25% and 0.50% doses of EMS. A high yielding mutant was isolated in M3 generation from 0.25% EMS. Various yield attributing traits like number of capsules/plant, capsule size, number of locules/capsule, number of seeds, seed size, number of seeds/capsule, 1000-seeds weight (g) and yield/plant (g) were enhanced significantly in comparison to control (untreated plant). The mutant was tested phytochemically (GC analysis) for confirming the variations in major quinonic phenol compounds like Thymoquinone (TQ)

and Thymol (THY). These compounds showed greater % peak area in mutant than in control. Based on observations, it was concluded that the moderate concentrations (0.25%) of EMS was efficient for improving this medicinal herb. The improved yield traits could be utilized by plant breeders in breeding programs and improved quinonic phenol compounds are important for pharmaceutical interest.

**Key words:** EMS, phytotherapeutics, yield, mutant, thymoquinone

PP101

ICABB-222

## EFFECT OF BENZIDINE AS AROMATIC SPACER IN ENZYME CONJUGATE ON BRIDGE HETEROLOGOUS ELISA FOR PREDNISOLONE

Divya Verma<sup>1,2\*</sup>, Sonu Chand Thakur<sup>1</sup>, T.G. Srivastav<sup>2</sup>

1. Centre for Interdisciplinary research in basic sciences, Jamia Millia Islamia, Jamia Nagar, New Delhi, India 2. Department of Reproductive Biomedicine, National Institute of Health and Family Welfare, Munirka, New Delhi

\*Corresponding author: ddivip@gmail.com

Prednisolone (PSL), a synthetic glucocorticoid, is widely used for the treatment of inflammatory and autoimmune diseases. It reduces the inflammation related symptoms such as pain, swelling and allergic reactions. It is used as an illegal drug for administration in animals for growth promoting purposes if used above permissible limit ( $4\text{--}10 \mu\text{g kg}^{-1}$ ). In this study, we have developed ELISA for the detection of prednisolone. We have incorporated Benzidine (aromatic spacer) between horseradish peroxidase (HRP) and PSL-21-hemisuccinate (PSL-21-HS) which has effect on the sensitivity of enzyme immunoassays. PSL-21-HS-bovine serum albumin (PSL-21HS-BSA) was used as an immunogen to raise the antiserum in New Zealand white rabbits. Enzyme conjugate for the homologous assay was prepared using PSL-21-HS and HRP as PSL-21-HS-HRP (without spacer). Enzyme conjugate for the heterologous assay was prepared using PSL-21-HS, Benzidine and HRP as PSL-21HS-Benzidine-HRP (with spacer) and the functional parameters of both homologous and heterologous assay were compared. Due to the presence of aromatic spacer in the enzyme conjugate, the affinity of heterologous assay changes from  $0.20 \times 10^{-8} \text{ mol/L}$  to  $0.14 \times 10^{-8} \text{ mol/L}$ . Sensitivity increases from 0.34 ng/mL to 0.04 ng/mL and ED<sub>50</sub> decreases from 8.53 ng/mL to 7.46 ng/mL in comparison to homologous assay

of prednisolone. Thus, the results of this study showed that incorporation of aromatic spacer in enzyme conjugate enhances the sensitivity, ED<sub>50</sub> and affinity of the developed assay.

**Keywords:** ELISA, Prednisolone, immunogen, enzyme conjugate, aromatic spacer, Benzidine

PP102

ICABB-227

## ANIMAL MODEL DEVELOPMENT FOR ANTI-OVULATORY STUDY

<sup>1</sup> Shubham Kumar, <sup>2</sup>Akshara Shukla, <sup>3</sup>Kumud Bala  
1, 2, 3 Amity Institute of Biotechnology,  
Amity University Uttar Pradesh, Noida-201301

Hormonal preparations that contain various combination of estrogen with progestin and progestin alone are well known as the contraceptives. These combinations in the contraceptives inhibit the release of follicle stimulating hormone (FSH) from the pituitary glands. The development of ovum is very much effected by the LH and FSH, they also help in the preparations of the lining of the uterus for the implantation of the embryo in the uterus. Progestin also makes the cervix mucus lining thick so that sperm cannot penetrate to get fertilized. The contraceptive present in the market consists of levonorgestrel (analogue of progesterone) and ethinyl estradiol (analogue of estrogen) in different concentrations. The concentration level has been regulated many times since the commercializing of the first contraceptive pill. The concentration of the dose of estrogen in pills has reduced from 50 to 30-35 mg and gradually to 20-15 mg. Pills are now segregated into higher and lower than 30 mg dose of estrogen level. This reduction has been made feasible due to the accessibility of new classes of progestin. These pills have severe side effects like, increased risk of heart attack and thromboembolism, risk of breast cancer, cervical, colorectal, and endometrial cancers and obesity. Thus the herbal compounds became the area of interest these days to reduce the side effect of the contraceptives. There are several herbs consisting of compounds that are having anti-ovulatory effect. This study is focused on the development of the animal model in order to monitor all the stages of reproductive cycle of female rats and further work is going on to tests the plant derived compounds for its anti-ovulatory effect.

**Key words:** herbal contraceptives, anti-ovulation, estrogen, progesterone

PP103

ICABB-238

## OXIDATIVE STRESS: CAUSE OF INFERTILITY

<sup>1</sup>Dhwani Gupta, <sup>2</sup>Harshdeep Kaur,  
<sup>3</sup>Akshara Shukla, <sup>4</sup>Kumud Bala

<sup>1,2,3,4</sup> Amity Institute of Biotechnology, Amity University Uttar Pradesh, Noida-201303

Fertilization and embryo development in vivo occurs in an environment of low oxygen tension. Oxidative stress has a role in etiopathogenesis of endometriosis, tubal factor infertility, and unexplained infertility. Oxidative stress (OS) has been identified as one factor that affects fertility status. ROS (pro-oxidants) include the hydroxyl radicals, superoxide anion, and hydrogen peroxide. There is a diverse range of antioxidants that limit the production of ROS, scavenge them, and repair cell damage. An imbalance between the pro-oxidants and antioxidants results in OS. Oxidative stress occurs when the generation of free radicals and active intermediates in a system exceeds the system's ability to neutralize and eliminate them. There is a complex relationship between ROS and antioxidants in the ovary. The increase in steroid production in the growing follicle causes an increase in P450, resulting in ROS formation. Oxygen deprivation stimulates follicular angiogenesis, which is important for adequate growth and development of the ovarian follicle. Oocyte metabolism and a lack of antioxidants combined with the follicular and oviductal fluid of the embryo causes an increase in ROS levels. Plasma levels of ascorbic acid (vitamin C) and  $\alpha$ -tocopherol (vitamin E) were significantly lower in women with recurrent spontaneous abortion. Use of nutritional supplements and antioxidants like vitamin C supplementation to protect against ROS and OS has proved beneficial. Oxidative stress leads to luteal regression, resulting in a lack of luteal support to a pregnancy. This study is focused on the determination and treatment of oxidative stress in females.

**Keywords:** Oxidative stress, infertility, antioxidants, ROS

## **ROLE OF ANTIOXIDANTS COENZYME Q AND VITAMIN E IN NEUROPROTECTION OF GLUTAMATE INDUCED DAMAGE IN RETINAL GANGLION CELLS**

**Shikha Upreti and Madhumita P. Ghosh**

*Amity Institute of Biotechnology, Amity University, AUUP, Noida*

Loss of vision in ophthalmic diseases like glaucoma, age related macular degeneration, optic neuropathy is associated with degeneration of retinal ganglion cells (RGCs). Retinal ganglion cells possess glutamate or NMDA (N-methyl-D-aspartate) type receptors which degenerate and cause these optic neuropathies. Our aim was to study the effect of analogues of Coenzyme Q and Vitamin E alone as well as in combination on glutamate induced damage of retinal ganglion cells. Intravitreally injected N-methyl D-aspartate (NMDA) was administered to Wistar rats weighing 100-200g to create an *invivo* model of retinal ganglion layer degeneration. NMDA insult followed by treatment with Coenzyme Q and Vitamin E (i.p) alone as well as in combination were given daily to the rats upto 7 days. Effect of treatment on RGCs was studied through morphological and immunohistochemical studies using cell proliferation marker BrdU. Coenzyme Q and vitamin E were more effective in combination than alone, in maintaining the linearity of the RGCs that were disrupted by NMDA. Hence, we propose coenzyme Q and vitamin E as a potential therapeutic combination to treat degeneration of glutamate receptors on retinal ganglion cells.

**Keywords:** Retinal ganglion cells (RGCs), N-methyl-D-aspartate (NMDA), Vitamin E, Coenzyme Q, Glutamate

## **DEVELOPMENT AND STABILITY ANALYSIS OF ESSENTIAL OIL (EO) LOADED MICROEMULSION FOR TRANSDERMAL APPLICATION**

**Manisha Singh\*, Arushi Pant and Rachana**

*Department of Biotechnology, Jaypee Institute of Information Technology, A-10, sector 62 Noida, Uttar Pradesh., India-201307.*

*Presenting author: Arushi Pant*

*E-mails: arushi.panth500@gmail.com, Corresponding author: manisha.singh@jiit.ac.in*

Essential oils (EO), ethereal oils, aetherolea or plant oils belongs to the class of highly volatile compounds which, due to their higher concentrated natural constituents acquire unique properties and hence, are being used for its wide range of health benefits. Their therapeutic benefits widely range from being a potential anti-fungal, anti-microbial, antidepressant, antiviral and antiseptic agents to the elevator of many CNS related behaviors like - anxiety, learning, memory, attention, arousal, relaxation, sedation and sleep. Furthermore, the effects on mood, pain and perception too, are being influenced by the use of essential oils. It also helps in treatment of epilepsy, stress, dementia by giving calming and soothing effects to the nerve cells. Further, EO's have shown potential benefits in treating transdermal disorders such as eczema, psoriasis, acne, fungal infections etc. Since, they are highly concentrated and volatile thus, there direct application might cause skin irritation, redness and itching. Therefore, to overcome these limitations, the EO's are loaded in a clear, thermodynamically stable microemulsion system which is reported to enhance its permeation through the transdermal route along with its antimicrobial properties. Microemulsions are specifically noted to enhance the deeper impregnation of the EO's inside the skin and they usually show the sustained compound release character leading to improved shelf life, and bioavailability. Hence, our present study is focused on formulating the tea tree oil (TTO) microemulsions. TTO is a therapeutically potential EO, which is extensively used in various skin infective and inflammatory conditions. The results exhibited the successful formulation of o/w TTO loaded microemulsions in nanometric size range with thermodynamic stability, hence, assisting enhanced permeability with sustained release.

**Keywords:** Microemulsion, Transdermal Disorder, Essential oils, Tea tree oil, nanometric size, stability.

PP106

ICABB-264

## SCREENING OF MULTI-DRUG RESISTANT BACTERIA FROM SEWAGE WATER FROM DIFFERENT SITES IN DELHI-NCR

**Kumar Shashank, Shubham Batra,  
Maansi Veermani, Neeta Bhagat, Sesha Charan and  
Sona Singh**

*Amity institute of biotechnology, Amity university, Uttar Pradesh*

Multi antibiotic resistance among pathogens is an ongoing public health problem. Infections caused by such pathogens have limited treatment options and have been associated with high mortality rates. Samples from various surface water-bodies (Najafgarh, kalindi kunj, hindon cut canal, INA and karnal bypass) across delhi reveal widespread presence of multi drug resistant strains. Susceptibility test for 20 antibiotics by Kirby-bauer method showed that Aminoglycosides form the best category (40%) with least resistance, followed by Carbapenems. Whereas Cephalosporin have the most resistance spread against them. Amongst 20 antibiotics tested, Doripenem proved to be best with a resistance of 13%, while Cefepime registered the highest resistance of 86%.

Among all the strains, maximum resistance to all classes of antibiotics was shown by strains of Karnal bypass.

**Keywords:** antibiotic susceptibility, cephalosporin resistance, carbapenems, Multi-drug resistance.

PP107

ICABB-265

## UNDERSTANDING CABLE BACTERIA - A BIOGEOBATTERY

**Ayushi Agarwal and Vibha Gupta\***

*Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201307, Uttar Pradesh, India  
E-mails: sangitaayushi@hotmail.com \*Corresponding author: vibha.gupta@jiit.ac.in*

Cable bacteria, found in marine sediments, is a filamentous bacterium that belongs to the family of *Desulfobulbaceae*. It is a biogeobattery by virtue of its ability to harvest electrons by sulphide oxidation in the deeper, oxygen free environment of marine sediments and to transfer them through its long filamentous body to the water surface for oxygen

reduction. Thus, inducing an electric field in the environment where electron donor and acceptor are distance apart in space. Interestingly, this live battery mediates long distance electron transport equivalent to electric cables used for long distance electrical signalling. These findings open new avenues of bioremediation of hydrocarbons by bioelectrochemical degradation and bio-electrical conducting wires or batteries. This review summarizes the current knowledge about these fascinating electroactive bacteria.

**Keywords:** Aquatic sediments, biogeobattery, Cable bacteria, Electrical potential.

PP108

ICABB-273

## ROLE OF DHA IN BRAIN DEVELOPMENT

**Manya Singh, Shubham Rajput, Garima Mathur\***

*Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201307, Uttar Pradesh, India  
E-mails: manyafincom@gmail.com, sr9999146261@gmail.com*

\*Corresponding author: Email: garima.mathur@jiit.ac.in

Omega-3 fatty acid *docosahexaenoic acid (DHA)* remains vital for adequate brain development and its functions. It is vital not only for infant and toddlers but also through all ages of a person's life. Infants provided with DHA rich foods show better learning ability, attention and cognitive performance. DHA, an omega-3 fatty acid, anatomically is a key formative constituent of the lobes of cerebral cortex, human brain, retina and skin. DHA constitutes 60% of the polyunsaturated fatty acids (PUFAs) in the retina and 40% of PUFAs in the brain. DHA is considered vital for growth of eye, nerve tissues and further research confirms that DHA decreases risk of coronary and circulatory disease. Deficiency of DHA thus triggers cognitive decline which can result in problems with attention, learning and brain dysfunction. Major dietary sources of DHA are alpha-linolenic acid or seafood oil or breast milk. Among herbivorous, body produces internally from alpha-linolenic acid, a type of omega-3 fatty acid manufactured by plants. Alpha-linolenic acid is a major resource of omega-3. Sea fish, breast milk, walnuts, almonds, flaxseeds are rich in omega-3 fatty acids. Body consumes this directly or infants get it from mother's milk. Research indicates that DHA supports optimum levels of neurotransmitters which act as chemical messengers among cells. DHA may enhance the fluidity of cell membranes and improve their ability to release neurotransmitters and increase density of

dendrites, property related to well-developed learning. Researches unanimously indicate DHA to be critical for brain development, health and its optimum function.

**Keywords:** Docosahexaenoic acid, Cognitive, Neurotransmitter, Omega-3 fatty acid.

PP109

ICABB-150

## THERAPEUTIC USES OF COMMON INDIAN PLANTS FOR TREATMENT OF BRAIN TUMOR

**Shashank Awasthi<sup>1</sup>, Tanya Gupta<sup>1</sup>, Saumya Yadav<sup>1</sup>, Manisha Singh<sup>1</sup> and Rachana<sup>1\*</sup>**

1. Jaypee Institute of Information Technology, A-10, Sector-62, Noida, Uttar Pradesh 201309

\* Corresponding author: rachana.dr@gmail.com

Cancer is the succeeding principal reason of demise globally, though; enormous researches have been made in the regulation and treatment of cancer. There are still a lot of significant deficiencies and rooms for the improvement for cancer therapy. Modern day's anti-cancer drugs are not 100% efficacious and are mostly associated with a lot of side effects. The most frequent primary brain tumor in adults which is characterized by a highly aggressive phenotype is Glioblastoma. In the process of looking for the safer and effective treatment for Glioblastoma multiforme, scientists are looking back towards natural therapies, based on plant-derived products, for cancer treatment. Many plant products are already in use, and in the present study, road side plants such as: *Alstoniascholaris*, *Neriumindicum*, *Callistemon citrinus*, *Calliandraportoricensis*, *Ficuscarica*, *Ficusbenghalensis*, *Magiferaindica* and *Syzygiumcumini* will be discussed for their mechanism of against brain cancer. Plant like *Alstoniascholaris* and *Neriumindicum* etc. have phytochemicals have shown very optimistic anti-tumor properties in vitro. All these plants contain various groups of compounds such as: Alkaloids, Flavanoids and other cancer fighting and/or immune boosting compounds which are responsible for its anti-tumor properties. This study targets on phytochemical compounds as anticancer agents against Glioblastoma with their mode of action.

**Keywords:** Brain tumor, Glioblastoma, Alkaloids, Flavanoids

PP110

ICABB-225

## HERBAL REMEDIES FOR RHEUMATOID ARTHRITIS:- A REVIEW

**Sakshi<sup>1</sup> and Reema Gabrani<sup>1\*</sup>**

1. Department of Biotechnology, Jaypee Institute of Information Technology, Sector 62, Noida, U.P. India<sup>1</sup>  
E-mail: sakshi.june@gmail.com,

\*Corresponding author: reema.gabrani@jiit.ac.in

Rheumatoid arthritis (RA) is one of the main diseases in the world which affects many people. It is an inflammatory disease of the synovium resulting in pain, stiffness, swelling, deformity and eventually loss of function and mobility in the joints. Improper diet and lack of exercise stand as two basic pillars in causing this disease. Hence there are different treatments available for arthritis like non-steroidal anti-inflammatory drugs and steroids which can relieve pain and control disease to a certain extent but with side effects. Alternate therapeutic measures promise relief to rheumatoid arthritis patients with minimal side effects. There are many herbal therapies that mediate their action by blocking the activity of immune cells and their secreted molecules thus reducing inflammation in the joints. Herbs that have shown potential to treat RA like *Curcuma longa* (turmeric), *Zingiber officinalis* (ginger), *Oenothera biennis* (evening primrose), *Ribes nigrum* (blackcurrant), *Nyctanthes arbor tristis* (harsingar), *Commiphora mukul* (guggulu), *Ananas comosus* (pineapple), *Tripterygium wilfordii* Hook F (TWH) (thunder god wine). These herbs have shown to inhibit various inflammatory cytokines (IL-1, TNF- $\alpha$ ), and down-regulate the expression of inflammatory gene products such as COX-2 and MMP-9 which are major players in the development of RA. It is seen that these herbs cause reduction of pain, stiffness and improve function and tolerability in knee pain. Thus many studies have asserted the role of several herbs in inflammation remission.

**Keywords:** *Curcuma longa*; Herbal remedy; TNF- $\alpha$ ; *Zingiber officinalis*.

**ANTIFUNGAL PROPERTY OF  
BACTERIAL ISOLATES FROM FIROZ  
SHAH KOTLA FORT AGAINST  
PHYTOPATHOGENS**

**Saloni Sachdeva, Priyansh Srivastava,  
Nawaz Alam, Shreshtha Dubey, Akriti Jain and  
Indira P. Sarethy\***

*Department of Biotechnology Jaypee Institute of Information  
Technology A-10, Sector-62 NOIDA-201309*

\*Corresponding author: [indirap.sarethy@jiit.ac.in](mailto:indirap.sarethy@jiit.ac.in)

Plant diseases, which cause losses upto 26% in yields, impair the quality of produce to the disadvantage of producers as well as consumers. To counter these diseases causing pathogens, presently there exist over 200 chemical fungicides in agriculture and horticulture worldwide. But the increase in resistant strains of pathogens and public concern about chemical fungicides has encouraged scientists to look for better and safe alternatives. Keeping in mind environmental requirements, microbial metabolites can be efficiently used as substitutes of chemical fungicides. Biofungicides can be used directly as fungicides or as leads in designing synthetic products. The genus Bipolaris is considered as a potential agent for economic loss as they are associated with diseases in high value field crops and Rhizopus is associated with spoilage of fruits and other food material. In this study, selected bacterial strains (FK-109, FK-128, FK-142, FK-143 and FK-221) isolated from Firoz Shah Kotla Fort, Delhi were tested for their antifungal property against phytopathogenic fungi (*Rhizopus oryzae*, *Bipolaris maydis* and *B. sorokiniana*), using the disk diffusion method and their zones of inhibition measured. Amongst these, FK-143 showed best activity against *R. oryzae*, *B. maydis* and *B. sorokiniana* and FK-128 showed inhibition against *B. maydis*. Isolates FK-109, FK-142 and FK-221 were less effective. The bacteria described here have a potential to be used in agriculture sector, based on further characterization studies.

**A BIOLOGICAL APPROACH FOR RAPID  
SYNTHESIS OF SILVER  
NANOPARTICLE FOR WASTE WATER  
TREATMENT**

**Tithi Mehrotra<sup>1</sup> and Rachana Singh<sup>1\*</sup>**

<sup>1</sup>Water Quality Monitoring and Bioremediation Lab, Amity Institute of Biotechnology, Amity University Uttar Pradesh - 201313, India.

E-mails: [tithimehrotra\\_6@yahoo.com](mailto:tithimehrotra_6@yahoo.com), \*Corresponding author:  
[rsingh2@amity.edu](mailto:rsingh2@amity.edu)

The biological approach for the synthesis of metallic nanoparticles provides an eco-friendly substitute to the conventional physical and chemical methods. Cell-mediated synthesis of silver nanoparticles using microorganisms are reported to be slow, hence the present study demonstrates a rapid bio-reductive synthesis method by using a rare *Bacillus* species isolated from the domestic effluent. The synthesis of silver nanoparticle was confirmed by UV- Visible Spectroscopy, its morphology by Scanning Electron Microscopy (SEM), purity by Energy Dispersive X-ray analysis (EDX) and size by Dynamic Light Scattering (DLS). Our work suggests various applications of silver nanoparticles in the treatment of different effluents. The green synthesized nanoparticle was effective in degrading Acid black 24 dye from textile effluent up to 95% in ~6 hours of exposure time. Also, the application of silver nanoparticle in treating domestic wastewater was observed, which was confirmed by the reduction in BOD value from 160 mg/L to 20 mg/L and COD value from 150 mg/L to 60 mg/L. Study of the effect of effluent treated by biologically synthesized silver nanoparticles on seed growth was also checked by phytotoxicity analysis on *Vigna radiata* which showed an enhanced seed growth after treatment with the nanoparticle as compared to the growth in untreated effluent.

**Keywords:** Biological, eco-friendly, green, silver nanoparticle, dye degradation, domestic wastewater, phytotoxicity analysis.

## EPIGENETIC CHANGES IN GLIOBLASTOMA AND TARGETED THERAPIES

Nidhi Jadon, Megha Gautam, Reema Gabrani\*

Jaypee Institute of Information Technology, A-10, Sector 62, Noida  
 E-mails: nidhijadon.812@gmail.com, \*Corresponding author:  
 reema.gabrani@jiit.ac.in

Glioma is the most common type of brain tumor with poor prognosis and high mortality rate. It comprises of more than 80% of malignant brain tumors. Gliomas are classified based on their histology as LGG (Low grade gliomas) and GBM (glioblastoma). Treatment includes surgical removal followed by radiation and chemotherapy with temozolomide but even after such aggressive treatment median survival rate is only for 1-2 years. Brain tumor which is formed due to GBM are malignant and grows back aggressively. Epigenetics can be defined as the change in gene expression without change in DNA sequence. Epigenetic modifications play a causal role in a variety of human diseases including metastasis and chromosomal aging. The epigenetic changes such as DNA methylation, interruption of LINE & SINE family or hypermethylation of HOXA11(Homeobox protein A-11 encoded by HOXA11 gene), histone acetylation or loss of acetylation can lead to long term changes in gene expression responsible for malignant brain tumours. Hypermethylation of miRNA such as miR-21 plays a crucial role in silencing of tumor suppressor genes. Silencing of certain genes such as O6 methylguanine methyltransferase (MGMT), p53 and p16 are the cause of malignant brain tumours. Epigenetic alterations can be revised by using epigenetic therapy or epigenomic influence techniques. Various therapeutic strategies have been developed for GBM include telomerase inhibition, use of HDAC (histone deacetylase) inhibitor medicines like hydroxamic acid-based compounds vorinostat, panobinostat, belinostat, and the depsipeptide romidepsin, MGMT inhibitor, temozolomide and nitrosourea.

**Keywords:** Glioblastoma; HOXA11; HDAC (histone deacetylase); MGMT (Methylguanine methyltransferase); p16; p53.

## WITHANIA SOMNIFERA: A REJUVENATOR

Shalini Tyagi, Vipra Bhardwaj and Garima Mathur\*

Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201307, Uttar Pradesh, India  
 E-mails: tyagi.shalini4@gmail.com, vipravibhas@bhardwaj.com,  
 \*Corresponding author: garima.mathur@jiit.ac.in

*Withania somnifera* belonging to family Solanaceae is commonly known as "Ashwagandha" or "Asgandh". Owing to its diverse medicinal properties, it is considered as a wonder herb. *W. somnifera* draws its generic name on English paleobotanist „Henry Thomas Marie Wintham while specific name, 'somnifera' is a combination of two latin words *somnus* (sleep) and *ferere* (to bear) meaning sleep inducing plant. Ashwaganda roots are compared with ginseng roots for their restorative properties of vigor and vitality, hence been given the name "Indian Ginseng". The present review discusses the morphological, cytogenetical and pharmacological characteristics of plant. It is one of the most sought Ayurvedic medicinal herbs (traditional medicinal system of India) with immense therapeutic properties mainly including anti-cancerous, sedative, anti-inflammatory, anti-tumor, antibacterial, anti-spasmodic and antioxidant. It is a potent adaptogen for enhancing body's resilience to stress. *Withania* is known as memory booster which enhances the functioning of central nervous system; it helps body in combating neurodegenerative disorders such as Parkinson's, Huntington's and Alzheimer's diseases. Keeping in view of renewed global interest in traditional ethnopharmacy, natural stock of herb is reassessed in search of remarkable bioactive principles with little or no side-effects on human population.

**Keywords:** Adaptogen, Antioxidant, Neurodegenerative disorders, ethnopharmacy, secondary metabolites, *Withania somnifera*.

---

## CARBON SEQUESTRATION: A SOLUTION TO GLOBAL PROBLEM

Arushi Saxena and Pammi Gauba\*

*Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sector-62, Noida, Uttar Pradesh-201307*

\*Corresponding author: pammi.gauba@jiit.ac.in

---

Over the century the human and industrial development has led to a large increment in fossil fuel consumption and CO<sub>2</sub> emissions, resulting in increase in atmospheric CO<sub>2</sub> concentration. It is believed this is responsible for the rise in global temperature resulting in glacial melting, rise in sea levels and ocean acidification. In recent years, researchers have come up with the development of Carbon Capture and Sequestration (CCS) technologies. With the help of these technologies, waste carbon dioxide is captured from large point sources such as fossil fuel stations, preventing its release into the atmosphere. Carbon dioxide sequestration has emerged as a key technology pathway for reduction of greenhouse gas emissions. Mainly there are three classes of target reservoirs which are capable of sequestering large volumes of CO<sub>2</sub>: Saline formations, Depleted oil and gas fields and Deep coal seams. Basically, there are three main stages in the CCS chain: Carbon reduction technologies, transport and storage. The technology has been approved by IPCC and provides a way as a mitigation option for developing countries like India and has already been mitigated as an option for developed countries like America. The current target of India is 20% reduction in CO<sub>2</sub> emissions by 2020. Development of sequestration technology would surely assure ample, low-cost energy for the century, giving better alternatives. The aim is to study the processes involved in sequestering the carbon deeply and also to explore various carbon mitigation, sequestration technologies and potential in Indian context.

**Keywords:** Carbon, Sequestration, acidification, Saline formations, mitigation, IPCC

---

## GUT-BRAIN CONNECTION AND MENTAL HEALTH

Advika Gupta, Sonia Purswani, Garima Mathur\*

*Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201307, Uttar Pradesh, India*

E-mails: advika.gupta27@gmail.com, soniapurswani28@gmail.com,

\*Corresponding author: garima.mathur@jiit.ac.in

---

A typical human adult carries hundred trillion microbes in the body, representing a combined microbial genome much greater than the human genome. Studies have proven that the gut microbiota composition can regulate certain aspects of emotional and neuropsychological functioning by communicating with the Central Nervous System (CNS) through an intricate connection between the gut and brain, known as the Gut-Brain Axis. Evidence also suggests that our diet plays a crucial role in programming the gut microbiota composition, diversity and its functionality throughout life. Gut dysbiosis can lead to psychiatric and metabolic disorders. In patients with ASD (Autism Spectrum Disorders), a variety of GI symptoms have been reported and these disturbances might be linked to gut dysbiosis representing the disruption of "gut-brain axis." The use of prophylactic interventions such as probiotics, omega-3 fatty acids or prebiotics may represent a good non-pharmacological option in the treatment of GI disturbances in ASD patients and underlying anxiety or depression in Irritable Bowel Syndrome (IBS) patients. Hence, the gut brain axis and gut microbiota composition of an individual becomes an attractive area of research, presenting a paradigm of opportunities for the treatment and prophylaxis of metabolic and neurological disorders.

**Keywords:** Gut-Brain Axis, Gut Microbiota, Probiotics, Prebiotics, Irritable Bowel Syndrome, Autism Spectrum Disorders

PP117

ICABB-034

## **DECOLOURIZATION OF TEXTILE AZO DYE DIRECT RED 31 BY IMMOBILIZED SCENEDESMUS RUBESCENS ISOLATED FROM TEXTILE EFFLUENT**

**Surbhi Sinha\* and Rachana Singh**

*Amity Institute of Biotechnology, Amity University, Noida, Uttar Pradesh*

*E-mails: rsingh2@amity.edu, \*Corresponding author: ssinha2@amity.edu*

The increase in the existence of textile dyes constitutes a major environmental toxicity hazard; resulting in the establishment of the novel and facile methods for the removal of these dyes from aqueous solution. Physical, chemical and electrochemical methods for the ouster of dyes have restricted use since they have many limitations in comparison with the biological methods. The objective of this research was to test the effects of immobilization and some experimental conditions on the decolourization of an azo textile dye, Direct Red 31 (DR 31) by *Scenedesmus rubescens* isolated from the textile effluent. Decolourization of free and immobilized *Scenedesmus rubescens* was examined by observing the decrease in the absorbance of dye at various experimental \*conditions like contact time, initial dye concentration and pH. Immobilized alga showed maximum decolourization of 98.76 % in 4 days with 20 mg L<sup>-1</sup> of dye at pH 3. The present method is easy to use, cost-effective and devoid of technical problems.

**Keywords:** Algae, Textile dye, Decolourization, contact time, pH

PP118

ICABB-088

## **PESTICIDE DEGRADATION BY MICROORGANISMS**

**Sakshi Bhadouria, Richa Verma, Mahender Singh Rawat, Parul Chauhan, Dr. Pammi Gauba\***

*Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sector-62, Noida, Uttar Pradesh-201307  
\*Corresponding Author: pammi.gauba@jiit.ac.in*

Pesticides are used all over the world to manage agricultural pests as they destroy and repel unwanted pests. The extensive use of pesticide causes imbalance in properties of soil, water and air environments as they cause natural degradation. This problem is

enhanced because of biomagnifications. The available methods for pesticide degradation (physical or chemical) are either incomplete or costly. Bioremediation is a novel process which utilizes the ability of microorganisms to remove pollutants from contaminated sites. Bioremediation provides an eco-friendly, economical and efficient method for detoxification of pesticides. It is seen that most of the time degradation occurs through the activity of microorganisms, especially the fungi and bacteria. Biological degradation by organisms can efficiently remove pesticides from the environment, especially organochlorines, organophosphates and carbamates used in agriculture. It is important to understand the molecular mechanisms involved in enzymatic catalysis, so that it will be possible to design new alternatives and/or efficient tools for the treatment of pesticide residues or for the bioremediation of contaminated sites. This information could be used in the future to treat pesticide residues in the field (such as waste resulting after washing pesticide containers), or the obsolete pesticides.

**Keywords:** Biodegradation; Bioremediation; Biomagnification; Pesticides.

PP120

ICABB-040

## **ALLELOPATHIC EFFECT OF SYZIGIUM CUMINI AND OCIMUM TENUIFLORUM PLANTS**

**Divya Batra, Abha Singh, Akash Yadav, Raina Jana Pragya Vats, Shantanu Pawar and Neeraj Wadhwa\***

*Department of Biotechnology, Jaypee Institute of Information Technology, Noida, Uttar Pradesh, India  
\*Corresponding author: neeraj.wadhwa@jiit.ac.in*

Allelopathy is a biological process in which an organism produces biochemicals which affect the growth, germination survival, and reproduction of other organisms. These biochemicals are also called as allelochemicals may either affect target organisms and the community positively or negatively. Allelopathy has several applications such as controlling weed population, plant growth enhancement, crop nutrition enhancement etc. Identification of plant species with significant allelopathic potential has been a target of numerous researches aiming to use them to control crop weeds. For our experiment we took medicinal plants of *Syzygium cumini* and *Ocimum tenuiflorum* plants, Effect of crude extract of these medicinal plants on germination of moong, white cotton and black cotton by observing the change in the radicle length of

these seedlings with the change in concentrations of extract solution.

Medicinal plants jamun and tulsi play a very vital role in medicinal and Ayurveda branch in India and are easily accessible.

PP121

ICABB-041

## DIATOMS AS A FUEL: A FUTURISTIC APPROACH

**Akash Yadav<sup>1</sup>, Raina Jana<sup>1</sup> and Neeraj Wadhwa<sup>1\*</sup>**

1. Department of Biotechnology, Jaypee Institute of Information Technology, Noida, Uttar Pradesh, India

\*Corresponding author: neeraj.wadhwa@jiit.ac.in

Changes in the climate and ecological imbalances caused by burning of fossil fuels have lead to development of renewable, carbon-neutral and economically viable alternatives which can replace these fossil fuels. However, the algal feedstocks are one of the most promising fuels in today's times. This review focuses on a particular algal taxon "diatom" which is a potential fossil fuel of the future. It has been estimated that microalgae an ideal biodiesel feedstock which can be proved to be very beneficial in our near future to replace the petroleum based fossil fuels. Due to the static costs associated with oil extraction and the biodiesel processing and variability of the algal biomass production, cost saving efforts for the algal oil production and the focus on production of oil rich algae is being done. It has been estimated that the yields obtained by diatoms as a production basis are sufficient to satisfy the total oil needs of The United States, and it only uses 3 to 5 % of the total land area. Hence, the futuristic approach needs the enhancement of the algal biology and culture system engineering so as to produce the lower algal biofuel production as well as extract large value- added products such as large quantities of proteins, carbohydrates as well as other nutrients for the use of animal-feed besides biofuel.

PP122

ICABB-042

## SCREENING AND CHARACTERIZATION OF MICROORGANISMS FOR ANTI- MICROBIAL ACTIVITY FROM THE BIODIVERSITY-RICH TIMLI FOREST RANGE, INDIA

**Nidhi Srivastava<sup>1</sup>, Ipsita Nandi<sup>1</sup>, A. Ibeyaima<sup>1</sup>,  
Sanjay Gupta<sup>1\*</sup>, and Indira P. Sarethy<sup>1\*</sup>**

1. Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sector-62, Noida-201309, India

E-mails: nidhu.85@gmail.com nandi.ipson@gmail.com

,ahongeb@gmail.com, \*Corresponding author: sanjay.gupta@jiit.ac.in  
,indirap.sarethy@jiit.ac.in

Emerging antimicrobial drug resistance is threatening global health. The slow pace of discovery of new, effective drugs and combinatorial chemistry being largely unsuccessful has resulted in shifting the focus back to natural products as sources of lead molecules for antimicrobial drugs, due to their structural diversity. Investigation of under-explored habitats for potentially novel microorganisms provides for wider chemo diversity. In our study soil samples have been collected from the unexplored Timli Forest Range (Shivaliks), Dehradun, India. By using selective isolation procedures, bacteria and fungi were isolated and were characterized for antibacterial and antifungal activity. A total of fifty eight distinct colonies of bacteria and fungi were obtained. UK-274, UK-281, UK-282 and UK-285 were selected on the basis of their broad spectrum antibacterial and antifungal activity and identified by 16S rDNA sequencing. UK-274 showed 97.71% similarity with *Actinomadura nitrigenes*, UK-281 97.97% similarity with *Streptomyces niveiscabiei*, UK-282 97.29% similarity with *Kitastospora psammotica*, and UK-285 showed 98.14% similarity with *Streptomyces niveiscabiei*. The low similarity match percentages indicated taxonomic novelty at the genus/species levels, further confirmed by phenotypic and colonial differences with the corresponding matching strains. Metabolite fingerprinting of antimicrobial fractions of isolate UK-282 provides an indication of potentially novel compounds and is discussed further.

## PHYTOREMEDIATION: A GREEN SOLUTION FOR HEAVY METAL DEGRADATION

Arpita Roy<sup>1</sup>, Sanskriti Ravi<sup>1</sup> and  
Navneeta Bharadvaja\*

1. Plant Biotechnology Laboratory, Department of Biotechnology,  
Delhi Technological University, New Delhi-42, India  
E-mails: sanskritiravi@yahoo.co.in, arbt2014@gmail.com,  
\*Corresponding author: navneetab@dce.ac.in

Presence of heavy metals in soils is one of the major ecological concerns and poses risk to the life. A number of human health risks are associated with the presence of heavy metals that enter into the food chain through contaminated soil and water. Different physical, synthetic and natural strategies are being utilized to expel heavy metals and metalloids from soils. Among them, phytoremediation is a good strategy to remove heavy metals from soils and have been proven as an economical and effective technique. Phytoremediation technique utilizes plants for the uptake of heavy metal contaminants from the soil by using plants abilities to suck the heavy metals. This technique can also be used for the removal of other environmental pollutants like organic pollutants that includes poly chlorinated biphenyls (PCBs), poly aromatic hydrocarbons (PAHs) and pesticides. There are several plants which have natural ability to uptake heavy metals and organic pollutants from soil, air and water. Phytoremediation consists of four different plant based technologies, each having a different mechanism of action for the remediation of metal polluted soil, sediment or water. There are different methods of phytoremediation which includes (a) phytofiltration (b) phytoextraction (c) phytostabilization (d) phytovolatilization. The present review provides current knowledge about phytoremediation and its different techniques are discussed.

**Keywords:** Phytoremediation, Heavy metals, phytoextraction phytostabilization

## ROLE OF PROBIOTICS IN PROPHYLAXIS OF *HELICOBACTER* *PYLORI* INFECTION

Kashyapi Chakravarty<sup>1</sup> and Smriti Gaur<sup>1\*</sup>

1. Department of Biotechnology, Jaypee Institute of Information  
Technology, Sector - 62, Noida, U.P., India  
\*Corresponding author: smriti.gaur@jiit.ac.in

*Helicobacter pylori*, a pathogenic bacterium, has been known to be the root cause of numerous gastrointestinal disorders. In patients showing symptoms of its infection, antibiotic therapy is a likely treatment. However, the high cost of antibiotic therapy, associated antibiotic resistance along with other adverse effects has led to the use of probiotics for *Helicobacter pylori* treatment. In recent times, Probiotics have played an essential role as an alternative or complementary prophylaxis for gastrointestinal diseases, thus minimizing antibiotics' usage and their side effects. Probiotics are live microbial agents that exude beneficial effects on their hosts when administered in proper dosage. The organism has been reported to be inhibited to a great extent by probiotics and research employing animal models has shown a significant reduction in *H. pylori*-associated gastric inflammation. In human clinical trials it has been observed that treatment with probiotics alleviated gastritis symptoms caused by *H. pylori* and reduced colonization of the organism. However, the complete eradication of *H. pylori* infection has not yet been reported by the administration of probiotics alone. Complement treatment with probiotics have shown to benefit infected individuals by decreasing harmful effects of *H. pylori* eradication treatment. Long-term administration of probiotics might have favourable outcomes in *H. pylori* infection especially by decreasing the risk of development of diseases caused by increased levels of gastric inflammation. One such chronic condition is gastric ulcer which occurs due to considerable damage to mucosal barrier by *H. pylori* colonization. This review provides a brief description of the promising role of probiotics as an alternative treatment to control *H. pylori* infection and consequently the management of various gastrointestinal disorders among populations with special focus on gastric ulcer.

**Keywords:** Probiotics, *Helicobacter pylori*, Gastrointestinal Disorders, Gastric Ulcer

PP125

ICABB-051

## IMPACT OF ANTIBIOTICS ON PLANT GROWTH

Rupali Barnwal<sup>1</sup> and Dr. Pammi Gauba<sup>1\*</sup>

1. Department of Biotechnology, Jaypee Institute of Information Technology  
Sector-62, Noida, U.P. India-201307  
\*Corresponding author: pammi.gauba@jiit.ac.in

The production and use of veterinary antibiotics has increased rapidly worldwide over the last few decades. However, when these antibiotics are excreted or when used as a part of organic manure, they are spread over the crop land hence plant growth and development might be affected. Impacts on human health through the consumption of antibiotic exposed crop plants have been intensively investigated. Information is still lacking on the effects of antibiotics on plants themselves, particularly on crop species, although evidence suggests adverse effects of antibiotics on growth and performance of plants. This study evaluates the effects of the two antibiotics namely chlortetracycline and tetracycline. Tetracycline, chlortetracycline and tylosin had very little effects on soil respiration while sulfamethoxazole, sulfamethazine and trimethoprim showed temporal effects on properties like soil respiration. Sulfonamides (sulfamethoxazole and sulfamethazine) and trimethoprim were found to be most toxic to plant growth in soil. The main aim and objective of this study is to evaluate experimental evidence of plant-pharmaceuticals interaction, their uptake and their removal by plants and to suggest an open area of research in this new field.

**Keywords:** Antibiotics, Sorption, Degradation and Soil respiration.

PP126

ICABB-053

## REMEDIATION OF NITRATE BY USING MICRORGANISMS

Preeti Thakur<sup>1</sup>, Dr. Pammi Gauba<sup>1\*</sup>

1. Department of Biotechnology, Jaypee Institute of Information and Technology, Noida  
E-mails: preetithakur603@gmail.com,  
\*Corresponding author: pammi.gauba.jiit@ac.in

Nitrate is second leading pollutant in India and emanate due to anthropogenic activity like enormous use of chemical fertilizers in agriculture. Therefore,

nitrate is major concern of our environment. Plants depend upon Nitrate for their growth. These are frequently used in chemical fertilizers to augment the quality of soil. High Practice of using chemical fertilizers elevates the concentration of nitrate in soil along with water. Permissible limit of nitrate is 0.1mg/l for drinking water and 1mg/l for aquatic life. The level of nitrate reported so far as up to 400ppm in ground water. Nitrate contamination has therefore emerged as a global problem and its potential threat marked as on environment sustenance and on human health. High concentration of nitrate arise some environmental issues like eutrophication. Surplus load of nitrate is carcinogenic in nature and causes blue baby syndrome. Besides this, methemoglobin condition in animals. The objective of current study is to identify nitrate remediating microbes from various environmental sites which are heavily polluted from industrial discharge. The isolated microbes can be used for the treatment of waste water in future.

**Keywords:** Nitrate, Blue Baby Syndrome, Methemoglobin, Eutrophication, Carcinogenic.

PP127

ICABB-055

## FUNGAL CHITOSAN AND ITS APPLICATIONS

Sakshi Vashisth<sup>1#</sup>, Siddhant Khandelwal<sup>1</sup>,  
Sonia Purswani<sup>1#</sup>, Advika Gupta<sup>1#</sup>,  
Himanshu Mishra<sup>1#</sup>, Vipra Bhardwaj<sup>1#</sup>,  
Garima Mathur<sup>1\*</sup>

1. Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201307, Uttar Pradesh, India  
E-mails: sakshivashisth96@gmail.com, advika.gupta27@gmail.com, himanshumishra@gmail.com, siddhant.jaypee@gmail.com, soniapurswani27@gmail.com, vipravibhas@bhardwaj.com,  
\*Corresponding author: garima.mathur@jiit.ac.in  
#Equal contribution

Chitosan, the deacetylated derivative of chitin, is a linear copolymer of N-acetylglucosamine and D-glucosamine with more than 40% degree of deacetylation (DD). It is polycationic, antimicrobial, nontoxic, biodegradable biopolymer that have been extensively used in various biomedical sectors. Chitosan is commercially produced by chemical deacetylation of crustacean chitin with strong alkali, creating environmental pollution. Inconsistent composition of raw material often produces heterogeneous mixture (inconsistent physicochemical properties) of chitosan that further affects its application. Alternatively, isolation of chitosan from fungal cell wall appears to be cost effective method to

overcome these limitations. The interest in production of chitosan from fungal sources has gained recently due to potential advantages such as medium molecular weight, higher DD, consistent physicochemical properties, biocompatible, biodegradable etc. Fungal chitosan is used in vast array of industrial and biomedical applications such as food, paper, wastewater, tissue engineering and as a carrier for drug delivery. To broaden the scope of fungal chitosan in possible application sectors, fungal chitosan blends can be fabricated to improve its physicochemical properties. This abstract highlights the review of fungal chitosan, its physicochemical properties and FC based blends and their applications.

**Keywords:** Chitosan, Fungal Chitosan, Tissue engineering, Biocompatible, Blend membrane, Biodegradable.

PP128

ICABB-068

## FIGHTING DEPRESSION WITH OMEGA-3 FATTY ACIDS

**Sakshi Vashisth, Advika Gupta, Ashmita Nautiyal, Merin Lawrence and Garima Mathur\***

Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201307, Uttar Pradesh, India  
 E-mails: sakshivashisth96@gmail.com, advika.gupta27@gmail.com, nautiyalashmita96@gmail.com, merinlawrence95@gmail.com, \*Corresponding author: garima.mathur@jiit.ac.in

Omega-3 fatty acids such as DHA (Docosahexaenoic acid) and EPA (Eicosapentaenoic acid) are essential PUFAs which are the key components of bio membranes and play a vital role in cell integrity, development, maintenance and function. DHA and EPA are long chain polyunsaturated fatty acid (LC-PUFA) which has beneficial effects on cognitive function, neurological and cardiovascular system and anti-inflammatory benefits. Due to these properties, omega-3 fatty acids have positive role in the treatment of neurological disorders such as Depression. Depression is a major depressive disorder affecting more than approximately 300 million people worldwide, estimated by WHO. It is characterized by multifaceted, polygenic and a multi-factorial brain disorder affecting mood of an individual with associated symptoms like anxiety, lethargy and fatigue. It is leading cause of poor quality of life and disability worldwide, causing huge social and economic loss. Pharmaceutical drugs available for treatment have associated side-effects. There are multiple studies which show that EPA and DHA are proving to be very

effective against the treatment of Depression and other psychiatric disorders. Various epidemiological studies have shown a correlation between increase in depression symptoms and lower consumption of dietary omega-3 fish oil. Patients with depressive symptoms are found to have lower serum concentrations of essential fatty acids. This abstract highlights the positive role and impact of omega-3 fatty acids in the treatment of depression.

**Keywords:** Depression, DHA, EPA, PUFAs, Omega-3 fatty acids.

PP129

ICABB-073

## BIOLOGICAL CONTROL OF POST-HARVEST DISEASES IN AGRICULTURAL GRAINS

**Rashi Prakash, S Krishna Sundari\***

Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sector -62, Noida, Uttar Pradesh, India-201307; E-mails: rashiprakash8@gmail.com, \*Corresponding author: krishna.sundari@jiit.ac.in,

The study focuses on the post-harvest diseases in agricultural grains and potential methods for biocontrol. Post-harvest diseases are those that infect various agricultural products (*viz.*, grains, pulses, vegetables, fruits) after their harvest. These diseases contribute to nearly 30% of the overall food losses in many countries. They appear either at pre-processing, transport, storage, drying, processing, packaging and / or marketing level. However, majority of these diseases occur during the storage stage. This may be due to fluctuations in humidity and temperature which leads to growth of certain bacteria and fungi under improper or poorly maintained storage conditions. In order to control the losses at storage level, biological control agents are studied by researchers internationally. These biocontrol agents reportedly work through the mechanisms of antagonism and competition for nutrients, thereby inhibiting the growth and spread (multiplication) of causative agents of these post-harvest diseases. The review presents the potential applications of biocontrol agents both at national and international levels. Biocontrol agents like *Pichia anomala*, *Pichia guilliermondii*, *Bacillus subtilis* and *Aspergillus flavus* have demonstrated their ability to reduce crop (crop-product) deterioration when added to respective crops (crop-products) while storage. *Pichia anomala* has shown to suppress the activity of *Penicillium roqueforti*, which is a prevalent fungi found in stored wheat grains. Similarly, *Rhodococcus*

*erythropolis* has also shown to completely inhibit the growth of *Aspergillus flavus* and subsequent aflatoxins in stored sorghum grains. Some of the commercially available biocontrol products in the market for the control of post-harvest diseases are BINAN-T, F-Stop, Ecofit and Sun-derma. In the near future there can be more biocontrol agents commercially available owing to their efficiency, ease of access, safety, and economic stability.

**Keywords:** Post-harvest, biological control, biocontrol, antagonism.

PP130

ICABB-075

## IMPACT OF HEAVY METALS ON MEDICINAL HERBS

Sakshi Bajpai<sup>1</sup> and Dr. Pammi Gauba<sup>2\*</sup>

1. Student, Department of Biotechnology, Jaypee Institute of Information Technology, Noida, India. 2. Associate Professor, Department of Biotechnology, Jaypee Institute of Information Technology, Noida, India.

\*Corresponding author: pammi.gauba@jiit.ac.in

Herbs are being used as preventive and therapeutic medication for centuries. People across different countries and cultures have long applied and imbibed infusions of countless indigenous plants. In India, the ancient practise of Ayurveda utilized the medicinal properties of traditional herbs. In the recent years, high concentration of heavy metals in the environment, particularly soil, as a result of anthropogenic activities such as mining, industrial and agricultural effluent, excessive use of pesticide etc. has led to a drastic increase in heavy metal concentration in the soil that has resulted in accumulation of metals and their residues in medicinal herbs and their products which in turn alters the elemental composition of herbal residues. In this paper, we have discussed the various sources of metal contamination in the environment, the major metals associated with human health hazard, the mechanism and impact of accumulated heavy metal on plant secondary metabolites, herbal products. The paper also discusses the toxicity associated with deliberate addition of metals to herbal products and the biophysical techniques that are utilized to quantify the metal content in herbal products. The paper aims to highlight the need of stringent regulatory guidelines and suggests some safety parameters that must be evaluated and ensured prior the approval and sale of herbal products in Indian market.

**Keyword:** Heavy metal, herbal products, toxicity, metal accumulation.

P131

ICABB-076

## GUT EMOTIONS: PSYCHOBIOATICS AS AN ADJUVANT THERAPY IN DEPRESSION AND ANXIETY DISORDERS

Avishi Aggarwal, Twinkle Wahi, and Smriti Gaur\*

Department of Biotechnology, Jaypee institute of Information Technology, Noida, Sector 62, Uttar Pradesh, India

E-mails: avishiaggarwal18@gmail.com, \*Corresponding author: smriti.gaur@jiit.ac.in

The term probiotic is defined as live microorganisms that are known to provide health benefits when consumed. There are many benefits of using probiotics, such as improving immune health, reducing gastrointestinal discomfort or relieving constipation. Probiotics may play role in the treatment of many psychiatric illnesses from depression to schizophrenia. It has been suggested that probiotic bacteria have beneficial effects on the symptoms of mental disorders such as depression and anxiety. "Psychobiotics" is the term given to such probiotics. Depression and anxiety are two different disorders, but people with depression often experience symptoms similar to those of an anxiety disorder such as irritability, nervousness and problems like sleeping and concentrating. It has been seen that changes in intestinal bacteria may play a role in neuropsychiatric conditions such as anxiety or depression. The intestine has its own separate nervous system, and generates many neurotransmitters (GABA, dopamine, acetylcholine and serotonin) that the brain generates. There is a bidirectional relationship between the central nervous system and gut referred to as the gut-brain axis which allows the gut to receive and send signals to and from the brain. Psychobiotics influence the mood by reducing stress hormone i.e cortisol, formation of neurotransmitters and regulating the body's response to inflammation. There are many strains of probiotics that can be used as psychobiotics like *L. helveticus*, *L. rhamnosus*, *B. longum*, *B. breve* etc. Prebiotics such as Galacto-oligosaccharides can also be used as psychobiotics. It has been understood that healthy gut play a critical role in human development such as immune development and metabolism. The potential of probiotics to be used as a novel treatment for mental disorders could have a major impact on those seeking antidepressant treatment by reducing the latency and side effects linked with antidepressants.

**Keywords:** probiotics, depression, anxiety, neurotransmitters, gut-brain axis, prebiotics

## RUTIN: EXTRACTION AND BIOLOGICAL ACTIVITIES

Twinkle Wahi, Avishi Aggarwal, Diksha Rathore,  
and \*Smriti Gaur

Department of Biotechnology, Jaypee institute of Information Technology, Noida, Sector 62, Uttar Pradesh, India  
E-mails: twinklewahi.tw21@gmail.com,

\*Corresponding author: smriti.gaur@jiit.ac.in

Rutin ((32, 42, 5, 7-tetrahydroxy-flavone-3-rutinoside) also called rutoside, quercetin-3-O rutinoside and sophorin, is a flavonol glycoside present in many foods especially buckwheat, apricots, grapefruit etc. It is receiving increasing attention due to its various health benefitting biological activities such as anti-oxidant, anti-inflammatory, etc. The major disadvantage associated with rutin is its poor bioavailability, mainly caused by its poor stability, low aqueous solubility, and limited membrane permeability. Additionally the low liposolubility of rutin also limits its practical use for topical applications. Both conventional and innovative methods have been reported for the extraction of rutin from natural sources. However, current trends on extraction process have been focused on the discovery and design of green and sustainable extraction techniques to optimize the extraction of rutin. Rutin has shown a wide range of pharmacological applications due to its significant antioxidant properties. Conventionally, rutin is used as antimicrobial, antifungal, and anti-allergic agent. Current research has shown its pharmacological benefits for the treatment of various chronic diseases such as cancer, diabetes, hypertension and hypercholesterolemia. However, the observed effects *in vitro* do not always translate into the clinic because of rutin poor bioavailability. To overcome this barrier, researchers have focused towards different strategies that, in principle, will enhance bioavailability and ultimately health benefits. Drug delivery systems based on nanoparticle systems, and phospholipid complexes are some of the rutin formulations with increased bioavailability. Additionally, derivatives of rutin obtained from chemical or enzymatic transformation have been also demonstrated not only to possess increased solubility but also enhanced biological properties.

**Keywords:** Rutin, anti-oxidant, anti-inflammatory, bioavailability

## EFFECT OF DIFFERENT LIGHTS ON THE GROWTH AND DEVELOPMENT OF ENDANGERED MEDICINAL HERB *RHODIOLA IMBRICATA*

Archit Pundir, Anaida Kad, Shubham Sharma and Hemant Sood\*

Dept. of Biotechnology and Bioinformatics, Jaypee University of Information Technology, Waknaghatal, (H.P.), India (PIN-173 234)

\*Corresponding author: hemant.sood@juit.ac.in

*Rhodiola imbricata* EDGEW (Family: Crassulaceae; Common name: Golden root) is a herbaceous, dioecious, perennial plant. It is indigenous to the Trans-Himalayan regions and exclusively found in Indus and Leh valleys of India. This plant has been used extensively in Ayurvedic, Unani, Chinese and Tibetan folk medicines. *R. imbricata* has various pharmacological activities like hepatoprotective, radioprotective, neuroprotective, immunomodulatory, anticancerous etc., which is attributed to the presence of phytochemicals such as salidroside, p-tyrosol, rosavin, etc. In this study, we have analysed the effect of white fluorescent light (WFL) of 3000 lux intensity and artificially created photosynthetic light (PSL) of 4000 lux intensity by using combination of LEDs on the growth and development of the plant under optimized culture conditions. *R. imbricata* shoot apex and leaf explants were cultured in triplicates on MS medium supplemented with BAP (1 mg/l) and IBA (2 mg/l) for shoot production and MS media + TDZ (1mg/L) for callus induction under WFL and PSL at 15±10C. The in-vitro grown shoots were observed for growth and development parameters at both conditions in which 1.639 g/flask biomass was observed in WFL incubated plants as compared to 1.289 g/flask in PSL and callus biomass obtained was 0.897 g/flask in WFL and 0.269 g/flask in PSL. The inter-nodal length of 1.7cm was observed in shoots grown under PSL as compared to 0.25cm shoots and 0.35 cm in callus regenerated shoots incubated in WFL. Chlorophyll content was estimated using spectroscopic analysis. The chlorophyll concentration in the plant tissue incubated in WFL was 152mg/g and 150mg/g in shoots regenerated from callus as compared to 53.6mg/g in PSL grown shoots. Thus, WFL incubated shoots showed 2.8 folds more chlorophyll content than PSL shoots which could be contributing for better survival of these developed plantlets under field conditions. So, this is reported for the first time in *Rhodiola imbricata* that alternative and economic sources

of light like LEDs could be used for large scale micro-propagation of plants with sustainable growth which could also be extended for production of the significant phytochemicals.

**Keywords:** Artificial photosynthetic light, White fluorescent light, chlorophyll estimation, *Rhodiola imbricata*.

PP134

ICABB-114

---

## OPTIMIZATION OF CAROTENOID PRODUCTION BY YEAST STRAINS FROM DIFFERENT SOURCES USING AGRO-RENEWABLE WASTE

Kumari Sweta, Gunjan Singh, Arshad Jawed,  
Debarati Paul\*

Amity Institute of Biotechnology, Amity University, Noida, U.P  
E-mails: swetariteshsinha@gmail.com, gunjan.singh15@gmail.com,  
arshadjawed29@gmail.com, \*Corresponding author: dpaul@amity.edu\*

---

Microbial synthesis of carotenoids has gained more interest as an alternative to synthetic carotenoid production due to its easy extraction and high yield. In this study, the microbial pigment production by yeast strains isolated from different sources was evaluated under different growth conditions and nutrient composition. Different agro-renewable waste were used as carbon source for different yeast strains to obtain maximum amount of microbial carotenoid. Yeasts are unicellular eukaryotic organism and good carotenoid producer. They have simple nutritional requirements and so they can grow rapidly on inexpensive substrates in large quantities, thus providing a cost effective method of adequate utilization of waste. This work aimed at identifying efficient carotenoid pigment producing yeast strains by utilizing potential inexpensive natural substrates from waste to minimize the production cost of pigments. Total six pigment producing yeast isolates were obtained from soil, fruits, flowers, agro-industrial wastes, and processed product in decomposition and grown in different medium (1) minimal medium, (2) waste extract medium and (3) hydrolysate from dry paddy straw in an orbital shaker, using 10% (w/v) of inoculum (300C, 120 rpm for 48 h) and incubated for 120 h. Maximum carotenoid content in the yeast cells was produced during stationary phase after 5 days of growth. Among 6 isolates, *Rhodotorula glutinis* ATCC 204091 showed maximum intracellular pigment production of 62 mg/g of dry cell mass in waste extract medium whereas the pigment production from the strain isolated from flower and fruit and vegetable

waste was 40 mg/g of dry cell mass in waste extract medium. This study enables the efficient utilization of vegetable and fruit waste and also other agricultural waste for carotenoid production through microbial fermentation. The carotenoids may be used as nutraceuticals, anti parasitic agent, anti cancerous, and anti oxidants in animal feed and also in cosmetic preparation.

**Keywords:** carotenoids, yeast, *Rhodotorula*, waste, carbon sources

PP135

ICABB-117

---

## CHITINOLYTIC BACTERIA: AS BIOCONTROL AGENT

Monika Gupta<sup>1</sup>, Ajit Varma<sup>1</sup> and  
Bishwajeet Paul<sup>2\*</sup>

1. Amity Institute of Microbial Technology, Amity University, Noida (U.P) – 201303, India 2. Department of Entomology, Indian Agriculture Research Institute, New Delhi, India  
E-mails: mgupta4@amity.edu, \* Corresponding author: bishwajeet\_paul2011@yahoo.com

---

**Abstract:** **Problem statement:** Chitin, a common constituent of insect exoskeleton, could be hydrolyzed by chitinase. The research was conducted to screen chitinolytic bacteria isolated from bulk soil to determine their chitinase activity in degrading chitin of *Spodoptera litura* (Lepidoptera). Lepidopterans are recognized as an important pest of Brassicaceae crops.

**Approach:** Screening and effect of the chitinase treatment on *S. litura* were studied. **Results:** A total of 28 isolates formed clear zone on solid chitin media. Six isolates, i.e., MCPB1, MCPB2, MCPB3, MCPB4, MCPB5 and MCPB6 had the highest zone clearance area on chitin media plates. At initial levels to test the efficacy of these isolates against *S. litura* larvae (10 days old), larvae were allowed to feed upon the diet mixed with different concentration of these bacterial isolates. The effect was observed using a microscope and sterile water was used as a negative control. Observation showed that crude enzyme of isolates could degrade chitin of *S. litura* gut lining as a result larvae stop feeding upon the diet and die due to starvation and puncture in gut lining. **Conclusion:** Through preliminary insect bioassay it is concluded that chitinase produced by bacterial isolates has potential application as biocontrol agents for *S. litura*.

**Key words:** Chitin degrading bacteria, *S. litura*, insect bioassay, biocontrol

---

## **BRASSINOSTEROID-SEED TREATMENT REGULATES BIOCHEMICAL RESPONSES OF BRASSICA JUNCEA SEEDLINGS UNDER INSECTICIDE STRESS.**

**Anket Sharma<sup>1\*</sup>, Vinod Kumar<sup>1</sup>,  
Ashwani Kumar Thukral<sup>1</sup>, Renu Bhardwaj<sup>1</sup>**

*Plant Stress Physiology Lab, Department of Botanical and Environmental Sciences, Guru Nanak Dev University, Amritsar-143005, India.*

\*Corresponding author: anketsharma@gmail.com

---

Crop plants are generally attacked by insect pests, which lead to reduction in the crop yield. To control this yield loss, pesticides are widely utilized. However, the application of pesticides also causes toxicity to the crop plants which result in their impaired growth and photosynthesis accompanied by enhanced oxidative stress. The present study was designed to assess the effects of 24-epibrassinolide (EBR) on *Brassica juncea* seedlings germinated in presence of a systemic insecticide, imidacloprid (IMI). Ten days old seedlings were analyzed for antioxidative defense response, protein content, amino acid profiling and elemental composition. It was observed that imidacloprid application significantly decreased the content of protein, amino acids as well as various elements in *B. juncea* seedlings. However, it has been noticed that after EBR application, the antioxidative defense system gets activated under IMI toxicity, accompanied by recovery of protein, amino acid content as well as elemental composition of seedlings.

**Keywords:** *Brassica juncea*, Indian mustard, insecticide stress, oxidative stress.

---

## **INTERDEPENDENCY OF SOIL QUALITY AND MICROBIAL ACTIVITY: A REVIEW**

**Soumya Soni<sup>1</sup>, Purnam Hoshe Ruba<sup>1</sup>,  
Mahima Maheshwari<sup>1</sup>, Krishna Anand Dwivedi<sup>1</sup>,  
Asmita Arora<sup>1</sup>, Akshra Gupta<sup>1</sup>, Archana Kumari<sup>1</sup>  
and S Krishna Sundari<sup>1\*</sup>**

*1. Jaypee Institute of Information Technology, A-10, Sector-62, Noida, Uttar Pradesh 201309*

*E-mails: skrishnasundari@gmail.com,*

*\*Corresponding author: krishna.sundari@jiit.ac.in*

---

Soil is the abode of an incredibly diverse ecosystem of which micro-organisms form a principle part. Soil quality is variously affected by the presence of these microbes and the soil-microbe associations can have a host of relationships governed by myriad factors. Also, agricultural demography and output depends to a large extent on the nature of the soil. Hence, the study of interdependence of soil and microbial activity therein, is highly beneficial to the entire agriculture sector. The Soil quality mainly refers to the "capacity of the soil to function as a vital living system". It is shaped by its physical, chemical & biological properties. The micro-biological processes spearheaded by microorganisms in soil can be one of the potential indicators of soil quality. This review paper deepens our understanding about the correlation between soil quality and microbial activities. This paper revisits the extensively used physical and chemical indicators of soil quality viz., concentration of macro & micro nutrients (N, P, K), pH, electrical conductivity, chloride & Calcium-Magnesium ion concentration, porosity, water retention capacity, percentage humidity and cation exchange capacity. It also gives a fresh insight and a new perspective in improving soil productivity, sustainability and growth of Agrarian sector.

**Keywords:** Soil quality; Soil microbial activity; Physical, chemical and biological properties.

## A STUDY ON THE DYNAMIC ASSOCIATIONS BETWEEN SOIL QUALITY AND MICROBIAL ACTIVITY IN SELECTED REGIONS OF NORTH INDIA

Akshra Gupta<sup>1</sup>, Asmita Arora<sup>1</sup>,  
 Krishna Anand Dwivedi<sup>1</sup>, Mahima Maheshwari<sup>1</sup>,  
 Pratibha Yadav<sup>1</sup>, Purnam Hoshe Ruba<sup>1</sup>,  
 Soumya Soni<sup>1</sup>, S Krishna Sundari<sup>1\*</sup>

1. Jaypee Institute of Information Technology, A-10, Sector-62, Noida,  
 Uttar Pradesh 201309

E-mails: skrishnasundari@gmail.com,\*Corresponding author:  
 krishna.sundari@jiit.ac.in

Agriculture forms the main building block of Indian economy, as a large number of Indian population rely on agriculture for their living. Agriculture practices and crop yield are known to be directly linked to soil quality. Soil quality is the potential of soil to function in an ecosystem providing a reflection of plants and animal health, its biological productivity and microbial activity along with environmental quality. Soil is known to inhabit a wide range of microorganisms which in turn contribute to soil quality. The present study intends to understand and observe the associations between soil quality and soil microbial activity. In our study, we collected soil samples from various districts of North India and analyzed them for various parameters indicative of soil quality grouped as physical and chemical parameters. The physical parameter included tests such as water retention capacity, percentage humidity, porosity and chemical parameters studied were pH, electrical conductivity (EC), cationic exchange, macro and micro nutrient content in soil. Further we studied soil microbial activity to understand the correlation of microbiota with soil quality for which we conducted methylene blue assay, turbidity assay, respiration assay, enzyme activity & total DNA content. Agreeing with our hypothesis, our results brought to fore, the interdependency between different soil parameters and the activity of microbes present in the soil samples.

## INVESTIGATION OF ALTERNATIVE SPLICING MODULATION OCCURRING ON INFECTION OF TOMATO LEAF CURL NEW DELHI VIRUS (ToLCNDV) IN TOMATO (*Solanum lycopersicum* L.)

Manoj Prasad<sup>1</sup> and Shweta<sup>1\*</sup>

National Institute of Plant Genome Research, New Delhi-110067

\* Corresponding author: shweta.bioscience@nipgr.ac.in

Tomato leaf curl disease (ToLCD) is one of the most devastating diseases of tomato that causes significant yield loss in tomato, in tropical and subtropical climates especially in South and Southeast Asia. This severe disease is caused by Tomato leaf curl New Delhi virus (ToLCNDV), a species of the genus Begomovirus, family Geminiviridae, transmitted by whiteflies (*Bemisia tabaci* Genn.). Alternative splicing (AS) is involved in regulating plant growth and development, flowering, circadian clock function, and stress responses. Alternative splicing occurring at the genomic level during plant-microbe interaction is not yet completely explored. We had employed high-throughput NGS RNA sequencing technology to generate a spliceosome map of *S. lycopersicum* infected with Tomato leaf curl New Delhi virus (ToLCNDV) upto the isoform-level. Comparative analysis of AS pattern identified in *S. lycopersicum* in response to virus infection was compared to monocot (*Oryza sativa*) and dicot (*Arabidopsis thaliana*) plants to estimate the conserved ratios of the AS types. Huge number of AS events were observed in *S. lycopersicum* but AS ratios were least affected. AS event was observed in several immune-responsive genes, R genes, ubiquitin and RNA silencing genes. Research insights of this study about AS landscapes during plant-virus interaction will trigger a new paradigm of plant defense. It will be helpful in employing effective defense strategy against ToLCNDV.

**Keywords:** Tomato leaf curl disease, Begomovirus, Alternative splicing, Tomato leaf curl New Delhi virus

## BIOCHEMICAL AND PHYTOCONSTITUENT STUDY OF PLANTS GROWN IN FLY ASH AMENDED SOIL: A WASTE MANAGEMENT APPROACH.

**Ayushi Varshney<sup>1\*</sup>, Sumedha Mohan<sup>2</sup> and Praveen Dahiya<sup>3</sup>**

*Amity Institute of Biotechnology, Amity University, Noida, U.P., India.*

\*Corresponding author: ayushi.alg@gmail.com

Fly ash is an important combustion residue and the most conversant industrial by-product. It is a source of various micronutrients and macronutrients that are essential for plant growth. The striking variations towards the sensitivity of fly ash are observed in the plant growth performance including Phytoconstituent and biochemical parameters. The growth and metabolism of plant was studied in different soil with different concentration of fly ash amendment. This study is an attempt to know the impact of fly ash on Phytoconstituent level and biochemical parameters of the plants and also to determine the possible utilization in various agricultural practices. Fly ash contains heavy metals which may prompt the production of bioactive components and thereby can enhance the medicinal potential of that plant. At high concentration of Fly ash amended soil, the experiment shows deleterious effect, the maximum being 100% fly ash with no amendment of soil. This shows that at high concentration of heavy metals in fly ash generated from thermal power plant have harmful impact on plants due to their toxic concentration. At low concentration of fly ash amended soil, heavy metals are better for plant growth, production of bioactive components and also for the medicinal potential of plants. The large scale use of fly ash in agriculture holds the potential to increase on an average 10 to 15% of yield and growth performance of the plants.

**Keywords:** Fly ash amended soil, biochemical parameters, Phytoconstituent, heavy metals

## IMPACT OF LEAD ON LEGUMUNOUS PLANTS

**Mahender Singh Rawat, Parul Chauhan  
Richa Verma, Sakshi Bhadouria, Akshita Jain and Pammi Gauba\***

*Department of Biotechnology, Jaypee Institute of Information Technology, Noida*

*A-10, Sector-62, Noida, Uttar Pradesh-201307*

\*Corresponding author: pammi.gauba@jiit.ac.in

Pollution of natural resources by heavy metals is an issue that has impacted entire environmental & human population around the globe. The use of plant and their associated microbes for environmental cleanup is an emerging technology and also cost-effective, noninvasive alternative or complementary technology for engineering based remediation methods. In the environment, lead induces toxicity in plants, animals and microorganisms. Lead contaminants exist in insoluble form in the environment, and its associated toxicity poses threat of severe health hazards. Plant grown with lead showed decrease in biomass, this was found to be directly related to the concentration of lead. The root and shoot length also showed a decrease with increase in concentration of heavy metal. Impact of lead on leguminous plants *Vigna radiata* & *Vigna mungo* was seen by growing them in different concentrations of this heavy metal. They were grown for 3 weeks & the parameters noted were length of whole plant, root length, shoot length, fresh weight & dry weight. Maximum toxicity of lead in *Vignaradiata* & *Vigna mungo* was observed at 500ppm when grown with different concentrations respectively. Both root and shoot length showed decrease with increase in the concentration of the pollutant. Maximum tolerance of lead by *Vigna mungo* was upto 700ppm whereas *Vigna radiata* shows tolerance up to 1000ppm. It could be concluded that at concentration greater than 500ppm, toxicity was induced in the plants.

**Keywords:** Toxicity; Remediation; *Vigna radiata*; *Vigna mungo*; Tolerance; Concentration; Environment.

## EQUILIBRIUM STUDIES OF Pb<sup>2+</sup> IONS BIOSORPTION FROM AQUEOUS SOLUTION USING *S. filipendula*

Ayushi Verma<sup>1</sup>, Shashi Kumar<sup>1</sup>, Surendra Kumar<sup>1</sup>  
and Chandrajit Balomajumder<sup>1</sup>

1. Department of Chemical Engineering, Indian Institute of Technology Roorkee, Roorkee – 247 667, Uttarakhand, India

This work reports biosorption of Pb<sup>2+</sup> ions onto *Sargassum filipendula* of seaweed in batch mode of operation. Elevated levels of Pb<sup>2+</sup> ions can be traced to industrial discharges from a variety of sources, such as electric battery manufacturing, lead smelting, and mining activities. The presence of lead in drinking water is known to cause various types of serious health problems leading to death in extreme exposure cases. The concentration of lead-ion in waste waters must be reduced to a level of 0.05 mg/L before discharging to waterbodies. In order to find out the effect of biosorbent dose on biosorption, all the experiments with different dosages of *S. filipendula* were carried out at constant pH 5.0, 35°C, 150 mg/L of initial Pb<sup>2+</sup> ions concentration and 150 rpm for 85 min. Experiments at different biosorbent dosages revealed that good biosorption capacity as well as high metal removal efficiency was observed at 0.5 g/L. The equilibrium of Pb<sup>2+</sup> ions biosorption was achieved at 60 min. The results revealed that *S. filipendula* removes 96 % of Pb<sup>2+</sup> ions from solutions containing 150 mg/L at temperature (35°C), pH (5.0), biosorbent dosage (0.5 g/L). The four isotherm models (Langmuir, Freundlich, Radke-Prausnitz and Fritz) were fitted to illustrate the equilibrium isotherms. The goodness of fit of the experimental data to the proposed isotherm models is generally attested by correlation coefficient R<sub>2</sub>. The experimental data are fitted to four isotherm models by using curve fitting tool of MATLAB 6.5 on Window XP. It was observed that the value of R<sub>2</sub> for Fritz is 0.99 greater than other models. Thus, it is concluded that Fritz was the more appropriate isotherm model for the removal of Pb<sup>2+</sup> ions by *Sargassum sp.* of seaweed.

**Keywords:** isotherm models, biosorption, lead, *Sargassum filipendula*

## EXPRESSION ANALYSIS OF CHITINASE CLASS-IV GENE OF *BRASSICA JUNCEA* IN RESPONSE TO HORMONAL TREATMENTS AND *ALTERNARIA BRASSICAE*

Zahoor Ahmad Mir<sup>1</sup>, Sajad Ali<sup>2</sup>, Prashant Yadav<sup>1</sup>,  
Apekshita Singh<sup>3</sup> and Anita Grover<sup>1\*</sup>

1 National Research Centre on Plant Biotechnology, New Delhi,  
2Centre of Research for Development (CORD), University of Kashmir,  
3Amity Institute of Biotechnology, Amity University, Noida  
\* Corresponding author: anitagrover@hotmail.com

Pathogenesis-related proteins (PRs) are one of the important antimicrobial weapons which can lead to increased resistance against an array of pathogens. Among them are PR3 proteins (Chitinases) which not only plays important role in combating plant biotic and abiotic stress but also in plant development. *Brassica juncea* is an important oil seed crop across the globe which is very prone to biotic and abiotic stresses. The aim of this study was to isolate and characterize a chitinase gene (class IV) from *B. juncea*. The expression pattern of chitinase class-IV gene showed maximum expression at 6hr after treatment with *Alternaria brassicaceae*. After jasmonic acid (JA), salicylic acid (SA) and abscisic acid (ABA) treatments, Chitinase-IV gene showed varied expression patterns hence suggesting their role in plant defense mechanism. Based on the expression studies, chitinase gene was significantly induced by JA but not by SA. These results further provide the evidence that chitinase IV genes can be used as JA signature in *B. juncea*. As chitinase IV gene was induced by both *A. brassicaceae* and JA, hence can serve as a potential candidate for improving disease resistance through genetic engineering.

## **ANALYSIS OF TRANSCRIPTOME AND METABOLOME RESPONSES DURING CR(VI) STRESS IN ROOTS OF ORYZA SATIVA**

**Sonali Dubey<sup>1</sup>, Vibha Rania<sup>1\*</sup>,  
Debasis Chakrabarty<sup>b2</sup>**

*1. Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201307, Uttar Pradesh, India  
E-mails: sonalidubey2007@gmail.com, \* Corresponding author:  
vibha.rani@jiit.ac.in, chakrabartyd@nbri.res.in*

Extensive usage of chromium (Cr) elevates its concentration in surface soil due to improper management of effluent discharge from industries associated to metallurgy, tanning and electroplating. In Asian countries rice serves as the major staple food and rice consumers are affected by substantial quantity of Cr due to contamination in cultivated land. This study focuses on Cr(VI) toxicity and understanding it's metabolism as molecular events underlying Cr(VI) toxicity and the defence responses in rice have been partially elucidated. Genome-wide transcriptome profiling in rice root was done and stress responsive genes were identified. Present study is helpful for the identification of genes accountable for tolerance, accumulation and defence response in plants with respect to Cr stress. Rice root metabolome analysis was also carried out to relate differential transcriptome data to biological processes affected by Cr (VI) stress in rice. Metabolome analysis propose that content of several metabolites including proline, lactate, fructose, uracil and alanine was significantly enhanced during Cr(VI) stress. The comparative analysis of both transcriptome and metabolome data provided us some various connections between genes and metabolic components. Detailed analysis of specific genes can lead to development of strategies for decontamination that can be used for environmental remediation of Cr(VI) pollution.

**Keywords:** Cr(VI) stress, Transcriptome, Metabolome, Rice, Root

## **PRODUCTION OF PROINSULIN IN MILK OF TRANSGENIC ANIMALS**

**Pranav Pancham<sup>1</sup>, Rachit Ananad<sup>1</sup>,  
Manisha Singh<sup>1</sup> and Rachana**

*<sup>1</sup> Department of Biotechnology, JIIT Noida, Sector 62, Noida, UP, India- 201309*

There is a major global need to produce large amount of Insulin to battle with diabetes. With the advances in genetic engineering methods, we are gaining the ability to tackle such problems, effectively. The first successfully purified Insulin was produced from a dog's pancreas by two Canadian Scientists to cure type 1 diabetes. Genetic engineering laid the foundation of producing and meeting the high demand of proinsulin (a precursor of Insulin). It was a major breakthrough, decoding the Insulin structure and locating the position of Insulin gene on human chromosome. Another major development was when Insulin was expressed in transgenic mice. Likewise other organisms, such as yeast, were also started being used successfully to produce human Insulin by manufacturing synthesize DNA. Earlier, vast killings of animals, was required to obtain Insulin. Currently, researchers are working on using transgenic rat's and cow's milk, to obtain Insulin at a very low cost, by introducing the human gene segments into the embryo of rats and cow, prior to implantation into the surrogate organism. Insulin can be purified from the milk after extraction of milk. Such practices have initially been tested on goats and cows to produce human proteins. In the present study, production of Insulin with various approaches will be discussed in detail.

**Keywords:** Genetic Engineering, Proinsulin, Transgenic, Insulin, Embryo, Implantation

## AZOTOBACTER VINELANDII STRAIN SRIA<sub>Z</sub>3 INFLUENCES PIRIFORMOSPORA INDICA GROWTH UNDER IN VITRO CONDITION

**Surbhi Dabral<sup>1</sup>, Yashaswee<sup>1</sup>, Prasun Bandyopadhyay<sup>1</sup>, Disha Rathi<sup>1</sup>, Deepesh Bhatt<sup>2</sup>, Ajit Varma<sup>1</sup> and Manoj Nath<sup>1\*</sup>**

1. Amity Institute of Microbial Technology, Amity University Uttar Pradesh, Sector 125, Noida, 201313, India 2. Department of Biotechnology, Shree Ramkrishna Institute of Computer Education and Applied Sciences, Veer Narmad South Gujarat University, Surat, Gujarat, 39500, India

E-mails: sdabral@amity.edu, yashaswee10501812@gmail.com, prasun.banerji@gmail.com disharathi28@gmail.com, deepesh987@gmail.com, ajitvarma@amity.edu,

\*Corresponding author: mnath1@amity.edu

In rhizosphere, microbes are a crucial component of plant growth and development. Among microbes, magic fungus- *Piriformospora indica* and a novel bacteria *Azotobacter vinelandii* are well known for plant growth promotion and stress alleviation. Notably, individual inoculation of the *P. indica* or *A. vinelandii* is reported to help a plant to cope up the stressful environment therefore it would be interesting to investigate the mutual interaction among these two microbes. The aim of the present study is to explore the interaction of *P. indica* and *A. vinelandii* strain SRIA<sub>Z</sub>3 under in vitro condition. Differential growth response of *P. indica* was observed after inoculation of SRIA<sub>Z</sub>3 on different days. Interestingly, enhanced *P. indica* growth in terms of hyphal radius and dry cell weight was found after 7 days of inoculation (DOI) of SRIA<sub>Z</sub>3. In addition, cell free supernatant of SRIA<sub>Z</sub>3 increased the *P. indica* spore germination as compared with control. Confocal microscopy based analysis also revealed better hyphal growth and sporulation after 7 DOI of SRIA<sub>Z</sub>3. Moreover, less sporulation and distorted *P. indica* hyphae were observed after co-inoculation of *P. indica* and SRIA<sub>Z</sub>3 on the same day. The finding of the present study will help to investigate the interaction of *P. indica* and SRIA<sub>Z</sub>3 with plants under stress conditions

**Keywords:** *Piriformospora indica*, *Azotobacter vinelandii* strain SRIA<sub>Z</sub>3, Microbial interactions, Confocal Microscopy

## ADVANTAGE OF GENETICALLY MODIFIED PHYTASE PRODUCING CROPS

**Akanksha Verma and Smriti Gaur\***

Jaypee Institute of Information Technology, Sector-62, Noida, Uttar Pradesh-201307

\*Corresponding author: smriti.gaur@jiit.ac.in

Myo-inositol hexakiphosphate phosphohydrolase well-known as phytase enzyme is a type of phosphatase enzyme that activates the hydrolysis of Myo-inositol hexakisphosphate i.e. phytic acid. Basically, it is a kind of digestive enzyme which dissolves the anti-nutrient or inedible phytic acid which is present in both plants and animal body. Phosphorous is the essential element required for optimal growth of animals but these phosphorous along with other vital minerals are present in bound form of phytic acid which cannot be consumed. Therefore, crops of cereal grains such as wheat, oats, rice, corn (maize), barley etc. and oilseed meals which are the primary source of animal feeds are need to be genetically modified. Overexpression of phytase enzyme was the main objective for transforming these crops genetically. This results in a greater reduction of feed costs as there is no need of additional supplementation of these enzymes in the animal feed. Another major issue which is resolved by these engineered crops is that it avoids algal bloom or eutrophication which further prevents environmental pollution as the excretion of the bound phosphorous along with other vital minerals through animals is reduced. Along with decreasing pollution these bioengineered crop plants with overexpressed phytase, improves both plant and animal nutrition as they provide the large amount of phytase enzyme. Various crop plants such as *Tobacco*, *rice*, *cotton*, *potato*, *sweet potato*, *soybean*, *maize*, *wheat*, *Arabidopsis*, *Chlamydomonas*, *Brassica napus* etc. have been genetically transformed with phytase gene and heterologous expression of these phytase enzymes has resulted in an improved consumption of inorganic phosphorous. This transgenic approach is a long-term approach which has proved to be the most versatile and cost-effective method.

**Keywords:** Phytase enzyme, phytic acid, transgenic crops, feed cost, environmental pollution

## ***IN VITRO ASSESSMENT OF PIRIFORMOSPORA INDICA UNDER SALINITY STRESS***

**Yashaswee<sup>1</sup>, Surbhi Dabral<sup>1</sup>, Disha Rathi<sup>1</sup>,  
Deepesh Bhatt<sup>2</sup>, Ajit Varma<sup>1</sup>, Manoj Nath<sup>1\*</sup>**

1. Amity Institute of Microbial Technology, Amity University Uttar Pradesh, Sector 125, Noida, 201313, India 2. Department of Biotechnology, Shree Ramkrishna Institute of Computer Education and Applied Sciences, Veer Narmad South Gujarat University, Surat, Gujarat, 39500, India  
E-mails: sdabral@amity.edu, yashaswee10501812@gmail.com, disharathi28@gmail.com, deepesh987@gmail.com, ajitvarma@amity.edu, \*Corresponding author: mnath1@amity.edu

Salt stress negatively affects plant growth that consequently leads to yield reduction. Plants employ several salt stress adaptive mechanisms in order to alleviate this stressful situation. Moreover, a fungal root endosymbiont-*Piriformospora indica*, is well reported for promoting plant growth and stress tolerance. The present study was planned to monitor the *in vitro* growth of *P. indica* under different salt conditions (0, 50, 100, 200, 300, 400, 500 mM NaCl). Here, we have analyzed the hyphal radius, sodium ion (Na<sup>+</sup>), reactive oxygen species (ROS) and cell death of *P. indica* under different salt concentrations. In general, growth of the *P. indica* showed reciprocal relationship with respect to salt concentrations. Notably, similar hyphal radius was observed in control (non-stressed) and 50 mM NaCl condition. The specific fluorescent indicators CoroNa Green, H2DCFDA and propidium iodide were used in salt stressed *P. indica* spores to analyze the sodium (Na<sup>+</sup>) ion, reactive oxygen species (ROS) and cell death respectively. Confocal based analysis indicated augmented level of Na<sup>+</sup>, ROS and cell death in *P. indica* spores under salt (50 and 100 mM NaCl) environment as compare with control. Further, work is still in progress to investigate the effect of *P. indica* on rice varieties under different salt stress conditions. The present study will provide a promising application of *P. indica* for sustainable agriculture, especially in the salinity affected areas.

**Keywords:** *Piriformospora indica*, ROS, Confocal Microscopy, Root endosymbiont, Salinity

## **ESTROGEN TOXICITY**

**Priyanka Sandal and Dr. Pammi Gauba\***

Department of Biotechnology, Jaypee Institute of Information Technology Sector-62, Noida, U.P. India-201307

\*Corresponding author: pammigauba@jiit.ac.in

Oestrogen is usually referred as female sex hormone as it is responsible for sexual and reproductive development in woman. It plays an important role in the development of female secondary sex characteristics. Environmental oestrogens are known as endocrine disruptors because they are said to harm the human endocrine system. Estrogen toxicity is caused because of these environmental estrogens. The glandular system releases estrogen directly into the bloodstream. But environmental estrogens can cause hormonal imbalances and may have an adverse effect one's overall health. Estrogen toxicity has been reported to have unfavourable effect on Postmenopausal Osteoporosis in mice, adult ovaries. These changes lead to in men and premenopausal women, excess of estrogen – a condition called estrogen dominance – causes toxic fat gain, water retention, bloating, and a host of other health and wellness issues. Detection of abundant amount of estrogen in the environment has raised concerns in recent years because of their potential to affect both wildlife and humans. Occurrence of estrogens in drinking water in the diet of children and adults has severe effects on their health and will ultimately affect their lifestyle.

**Keywords:** Oestrogen, Endocrine disruptors, Osteoporosis, Premenopausal, Estrogen.

## AUXIN PRIMING AND INDUCTION OF S-PHASE KINASE-ASSOCIATED PROTEIN1(SKP1) DURING TERMINAL HEAT STRESS IN WHEAT (*TRITICUM AESTIVUM L.*)

Praful Jaiswal<sup>1</sup>, Sharmistha Barthakur\* and A.N. Sahi<sup>2</sup>

1. ICAR-National Research Center on Plant Biotechnology Pusa Campus, New Delhi (India) 2. Amity Institute of Biotechnology, Amity University, Noida (India)

Presenting Author: jaiswalpraful1987@gmail.com

\*Corresponding Author: Sharmistha.Barthakur@icar.gov.in

Wheat plants are very sensitive to high temperature stress during grain filling. Complex networks of phytohormones and numerous key genes intricately regulate heat stress. Plant hormones play significant roles in signaling pathway to regulate abiotic stress response in plants, independently, synergistically or antagonistically. Auxin is one of the classic phytohormones effective during tropism growth and tissue differentiation. To study involvement of auxin during vegetative and grain filling stages of wheat under heat, seeds of popular wheat variety HD2967 were treated with 50ppm of IAA alone and in combination with high temperature exposure for specific period. Raised plants were also exposed to heat stress during post anthesis in field conditions in season. Various morphological physiological and biochemical analyses was carried out under ambient and heat stress. Post emergence, germination percentage and other physiological parameters were significantly enhanced after treatment relative to ambient conditions. However the grain analysis showed increase in the no of spikelet, no of grain and 1000 grain weight under both ambient and heat stress conditions. Treated plants also maintained better cell membrane integrity and leaf photosynthesis. Ubiquitin 26S proteasome system (UPS) is important in maintaining protein turn over, abiotic stress response and intricately involved in auxin signaling. Comprehensive transcript expression profiling of SKP1 which is an essential component of SCF complex (Skp1-Cullin-F-box protein) was carried out. Differential and highly modulated expression of SKP1 was observed under heat stress response. Results indicate positive impact of auxin priming during terminal heat stress in wheat and the data will be presented here.

**Keywords:** Priming, Phytohormones, Emergence, Ambient temperature, Proteasome system

## DEVELOPMENT OF AN ANTI-FUNGAL DRUG LOADED NANOEMULGEL FOR THE TREATMENT OF ORAL CANDIDIASIS

R. S. Narang<sup>1</sup>, Anmol Dogra<sup>2</sup>, Javed Ali<sup>3</sup> and Jasjeet Kaur Narang<sup>2\*</sup>

1. Department of Oral and Maxillofacial Pathology, Sri Guru Ram Das Institute of Dental Sciences and Research, Amritsar, Punjab;

2. Department of Pharmaceutics, Khalsa College of Pharmacy, Amritsar, Punjab 3. Department of Pharmaceutics, Jamia Hamdard, Hamdard University, New Delhi-110062;

E-mails: narangraman@yahoo.com, javedaali@yahoo.com,

\*Corresponding author: jasjeet2975@yahoo.com

Fluconazole, a potent antifungal drug has potential for the treatment of oral candidiasis. However, it suffers from the problem of poor aqueous solubility and low permeation, which in turn limits its application. The objective of the present investigation was to formulate a fluconazole based nanoemulgel which is thermodynamically stable, has improved aqueous solubility and exhibits improved mucosal penetration. The aqueous titration method was used for the formulation of the nanoemulgel. For the formulation, the solubility of fluconazole in various oils, surfactants, and cosurfactants was determined. Further the miscibility of the various solvents and cosolvents used was also evaluated. Based on the results of the study, the oil, surfactant, cosurfactant which exhibited maximum solubility of fluconazole were selected and aqueous titration method was used to formulate emulsions which were further sonicated using a probe sonicator to reduce the globule size to nanometer range. An optimized quantity of the gelling agent was incorporated in the optimized nanoemulsion to yield a transparent nanoemulgel. The nanoemulgel formulated was evaluated for optical clarity, homogeneity, viscosity, grittiness and spreadability. The results of the evaluation study revealed that the formulated Fluconazole loaded nanoemulgel was optically transparent, homogeneous, free from grittiness and having optimised viscosity and spreadability. The results of the study clearly indicated successful formulation of a nanoemulgel of fluconazole with its potential for the treatment of oral candidiasis.

**Keywords:** Aqueous titration method, Fluconazole, nanoemulgel, oral Candidiasis

PP152

ICABB-017

## WHEAT GLUTEN AND PUROINDOLINE AS EDIBLE FOOD COATING

Gaurav Kumar and Neeraj Wadhwa\*

*Department of Biotechnology, Jaypee Institute of Information Technology, Noida, Uttar Pradesh, India*  
*\*Corresponding author: neeraj.wadhwa@jiit.ac.in*

Quality attributes of Foods such as color, texture, flavor change on storage causing deterioration. One of the most important aspects in food technology is to understand and control the factors of food deterioration. Puroindoline is the main component of a new family of proteins that has been suggested to exert an antimicrobial activity. In the present study Puroindoline has been isolated from wheat endosperm by Triton X-114 phase partitioning method. The extract was further confirmed as Puroindoline by SDS-PAGE on the basis of molecular weight. And we report the yield to be 350 $\mu$ g per 10 gm of wheat flour. In present work we have attempted to control the deterioration of edible mushroom (*Agaricus Bisporus*) by coating them with the Wheat gluten films containing protein puroindoline. Browning of the Mushroom could be prevented when Puroindoline was integrated with wheat gluten. This fortified gluten biofilm can be used as edible packaging material to prevent the browning of the Mushroom.

PP153

ICABB-066

## IMPACT OF ANTIBIOTICS ON PLANTS

Ekta Bhatt and Dr. Pammi Gauba\*

*Department of Biotechnology, Jaypee Institute of Information Technology A-10, Sector-62, NOIDA-201309*  
*\*Corresponding author: pammi.gauba@jiit.ac.in*

There are multiple pathways through which Pharmaceutical compounds enter into the environment: it excreted in environment in the form of unmetabolized by-product via human excretion, rinsed off during showers and or discharged directly from the pharmaceutical industries as effluents. There are recent studies which show that these pharmaceuticals cause a variety of problems which may lead to death or deformities or toxicity in animals who consumed it via contaminated water. There are several studies which suggest the accumulation of pharmaceuticals in plants, but not much amount of work has been done on the toxic effect of these compounds. The main aim and

objective of this review is to collect the experimental evidence of plant-pharmaceuticals interaction, their uptake and their removal by plants and to throw some light on this area for research.

**Keywords:** Pharmaceuticals, Toxicity, environment, Accumulation.

PP154

ICABB-276

## EVALUATION OF ANTIMICROBIAL PROPERTY OF HEPARIN BINDING DOMAIN OF GOAT VITRONECTIN

Amith.K.C\*, Paritosh Joshi and  
 Prasant. K. K. Mishra

*M.V.Sc., Division of Biochemistry, Indian Veterinary Research Institute, Bareilly*  
*E-mails: srigandha.css@gmail.com, pj@ivri.res.in,  
 drprasanthbiochemistry@gmail.com*

Vitronectin (VN) is a multifunctional protein present in plasma and in the extracellular matrix. In this study, we are evaluating the antimicrobial property of heparin binding domain (HBD) of goat VN and studying its interaction with *S. aureus* considering the importance of this bacterium in animal husbandry. The goat VN is a 75 kDa protein with 444 amino acid residues. The HBD fragment extends from region 341-380 amino acids present in C-terminus of the VN. This fragment found to exhibit antimicrobial property was subjected to site-directed mutagenesis resulting in production of three mutants with deletion of specific amino acid residues from native VN, namely, HBD-FLD (341-380 amino acid deletion), HBD-R1D (341-355 amino acid deletion) and HBD-R2D (356-380 amino acid deletion). The created mutants were cloned in prokaryotic vector and raised in DH5 $\alpha$  competent cells. The competent cells containing our plasmid was bulk cultured and induced using IPTG. Following which purification was conducted using Nickel-agarose column chromatography to get our protein of interest. The purified proteins will then be subjected to antimicrobial assay by conducting serial dilution against *S. aureus*. By doing so we would be estimating the effect of each mutant against *S. aureus*. The whole study is to deduce the functionality of HBD and finding out whether VN could act as an antimicrobial peptide (AMP) against *S. aureus*. If the proposed study exhibits positive interference, then we could come up with a novel way for fighting Staphylococcal infection by formulating an AMP/pharmaceutical mixture.

**Keywords:** Goat Vitronectin, heparin-binding domain and antimicrobial peptide

## MOLECULAR CLONING AND FUNCTIONAL CHARACTERIZATION OF FATTY ACID HYDROXYLASE FROM PLANTS

**Kaushik Kr Dhar Dubey, Dr V Chimote,  
Dr V Ravi, Dr J S Yadav, Dr K C Upadhyaya,  
Dr A Kumar**

*Molecular Genetics Lab, Amity Institute of Biotechnology,  
Amity University, Noida, Uttar Pradesh-201303.  
E-mails: dubey.kaushik01@gmail.com, akumar@amity.edu*

Higher plants produce fatty acids that are predominantly stored in the form of Triacylglycerol (TAG) in oil bodies in the seed. Plant seed oil is the main source of fatty acids (FA) for human consumption. Many of these fatty acids also have various industrial applications and can supplement petroleum sources. Due to rising cost of petroleum and other increased concern about the non-renewable energy source, it is very needful to develop sustainable sources of high value FAs for both chemical as well as health related industries. So, to use oil seeds as bioreactors for commercial production of high value FAs, better understanding of biochemical pathways and other factors involved in increased production is required. Production of these fatty acid by transgenic plant, requires isolation of genes involved in their biosynthesis from plants. *Hiptage benghalensis* (*Malpighiaceae*) is a perennial herb native to India, Southeast Asia, which accumulates high levels of ricinoleic acid in its seeds. Castor is the only commercial source of a ricinoleic acid which is a hydroxy FA that is being used globally in chemical industry. Current study emphasizes on isolation of genes involved in biosynthesis of ricinoleic acid from wild plants which can act as reservoir of superior germplasm. It involves cloning of those genes and selection of allelic variants which will be further used for characterization using yeast as an expression system. Accumulation of hydroxy FAs at different stages of seed development will be done by GC-MS analysis and expression pattern will be studied using qRT PCR.

**Keywords:** TAG, hydroxy fatty acid, ricinoleic acid, castor, hiptage, germplasm

## ESSENTIALITY OF METHYLISOCITRATE LYASE

**Ashmita Nautiyal and Vibha Gupta\***

*Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201307, Uttar Pradesh, India  
E-mails: nautiyalashmita96@gmail.com, \*Corresponding author: vibha.gupta@jiit.ac.in*

Methylisocitratelyase (MCL) is an oxo-acid lyase which catalyzes the cleavage of methylisocitrate to succinate and pyruvate, the last step in methylcitrate cycle. The role of this cycle is  $\alpha$ -oxidation of propionate to pyruvate akin to glyoxylate cycle where acetate is oxidized to glyoxylate at the corresponding carbon. MCL is a homotetramer which is encoded by *prpB* gene of *prp* operon involved in propionate oxidation. Lack or loss of MCL activity is predicted to result in potentially toxic accumulation of propionyl-CoA metabolite and hence this enzyme is reported to be a virulent factor in several human pathogenic microorganisms such as *Mycobacterium tuberculosis*, *Candida albicans*, *Candida lipolytica*, *Aspergillus nidulans*, *Escherichia coli* etc. This study reviews the bactericidal essentiality of a metabolic enzyme for development of a unique potential drug target.

**Keywords:** MethylisocitrateLyase, Methylcitrate cycle, Glyoxylate cycle, propionate oxidation

## UNDERSTANDING CYSK FOR DEVELOPING FUTURE THERAPEUTICS

**Pallavi Joshi<sup>1</sup> and Dr. Vibha Gupta<sup>1\*</sup>**

*1. Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201309, Uttar Pradesh, India  
E-mails: joshipallavi5795@gmail.com,  
\*Corresponding author: vibha.gupta@jiit.ac.in*

CysK (O-acetylserinesulfhydrylase) is a pyridoxal-5'phosphate (PLP) dependent enzyme which catalyzes the second step of the *de novo* cysteine biosynthesis pathway by converting O-acetyl serine (OAS) into L-cysteine in the presence of sulfide. The first step of the cysteine biosynthesis involves formation of OAS from serine and acetyl CoA by CysE (Serine acetyltransferase). Together, these two enzymes form a bi-enzyme complex, termed Cysteine Synthase Complex (CSC) in the absence of OAS, the substrate

for CysK. This complex has an inhibitory effect on the activity of CysK as the C-terminal decapeptide of CysE penetrates into the active site of CysK and converts its open conformation to the closed one. Apart from its role in cysteine biosynthesis, several new studies report additional moonlighting functions of CysK in the bacterial cell. Significant of these are its role as transcriptional regulator and involvement of CysK in contact dependent toxin activation in many Gram-negative pathogens. These diverse roles of CysK have established it as a potential drug target. The aim of this study is to review structural and functional understanding of CysK for drug development efforts.

**Keywords:** CysK; Cysteine biosynthetic pathway; Cysteine Synthase complex; Moonlighting functions

PP158

ICABB-107

## ROLE OF ISOCITRATE LYASE IN ADAPTATION TO HOST ENVIRONMENT

Shreya Deb and Dr Vibha Gupta\*

Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201307, Uttar Pradesh, India  
 E-mails: shreyadeb0408@yahoo.in \*Corresponding author's E-mail: vibha.gupta@jiit.ac.in

Isocitrate lyase (ICL) is widespread in nature and functions in different physiological periods of life in many organisms. The key enzyme of glyoxylate cycle, it is generally induced in most bacterial and fungal cells under conditions of low glucose, low oxygen tension and especially in the presence of acetate, ethanol and high temperatures. Most microorganisms capable of utilizing acetate or other fatty acids as the sole carbon source utilize the glyoxylate cycle for the anaplerosis of oxaloacetate and the study of such alternative metabolic pathways that help in the survival of bacterial and fungal pathogens, thereby aiding in the persistence of infection inside host, is critical for public health. Substantial evidence exists on involvement of the glyoxylate cycle, and therefore ICL, in virulence and pathogenicity of several human pathogenic bacteria (*Mycobacterium tuberculosis*) and fungi (*Candida albicans*), as well as plant pathogenic fungi *Magnaporthe grisea* and *Leptosphaeria maculans* illustrating importance of this cycle and ICL in many host-pathogen systems. This study reviews the factors that influence the activity of ICL that aids in adaptation of such pathogen to its host environment for enhanced understanding in development of ICL as a potential drug target.

**Keywords:** Glyoxylate cycle, isocitratlyase, virulence, pathogenicity, *Mycobacterium tuberculosis*, *Candida albicans*, *Magnaporthe grisea*, *Leptosphaeria maculans*

PP159

ICABB-232

## APPLICATION OF NANOTECHNOLOGY FOR NITRIC OXIDE GAS IN THERAPEUTICS

\* Saumya Yadav<sup>1</sup>, Tanya Gupta<sup>1</sup>, Manisha Singh<sup>1</sup> and Rachana<sup>1</sup>

<sup>1</sup> Department of Biotechnology, JIIT Noida, Sector - 62, Noida 201309, India,

\*Presenting author: saumyayd@gmail.com

Researches and various clinical studies conducted in recent times proved that, gases can be highly useful as pharmaceutical agents against various diseases. Some of the most useful gases used in therapeutics are: carbon dioxide, oxygen and nitrogen etc. These gases have been used in past and still are in use to treat diseases like: pulmonary and cardiovascular disorders and lesions treatment etc. Nitric oxide is one of such gases, which was earlier considered as an atmospheric pollutant until, the discovery of its synthesis in cells of mammals. This led to further investigations to explore the use of nitric oxide in the treatment of pulmonary disease as, it acts like a vasodilator. In higher concentrations ( $\leq 500\text{nM}$ ), it shows apoptotic effects on cancerous cells, as well. It is also an immunomodulator and works with reactive oxygen species and reactive nitrogen species, to keep the immune system in balance. NO being gaseous molecule, is difficult to handle but, now a day's various approaches are being utilized to deliver it at the site of action. Nanotechnology is one such technology which is now in trend to serve this purpose. In the present study various approaches utilizing nanotechnology for its use in treatment, will be analyzed and discussed which have promises for better efficacy and less degree of side effects.

**Keywords:** Nitric oxide, Nano Technology, Pulmonary disease, Wound healing, Antimicrobial

## **ANALYSIS OF PILIN BIOSYNTHESIS GENES IN VIRULENCE OF AEROMONAS HYDROPHILIA**

**Nancy Garg<sup>1</sup>, Anukriti Verma<sup>1</sup>, Shivani Sharda<sup>1</sup>, Daad Saffarini<sup>2</sup>, Sheetal Shirodkar<sup>1\*</sup>**

*1. Amity Institute of Biotechnology, Amity University Uttar Pradesh Noida Campus, Noida 201313 2. Department of Biological Sciences, University of Wisconsin Milwaukee, Milwaukee, WI 53201*

\* Corresponding author: sshirodkar@amity.edu

*Aeromonas hydrophila* ATCC 7966 is a gram negative facultative anaerobe and is known to cause red fin disease in fishes as well as gastroenteritis, skin and soft tissue infections in humans. Aeromonas infection causes significant losses to the aquaculture industry worldwide. Several known virulence factors of Aeromonads include toxins such as aerolysin, hemolysin, cytotoxin and enterotoxins, type II, III, and VI secretion systems, and type IV (Tap) pilus. The genome sequence of *Aeromonas hydrophila* shows presence of several pilus assembly proteins, fimbriae and adhesins. These structures are predicted to play an important role in cell adhesion and biofilm formation. Biofilm formation assay with the wild type *Aeromonas hydrophilia* shows that it is capable of attaching to abiotic surfaces leading to formation of a biofilm. In the current study we are characterizing the role pilus biosynthesis operon AHA1450-1459 in virulence of *Aeromonas hydrophilia*. In silico analysis of the operon shows presence of pilus assembly proteins AHA1452(CpaB) AHA1457(TadB), AHA1458 (TadC) and AHA1559 (TadD) with transmembrane domains. AHA1451 encodes for a leader peptidase(PilD) which is involved in processing of the transmembrane AHA1450 encoded Flp pilin protein. Further studies involve mutagenesis and analysis of the annotated pilin biosynthesis genes and their role in virulence of *Aeromonas hydrophila*. The study may lead to identification of pili as a significant virulence factors that may be used as a drug targets for the treatment of this fish pathogen.

**Keywords:** *Aeromonas hydrophila*, Pilin, Biofilm Formation, Virulence

## **COMPREHENDING THE PATTERNS FOR COEXISTENCE OF RHEUMATOID ARTHRITIS AND ANKYLOSING SPONDYLITIS THROUGH GENE EXPRESSION PROFILING**

**Anukriti Verma, Divye Bhardwaj,  
\*Bhawna Rathi, Shivani Sharda**

*Amity Institute of Biotechnology J-3 Block, Amity University Campus, Sector - 125, Noida - 201303 (U.P.)*

\*Corresponding author: brathi@amity.edu

**Background/Rationale:** Rheumatoid Arthritis (RA) and Ankylosing Spondylitis (AS) are the most well-known rheumatic diseases. They are chronic inflammatory diseases that cause injury to the joints and ultimately depreciate physical fitness of patients. Though their etiology and symptomatology are different, cases of coexistence of RA with AS do exist.

**Aims/Objectives:** This study insight into finding the common potential and putative targets, functions and pathways in RA and AS using the bioinformatics analysis in order to improve diagnosis and treatment in patients having concomitant RA and AS.

**Materials and Methods:** The gene-expression datasets of RA and AS were downloaded from ArrayExpress. The data pre-processing and statistical analysis of these datasets was performed using Bioconductor R suite. The functional annotation and pathway analysis was performed using the DAVID tool, KEGG database and STRING database.

**Results and Discussions:** Gene expression data analysis of AS and RA patient datasets was done to explore the Differentially Expressed Genes (DEGs). In majority of datasets the common differentially expressed genes found were Sterile Alpha Motif Domain Containing 9 Like (SAMD9L) and Inhibin Beta A Subunit (INHBA). The functions and pathways for the above DEG's were regulation of metabolic process, cell differentiation, organ development, cell proliferation, cell differentiation and immune system process.

**Conclusion:** DEGs along with their associatory pathways might have the potential to be used as targets for the diagnosis and treatment of concomitant RA and AS and warrants for further experimental validation.

**Keywords:** Rheumatoid Arthritis, Ankylosing Spondylitis, Bioinformatics, Gene expression analysis, Functional and pathway analysis, Gene targets

PP162

ICABB-009

**Keywords:** Obstructive Sleep Apnea, miRNA, target genes, DEG

## IDENTIFICATION OF A DIFFERENTIALLY EXPRESSED GENETIC SIGNATURE IN OBSTRUCTIVE SLEEP APNEA

Sartaj Khurana, Anukriti Verma,  
Shivani Sharda, Sudeep Bose\*

Amity Institute of Biotechnology, Amity University, NOIDA

\*Correspondence author: sbose1@amity.edu

**Background:** Obstructive Sleep Apnea (OSA) is one of the most common disorders and is growing on a global scale as a major health concern. It is characterized by repetitive episodes of respiratory disturbance accompanied by oxygen depletion and sleep disruption. Literature has established a strong association between miRNA and adipogenesis/obesity supporting the fact that microRNAs are potential biomarker candidates. Therefore, identification of differentially expressed miRNAs and their potential targets is warranted to understand the underlying mechanism of OSA and associated cardiovascular and metabolic disorders.

**Aim:** The aim of this study is to identify the potential targets of the dysregulated miRNAs in OSA and to study their expression patterns

**Methods:** Gene expression datasets for OSA were retrieved from ArrayExpress. These were preprocessed using Bioconductor R suite to identify the Differentially Expressed Genes (DEG's) in OSA. The DEG's were mapped with the miRNA target genes and their functional and pathway analysis was performed.

**Results:** Some of the genes such as transforming growth factor beta receptor 2 (TGFBR2), phosphatase and tensin homolog (PTEN), a disintegrin and metalloproteinase (ADAM), sprouty homolog 1 and 2 (SPRY 1 and 2), myc were found to be differentially expressed miRNA targets and were found to play pivotal roles in metabolic disorders, diabetes, obesity and cardiovascular diseases that are strongly linked with OSA.

**Conclusion:** OSA is a heterogeneous disorder with multiple pathophysiological risks and is still under detailed study. The identification of a dysregulated miRNA signature and the expression pattern of miRNA targets and molecular pathways associated with OSA would suggest their role in OSA as potential biomarkers and widen our understanding of the risk factors for the disease as well as provide new avenues for potential treatment.

PP163

ICABB-027

## IN SILICO STUDIES OF UNCHARACTERIZED GENES OF *BRASSICA JUNCEA* L.

Vinod Kumar<sup>1,2\*</sup>, Anket Sharma<sup>1,2</sup>, Renu Bhardwaj<sup>2</sup> and Ashwani Kumar Thukral<sup>2</sup>

<sup>1</sup>Department of Botany, DAV University, Sarmastpur, Jalandhar, 144012, Punjab, India

<sup>2</sup>Department of Botanical & Environmental Sciences, Guru Nanak Dev University, Amritsar, 143005, Punjab, India

\*Corresponding author: vinodverma507@gmail.com

*Brassica juncea* L. is an important oil seed crop and also used as green leafy vegetable and the present study was designed to analyze the uncharacterized genes of *Brassica juncea* for secondary structure predictions and 3D modeling by using various bioinformatics tools. Pyre 2 tool was used for the secondary structure predictions and it was observed that in all the genes maximum values of alpha helix followed by TM helix, disordered and beta strand were found for the uncharacterized genes. I-TASSER web server was used to predict possible three-dimensional models for conserved domains of some uncharacterized genes of *Brassica juncea*. The built models were validated by 3D verify, PROCHECK and ERRAT server. Out of the eight genes studied only three genes, i.e., A0A023VW24, A0A023VX39 and A9LLE8 have qualified against recommended score for a high quality model and found to be sufficiently robust for future studies such as docking and simulation. This is the first and the baseline study in the uncharacterized genes of *B. juncea*.

**Keywords:** *Brassica juncea*, Pyre 2, I-Tasser, PyMOL

## COLON CANCER: RESISTANCE AND TREATMENT

Suvidhi Pandey<sup>1</sup> and Reema Gabrani<sup>1\*</sup>

1. Department of Biotechnology, Jaypee Institute of Information Technology, Noida  
 E-mails: pandey.suvi.3@gmail.com, \*Corresponding author: rmgabrani@gmail.com

Colon cancer persists as one of the most prevalent and deadly tumor types in both men and women worldwide inspite of widespread, effective measures of preventive screening, and also major advances in treatment options. Despite advances in cytotoxic and targeted therapy, resistance to chemotherapy remains one of the greatest challenges in long-term management of incurable metastatic disease and eventually contributes to death as tumors accumulate means of evading treatment. Drug resistance develops in nearly all patients with colon cancer, leading to a decrease in the therapeutic efficacies of anticancer agents. Fluorouracil (5-FU)-based chemotherapy is the major treatment for advanced disease. Different combinations of 5-fluorouracil (5-FU), oxaliplatin, irinotecan and other newly developed agents have been used to treat colorectal cancer. The combination of 5-fluorouracil (5-FU) and leucovorin has been the unofficial "standard" therapy for patients with colorectal cancer for over a decade. Thymidylate synthase (TS) is an E2F1-regulated enzyme that is essential for DNA synthesis and repair. TS protein and mRNA levels are elevated in many human cancers, and high TS levels have been correlated with poor prognosis in patients with colorectal, breast, cervical, bladder, kidney, and non-small cell lung cancers. Recently a number of new agents targeted against the enzyme thymidylate synthase have been synthesized and are in various stages of development. New oral 5-FU prodrugs such as UFT, S-1, and Capecitabine may help to overcome some of these difficulties. Eniluracil, a potent inhibitor of the enzyme dihydropyrimidine dehydrogenase, may also help by overcoming potential 5-FU resistance mechanisms, in addition to increasing its bioavailability. The antifolate-based inhibitors, Tomudex is in the advanced stage of development. Similar efficacy with 5-FU and a convenient schedule may suggest a role in future combination regimens. The generation wise development in the chemotherapy and advancement of drugs can provide a channel for better cure.

**Keywords:** 5-FU; Drug resistance; Prodrugs; Thymidylate synthase

## IDENTIFICATION AND MANIPULATION OF FNR PROMOTER OF SALMONELLA TYPHIMURIUM

Ajay Kumar<sup>1</sup> and Barkha Ratta<sup>1</sup>,  
 Swagatika Priyadarsini<sup>1\*</sup>

1. M.V.Sc., Division of Biochemistry, Indian Veterinary Research Institute, Bareilly  
 E-mails: ajayivri@gmail.com , barkhaivri@gmail.com,  
 \*Corresponding author: drswagatika.vet@gmail.com

*Salmonella Typhimurium* (STM) is a gram negative, motile, facultative intracellular bacilli belonging to family of Enterobacteriaceae. The organism contributes to majority of non typhoidal salmonellosis (NTS), a food-borne zoonotic disease occurring in a broad host range showing symptoms of acute inflammatory diarrhea to invasive systemic diseases like focal infections in immunocompetent and immunocompromised patients. The two critically important niches for STM are gastrointestinal tract (where it colonizes in the intestinal epithelium) and intramacrophage environments of the host. The global transcriptional regulator fnr (Fumarate and Nitrate reductase Regulator) gene of STM is solely responsible for adaptation of the organism to the anaerobic gastrointestinal environment of host. The inactive FNR[2Fe-2S]2+ is converted to active FNR[4Fe-4S]2+ in oxygen-limited condition thus activating virulent genes within *Salmonella* pathogenicity island 1 (SPI-1), newly identified flagellar genes (mcpAC, cheV) and the virulent operon (srfABC) of STM. In this experiment, we have identified the promoter (Pfnr) sequence of fnr gene of STMin-silico and amplified the sequence using specific primers followed by cloning and replacing the lac-promoter 2-galactosidase of pUC19 vector. Further strength of the promoter is to be reduced by introducing random errors using error prone PCR, followed by replacement of mutated Pfnr in place of lac-promoter of pUC19 vector. Here we are using 2-galactosidase gene as the reporter gene and the selection will be done by visualizing the intensity of blue color produced by colonies grown in the LB agar plates containing X-gal and IPTG. The highly mutated Pfnr with reduced strengthwill further be utilized to replace the normal Pfnr in the genome of wild STM to deoptimise the expression of fnr gene, thus decreasing the virulence, pathogenesis and colonization of the organism in the host.

**Keywords:** promoter, error prone PCR and 2-galactosidase

## ADVANCEMENT OF NANOTECHNOLOGY IN TUBERCULOSIS

**<sup>1</sup>Stuti Awasthy, Himanshu Sukhpal, Shivanika Shankar, Mayank Pareek,  
<sup>1</sup>Attinderpal Kaur and <sup>1</sup>Shweta Dang\***

1. Jaypee Institute of Information Technology, Sector 62, Noida, UP, 201309

E-mails:stutiawasthy@gmail.com, himanshusukhpal@gmail.com, shivanikashankar@gmail.com, mayankpareek5@gmail.com, attinderkahlon9@gmail.com, \*Corresponding Author : Shweta.dang@jiit.ac.in

Tuberculosis (TB) is still one of the main health threats of the world. It is an infectious disease caused by *Mycobacterium tuberculosis*. The bacteria infect various human organs such as lungs, kidney, liver etc. Some of the symptoms of the disease are chronic cough, blood containing sputum, fever, night sweats, weight loss etc. Nanotechnology has offered enormous improvement in field of diagnostics and therapeutics. A colorimetric sensing strategy employing unmodified gold nanoparticles for tuberculosis diagnosis has been developed which has made detection of *Mycobacterium* easy, accurate and less time consuming. Nanotechnology has also helped in overcoming the limitations associated with current line of treatment (i.e. less bioavailability, peripheral toxicity etc.). It has enabled drug delivery through various administration routes i.e. oral and inhalation route. Scientists have formulated intravenous nanoemulsion of Rifampicin and SQ641 in order to improve the solubility, stability and bioavailability of drug (up to 3.3 times) which further leads to reduction in dose frequency. These Nano-emulsions demonstrate better intracellular and *in vivo* efficacy (i.e. reduced degradation rate of drug) as compared to the conventional drugs and have even resulted in reduced cases of peripheral toxicity in individuals.

**Keywords:** Nanotechnology, Tuberculosis, Nanoparticles, Nanoemulsion, Bioavailability.

## ROLE OF MICRO RNA AS AN ONCOMIR AND TUMOR SUPPRESSOR

**Mansi Verma and Dr. Susinjan Bhattacharya\***

Biotechnology Department, Jaypee Institute of Information Technology, A-10, Sector 62 Noida

\*Corresponding author: s.bhattacharya@jiit.ac.in

microRNAs are small non coding RNA that target mRNA and regulate various metabolic pathways, cell cycles, etc. Dysregulation of miRNA can lead to serious health issues through translational repression of mRNA and can even cause cancer. In fact, they have a pivotal role in tumorigenesis. Some microRNAs promote tumor formation and thus act as oncogenes while others suppress tumor formation thereby acting as tumor suppressors. microRNAs are also involved in glioblastoma, leukemia, bladder cancer, pancreatic cancer and gastric cancer. MiR23a/b inhibit the apoptosis of gastric cancer cells by directly targeting an important tumor suppressor, programmed cell death 4 (PDCD4). Thus, miR-23a/b act as oncomirs in gastric cancer through the inhibition of PDCD4 translation. MiR-339 and mainly miR-766 reactivate the expression of tumor suppressor genes in colorectal cancer cell lines through DNA methyltransferase 3B gene inhibition. Collectively, loss of tumor suppressors and overexpression of oncogenes are the central driving forces for tumorigenesis. The network of oncogene- miRNA-Tumor Suppressor Gene (TSG) affects numerous tumor types and involves several oncogenes, miRNAs, and TSGs; hence it may contribute in the growth and progression of a variety of tumors. Therefore, targeting this network holds remarkable therapeutic potential for treatment of cancer. The molecular mechanism of microRNA provide a new avenue for treatment by providing new drug targets and also acts as a biomarker for diagnostics.

**Keywords:** microRNA, oncogene, tumor suppressor, cancer.

## APPLICATIONS OF NANOTECHNOLOGY IN COSMETICS

**Aayushi Bhatnagar and Dr. Sujata Mohanty\***

*Jaypee Institute of Information Technology, Sector 62,  
Noida, Uttar Pradesh*

\*Corresponding author: sujata.mohanty@jiit.ac.in

Nanotechnology has made its place in the cosmetic world and emerged as a new area, Nanocosmetics. Various cosmetic products, such as, creams, lotions, lipsticks, anti-wrinkle creams, sunscreens, shampoos, conditioners, eye-shadows, mascara, lip-liners, blush, soaps, perfumes are engineered with nano-emulsions to make less harmful to the skin, transparent and soft in touch. These engineered products are then commercialized in the market. In addition, nanoparticles are incorporated in the cosmetic products for UV filtering and efficient delivery of the active ingredients such as vitamins and anti-oxidants. Sunscreens are engineered with titanium dioxide ( $TiO_2$ ) and zinc oxide ( $ZnO$ ) to prevent the skin from the penetration of UV rays. Nanoparticles have more surface area than large particles and hence the active ingredients are absorbed more efficiently in the skin. Methods like sol-gel, pyrolysis, vacuum deposition, ball milling are used for preparation of these nanoparticles. Their dimensions can be determined with various microscopic techniques such as Transmission Electron Microscopy (TEM), Atomic Force Microscopy (AFM) and Scanning Tunnel Microscopy (STM). Niosomes help in development of creams and also prevents turning of hair into grey. L'Oréal has introduced its L'Oréal Revitalift double lifting anti-wrinkle cream which reduces wrinkles and tightens the skin due to presence of Pro-retinol A. Nanocosmetics has been proved to be industrially feasible.

**Keywords:** Nanotechnology, Nanocosmetics, Niosomes, Nanoparticles

## MYCOBACTERIAL RV1916 HAS ISOCITRATE LYASE ACTIVITY: A CONTROVERSY RESOLVED

**Monika and Vibha Gupta\***

*Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201307, Uttar Pradesh, India*

E-mails: monikaantil60@gmail.com,

\*Corresponding author: Email: vibha.gupta@jiit.ac.in

Despite a curable disease, tuberculosis (TB) is one of the leading causes of death worldwide. This is due to the ability of causative organism *Mycobacterium tuberculosis* (*Mtb*), to persist inside the host cells, leading to the long duration of TB therapy and therefore, development of drug resistant strains of *Mtb*. Novel drug targets against persistent *Mtb* is an immediate necessity for overcoming this global menace. Enzymes of glyoxylate pathway are propitious and proven drug targets for persistent *Mtb*. Isocitrate Lyase (ICL) is the key enzyme of glyoxylate pathway that converts isocitrate to succinate and glyoxylate, allowing growth on  $C_2$  compounds. In pathogenic H37Rv *Mtb*, two types of ICLs have been reported - ICL1 encoded by *icl* (Rv0467) is well characterized and homologous to eubacterial enzyme whereas ICL2 encoded by *aceA* (Rv1915/Rv1916) is more related to eukaryotic isocitrate lyase. The *aceA* gene exists as a split ORF in H37R<sub>v</sub> *Mtb* - designated Rv1915/*aceAa* and Rv1916/*aceAb*. Sequence investigation of H37R<sub>v</sub> *Mtb* ICLs reveal that the catalytic motif (KKCGH) is present in Rv0467 and Rv1915 but not in Rv1916. Bioinformatic analysis further indicate domain II of Rv1916 to be similar to peroxisome targeting signal of peroxins which break down long fatty acid chains via the  $\alpha$ -oxidation cycle. In addition, Rv1916 is also reported as a pseudogene in literature. Therefore, controversy exists on the role of Rv1916 - whether an ICL, or some other function or a pseudogene? This study reports cloning of *aceAb* (Rv1916) in the pET21c expression vector, induction and expression analysis of the prepared construct in *E. coli* BL21(DE3) cells along with large scale purification and biophysical/biochemical characterization of recombinant Rv1916 for resolving some of the controversies associated with this *Mtb* gene. The studies clearly demonstrate that the recombinant Rv1916 has significant ICL activity.

**Keywords:** Tuberculosis, *Mycobacterium tuberculosis* (*Mtb*), Isocitrate lyase(ICL), glyoxylate cycle, persistence

PP170

ICABB-106

## MOLECULAR IMAGING AND THEIR POTENTIAL USE IN NANOTECHNOLOGY

**Aparna Singhal, and Dr. Deepak Sharma**

Meerut College, Meerut, Ch. Charan Singh University  
E-mails: 25aparna1996@gmail.com, depshad@gmail.com

Recently there have been significant developments in the use of imaging techniques to identify and monitor diseased tissue *in vivo*. Physiological and pathological changes can be detected through the visualisation of tissue morphology and cell function. When diseases manifest, the biochemical activity of cells alters. Molecular imaging is described as the visualisation, characterisation and measurement of biological processes at the molecular levels in humans and other living systems. It uses radiolabelled molecules that produce signals by means of radioactive decay along with other molecules to image via means of sound, magnetism, or light (optical techniques of bioluminescence and fluorescence), as well as other emerging techniques. Modalities that fall within this technique include: molecular magnetic resonance imaging, magnetic resonance spectroscopy, optical bioluminescence, optical fluorescence, targeted ultrasound, single photon emission computed tomography, and positron emission tomography. Most molecular imaging procedures involve an imaging device and an imaging agent (probe). Advancements in molecular imaging require the development and application of sophisticated probes that are able to detect biological processes on the cellular and molecular level. These probes necessitate two key characteristics: a property that facilitates their accumulation at the site of interest and a property that allows them to be imaged. Nanoparticulate probes have demonstrated significant advantages over single molecule-based contrast agents. The latest developments in nanoparticulate molecular imaging contrast agents incorporate the appropriate contrast-generating materials, targeting groups, a biocompatible coating and the possibility for other functionalities such as a therapeutic drug. These agents allow for brighter, tissue-specific imaging to help visualise and help diagnose disease at the earliest stages and, in some cases, even before disease manifestation. Additionally, due to their careful nanostructure design, there is the potential to improve treatment efficacy and reduce undesirable side effects. Most significantly there has been a combination of

diagnostic imaging and drug delivery roles into unique singular nanoparticulate formulations that allow for real-time treatment tracking.

**Keywords:** Nanoparticles, Imaging, Synthesis, MRI, Contrast Agents

PP171

ICABB-124

## FOCUSED ULTRASOUND USED TO DELIVER NANOPARTICLES (NPs) ACROSS BLOOD BRAIN BARRIER (BBB)

**<sup>1</sup>Himanshu Sukhpal, <sup>1</sup>Ishita Bhatnagar,  
<sup>1</sup>Stuti Awasthy, <sup>1</sup>Kuldeep Nigam,  
<sup>1</sup>Atinderpal Kaur, <sup>1</sup>Shweta Dang\***

<sup>1</sup>Novel Drug Delivery Lab, Department of Biotechnology, Jaypee Institute of Information Technology, Sector 62, Noida, UP, 201309  
E-mails: himanshusukhpal@gmail.com, ishitabhatnagar02@gmail.com, stutiawasthy@gmail.com, kuldeepnigam1604@gmail.com, atinderkahlon9@gmail.com,\*Corresponding author: shweta.dang@jiit.ac.in

The blood-brain barrier (BBB) is a complex structure; made up of the endothelial cells of the brain capillaries, being highly selective in nature, makes it a challenge to the delivery of neurotherapeutics to the brain. Increasing the dosage of active molecules may result in side effects such as peripheral toxicity, skin rashes, sleep apnea, vomiting, etc. Nanotechnology in the recent years has attracted a lot of interest as a carrier for drugs, because of being a safe and a relatively untaxing method, along with its therapeutic nature. One of the most significant advances include the use of focused ultrasonic waves, to create a pressure of 0.4 MPa to 0.6 MPa on the endothelial cells of the brain capillaries of rats causing localized and temporary gaps in their BBB, resulting in the delivery of nanoparticles injected just prior to the sonication. PEG-coated polystyrene tracer drug bearing NPs (PS-NP+) (60 nm diameter) were delivered across the BBB in rats using 1 MHz Focused Ultra Sound (FUS). The percentage of PS-NP+ vessels producing clouds was increased to 50% at 0.6 MPa also a higher pressure resulted in a 4.6 fold increase in large PS-NP clouds. It was also verified that this method of delivery of NPs can be used to significantly increase the delivery of 60 nm NPs to 9L rat tumors. In another study, a blend of non-PEGylated and highly PEGylated polymers at an optimized ratio was also used to engineer brain-penetrating gene bearing NPs with a polyethylenimine (PEI) core polymer. The presence of mCherry gene delivered using PEI NPs, was immunologically detected in both glial cells and neuronal cell nuclei,

the expression of mCherry was homogeneously distributed throughout the sonicated area. Such encouraging results demonstrate the benefit of combining FUS-mediated delivery across the BBB with brain-penetrating NPs and the numerous applications of it in the industry.

**Keywords:** Blood Brain Barrier (BBB); Drug Bearing NP delivery; Drug delivery; Focused Ultrasound; Gene Bearing NP delivery; Nanotechnology; Ultrasound

PP172

ICABB-125

## NANOTECHNOLOGICAL REVOLUTION IN FOOD INDUSTRY

Shruti Singla, Vijeta Prakash, Varnika Suryavanshi, Raina Jana, Arushi Saxena and Sudha Srivastava\*

Department of Biotechnology, Jaypee Institute of Information Technology, Noida, UP- 201307 India.

\*Corresponding author: sudha.srivastava@jiit.ac.in

We report here applications of nanotechnology in food industry - Food Processing, Packaging, and Preservation. Conventionally used food packaging materials suffered from drawbacks like non-renewable in nature, cause of various health hazards and limited product shelf life. Last decade has witnessed technological advancement in food industry - employing nanotechnology to maintain and improve packaging conditions at the same time increase their shelf life, to deliver antioxidants, enzymes, flavours, anti-browning agents and improve the barrier properties by reducing oxygen flow. Furthermore, antimicrobial nanomaterials based food packaging has been developed to avoid spoilage of food products and hence increased shelf life. Lately, nanotechnology based edible packaging materials have been reported to increase the longevity of food products. Nanotechnological tools in food processing improve viscosification and gelation of food product to improve texture and appeal. Nanosensors for detection of oxygen in-package have also been instrumental in improving preservation of food products. In addition to this, we have also reviewed the possible Health Hazards caused by the usage of nanomaterials in food industries and in agriculture sector in view of Food safety.

**Keywords:** Nanomaterials, Nanosensors, Food Processing, Food packaging, Food preservation, Nanotechnology, Antioxidants

PP173

ICABB-129

## CHALLENGES IN CHAGAS DISEASE VACCINE DEVELOPMENT: ROLE OF BIOINFORMATICS AND NETWORKS

Akshay Jain, Vishal Mishra, Vivek Srivastava and Kamal Rawal\*

Department of Biotechnology, Jaypee institute of Information Technology, Noida, Sector 62, Uttar Pradesh, India

\*Corresponding author: kamal.rawal@gmail.com

Chagas is a vector borne disease caused by *Trypanosoma cruzi* and continues to be an important public health threat in South America, Mesoamerica, and South Texas, where it is one of the most common infections of poverty and an important maternal-child health threat. In addition to the public health impact of Chagas disease, now affecting up to 10 million people in the Western Hemisphere. This Triatomine bug infects the host through the bite or through intact mucosal membrane. Around 41,200 new cases occur annually in endemic countries & 14,000 infants are born with congenital chagas disease that resulted 10,300 deaths per annum. This disease has a serious economic impact on the United States & the other part of the world. In this disease acute infection can be lethal but they developed gradually into a chronic stage. Immunity against *T.cruzi* infection is still incomplete. Currently no medicine is available for protecting against this infection & prevents this disease but pharmacological treatments are depended on benznidazole and nifurtimox. Strategies used for Chagas diagnosis include microscopy, which detects parasites in tissues, quantitative PCR (qPCR), which measures levels of parasite DNA in host tissues, and serological methods, such as enzyme-linked immunosorbent assays (ELISA) and immunoblotting, which detect circulating *T.cruzi*-specific antibodies. Prevention is generally focused on decreasing the number of the insect. This is done by using sprays and paints containing insecticides, improving housing & sanitary conditions in certain areas. Here we discuss challenges and role of bioinformatics in development of therapeutic chagas vaccine. Out of 27 million Pubmed records, we will screen more than 60000 abstracts pertaining to Chagas disease (*T. cruzi*, Chagasic cardiomyopathy etc) using our semi-automated SVM based text mining system(Jaisri et al 2016, Plos one). A deep curation strategy shall be employed to eliminate false hits. We intend to screen over 1000 full length papers during the course of study using manual curation to validate the hits as well as improve the quality of datasets. Each short listed

molecule shall be linked to manually curated research article(s) for validation in a resource base. The portion of text denoting gene (molecule) or its interaction with other molecules in context of CD will be highlighted and shall be accessible through a dedicated web portal. The process shall be not only be executed for molecules of pathogen (*T. Cruzi*) but also for molecules implicated in host immune response (acute & chronic phases). This will be supplemented with screening of molecules involved in evolution of CD towards cardiac system (chagasic cardiomyopathy). Further, we will also explore literature pertaining to neuron-immuno-endocrine axis to understand the cross-talk between the HPA-axis (hypothalamic-pituitary-adrenal system), nervous and immune systems which are associated with the different clinical forms of Chagas disease.

**Keywords:** Chagas, *Trypanosoma cruzi*, Machine learning, Bioinformatics, Network system

PP174

ICABB-145

## ANALYSIS OF L6 SKELETAL MUSCLE CELLS PROTEINS EXPRESSED ON EXPOSURE TO DIVERSE GLUCOSE CONCENTRATION USING MALDI-TOF

Nancy Taneja<sup>1</sup> and Priyadarshini<sup>1\*</sup>

Jaypee Institute of Information Technology, A-10, Sector-62,  
Noida, Uttar Pradesh 201309

E-mails: priya.jiit@gmail.com,

\*Corresponding author: priyadarshini@jiit.ac.in

Type 2 Diabetes is a progressive metabolic disease characterise by hyperglycaemia due to inherited/acquired low insulin production. Proteins are the major component of all cellular processes. The alteration in the protein structure, function may contribute to the pathogenesis of many diseases including diabetes. Study of underlying molecular mechanisms action that lead to the development of Type 2 Diabetes is important for the prevention and treatment of the disease. Protein expression may alter after the exposure of the cells to different glucose concentrations and can provide crucial data about the pathogenesis of Type 2 Diabetes. L6 skeletal muscle cells were differentiated into myotubes and further exposed to different glucose (G) concentrations (0mM, 8mM, 16mM and 25mM) for 12 hours. Total cell protein was extracted and protein profile was studied using SDS-PAGE. Single distinct band was observed in SDS-PAGE in samples obtained from cells which were exposed to 8mM (G). The band was excised; in gel digestion was performed followed

by MALDI-TOF analysis. MALDI-TOF analysis revealed this band as SEC22 Homolog A, Vesicle Trafficking Protein (SC22A). Identified protein plays a crucial role in vesicle fusion and vesicle-mediated transport between the Endoplasmic Reticulum and the Golgi complex. It is also known for its role in cellular molecule transport by exocytosis.

**Keywords:** Type 2 Diabetes, L6 skeletal muscle cell, Proteins, SDS-PAGE, MALDI-TOF.

PP175

ICABB-151

## INVESTIGATION OF INTERACTIONS OF CAMPHENENE MOLECULE WITH OXIDATIVE ENZYMES: DOCKING STUDIES

Tanya Gupta<sup>1</sup>, Saumya Yadav<sup>1</sup>Shashank Awasthi<sup>1</sup>,  
Manisha Singh<sup>1</sup>, and Rachana\*

Department of Biotechnology, JIIT Noida, Sector -62, Noida 201309

\* Corresponding author: rachana.dr@gmail.com

Cells undergoing oxidative stress have different level of antioxidant (catalase and SOD) and oxidant enzymes (iNOS and MOP). This imbalance in their action can lead to inflammatory conditions ultimately resulting into the tumor progression. Various natural products included in our daily diet or otherwise have the potency to protect cells against oxidative damage. Many of our favourite fruits contain such components and not only their pulp but their peels also have many medicinal components. Camphene a monoterpenes is one of such molecules which is found in the peel and has been used as food supplements. But this molecule has not been explored much by the scientists. It is suggested to be a very good anti oxidant however, it is not known whether camphene can directly interact with antioxidant enzymes and impair their functions or not. The present study is aimed, to assess that how efficiently camphene molecule can bind to oxidant enzymes using Autodock 4.0. or if they can work as inhibitors of these enzymes. Further, the reliability and accuracy of docking results is validated by Ramachandran plot. Docking studies revealed that camphene has binding pockets xidant enzymes, camphene showed the good affinity towards inducible nitric oxide synthase with binding energy of -5.42 Kcal/mol and IC50 of 106.6μM as compared to AMT, a selective inhibitor (-4.63Kcal/mol, 401.72μM). Thus, results indicate that camphene can be a potent inhibitor for oxidant enzyme.

**Keywords:** Oxidative stress, Docking, Camphene, Cancer, Autodock

## CLOTHING AND EXPRESSION OF TRUNCATED ORF2 AS A VACCINE CANDIDATE AGAINST HEPATITIS E VIRUS

**Dibya Rani<sup>1</sup>, Baibaswata Nayak<sup>1\*</sup> and Sudha Srivastava<sup>2</sup>**

1. Department of Gastroenterology, All India Institute of Medical Sciences, Ansari Nagar, New Delhi-110029

2. Department of Biotechnology, Jaypee Institute of Information Technology, Noida, UP- 201309 India

E-mails: dibyajha0108@gmail.com, \*Corresponding author: sudha.srivastava@jiit.ac.in, baibaswata@yahoo.com

With an ever increasing cases of hepatitis E virus infection, associated deaths and still birth cases in pregnant women in developing countries, calls for immediate attention. We report, cloning and expression of two forms of truncated ORF2 of HEV. Truncated ORF2 DNA's as well as expressed proteins can be used as vaccine candidates since ORF2 has been reported to be immunogenic in nature. The expressed proteins were purified using Ni-NTA affinity chromatography. Further confirmation of the expressed protein was done through western blot employing anti-his antibody as well as HEV positive human sera. The gold nanoparticles and chitosan nanoemulsions were synthesized for immobilization of DNA (truncated ORF2's) and encapsulation of expressed proteins respectively. Nanomaterials were characterized using transmission electron microscopy as well as UV-Visible absorption spectroscopy. Toxicity of the synthesized nanomaterials was tested on HeLa cell lines before animal model studies could be performed with the above vaccine candidates.

**Keywords:** Nanoparticle, Nanoemulsion, Vaccine, Hepatitis E Virus.

## USE OF NANOTECHNOLOGY FOR THE TREATMENT OF SCHIZOPHRENIA

**Mayank Pareek, Himanshu Sukhpal, Shivanika Shankar, Ishita Bhatnagar, Atinderpal Kaur, Kuldeep Nigam and Shweta Dang**

*Jaypee Institute of Information Technology, Sector 62, Noida, UP, 201309*

*E-mail:mayankrpareek5@gmail.com, himanshusukhpal@gmail.com, kuldeepnigam16@gmail.com, shivanikashankar@gmail.com, ishitabhatnagar02@gmail.com, attinderkahlon9@gmail.com,*

*\*Corresponding author: Shweta.dang@jiit.ac.in*

Schizophrenia is a psychological disorder classified separately because it cannot categorized with other neural disorders due to its unusual symptoms and unknown reasons. The current medication for the treatment of schizophrenia includes dopamine receptors D1-D2 antagonists and NDMA inhibitors. Most commonly used antipsychotic drugs, which antagonizes D1, and D2 receptors are Clozapine, Haloperidol and Olanzapine. These drugs possess an inhibitory action by affecting the ventral tegmental area of dopamine receptors and result in decreased rate of occurrence of positive and negative symptoms of Schizophrenia. There are many limitations associated with these drugs such low oral bioavailability (Clozapine <27%, Haloperidol <50-60%, Olanzapine <40%) and high peripheral toxicity, the blood brain barrier is also great obstacle to the transport of exogenous substances into the brain, many studies have been carried out by researchers in order to overcome these challenges. In a study, clozapine solid lipid nanoparticles (SLN) were prepared and tested on rats, it was found that the amount of SLN consisting drug has increased significantly inside blood serum. In another study haloperidol nanoparticles (NP) were administered through intranasal route and drug efficacy were higher than the drug administered by intra peritoneal injection. It has been observed that nanoparticles and Nano emulsions of these drugs have higher bioavailability and lower peripheral toxicity; it demonstrates promise in the reduction of the drug dosage necessary to produce a therapeutic effect with antipsychotic drugs for the treatment of schizophrenia.

**Keywords:** Schizophrenia disease, Clozapine, Olanzapine, Haloperidol, Nanoparticles,

PP178

ICABB-164

## TOBACCO STEM SILVER NANOPARTICLES: A NEUROPROTECTIVE AGENT

**Yash Sharma\***, Nidhi Srivastava and Kumud Bala

*Therapeutic and Molecular Diagnostic Lab, Center of Medical Biotechnology, Amity Institute of Biotechnology, Amity University, Noida, Uttar Pradesh, India*

\*Corresponding author: [ysharma@amity.edu](mailto:ysharma@amity.edu)

The present study was approached to determine the neuroprotective ability of synthesize silver nanoparticles of stem of *Nicotianatabacum* (TSAgNPs). Aqueous extract of tobacco stem was used as bioreducing agent to synthesize nanoparticles. TSAgNPs were characterized by UV-Vis spectra scan, DLS and FT-IR. Antioxidant content in TSAgNPs was determined by Electron transfer assay (Total Flavonoid Count, Total Phenolic Content & DPPH Free Radical Scavenging), Enzymatic Biochemical assay (SOD, CAT, & GST) and Non enzymatic Biochemical assay (GSH Content & MDA Content). Neuroprotective ability was determined by observing *In Vitro* antioxidant activity of TSAgNPs on Rat PC-12 cells by exposing it to Hydrogen Peroxide as neurotoxic agent. This was found from this study that by UV-Vis spectra scan has shown the maximum absorbance at 456nm, whereas DLS has shown size of TSAgNPs i.e. 565.1 Dia(nm). FT-IR has confirmed the bioconjugate formation by giving intense bands at 3298.83, 2333.38, 1639.39, 1085.46 and 1038.83 cm<sup>-1</sup> wavenumber. Antioxidant content in TSAgNPs were found to be present and it has shown presence of Flavonoid content i.e. 74.85±0.22 mg QE/ g of TSAgNPs, Phenolic content i.e. 502±0.06mg QE/ g of TSAgNPs and DPPH free radical scavenging found to be 60% of inhibition. Enzymatic and nonenzymatic biochemical assay was determined and has shown the presence of maximum specific enzyme activity in TSAgNPs. *In vitro* antioxidant activity i.e. SOD, CAT, GST, GSH content & MDA content in Rat PC-12 cells was found to be maximum as the volume of TSAgNPs increased in cells against neurotoxic agent and this observation reveals the presence of neuroprotective ability. This can be concluded from the present study that TSAgNPs can be used as natural herbal remedy to treat the neurological disorders as neuroprotective agent and to make use of waste material i.e. stem of tobacco for therapeutic purposes.

**Keywords:** Silver Nanoparticles, *Nicotiana tabacum*, Stem, Neuroprotection, Rat PC-12 cells, Superoxide

dismutase, Catalase, Glutathione s transferase, Lipid peroxidation.

PP179

ICABB-167

## NANOFORENSICS: A TIGHTER KNOT FOR CRIMINALS

**Madhur Arya, Rahul Saxena and Sudha Srivastava\***

*Department of Biotechnology, Jaypee Institute of Information Technology, A-10 Sector 62, Noida, U.P. India*

E-mails: [madhuraryas@gmail.com](mailto:madhuraryas@gmail.com), [rahul.nano.amu@gmail.com](mailto:rahul.nano.amu@gmail.com),

\*Corresponding author: [sudha.srivastava@jiit.ac.in](mailto:sudha.srivastava@jiit.ac.in)

Forensic science is a powerful tool in a civil society to investigate and fight with the crime. Forensic techniques collect, preserve and analyze critical samples available at the crime spot. Different problems like volatility and extremely small amount of samples make this task more challenging. An amalgamation of forensic science with nanotechnology is a key to improve the existing techniques and overcome the challenges. Nanomaterials like silver, gold and titanium dioxide nanoparticles have been extensively used in detection of latent fingerprints. Using silver nanoparticles, fingerprints that are over a week old can be enhanced with the help of water insoluble residues of fingerprints. Various instruments powered by nanotechnology like atomic force microscopy (AFM) are able to predict even the time of death and age of a bloodstain. DNA structures and nanoparticles could also be used as nanocoding system for information encryption/decryption. Thus, nanotechnology can enhances the sensitivity of detection forensic evidences and could recreate the crime scene. Nanotechnology is likely to play a major role in the future in the field of forensic science to deliver more selective and more sensitive ways to detect and reveal cases along with infallible evidence.

**Keywords:** Nanoforensics, Nanotechnology, Forensic science, Latent fingerprint, Atomic force microscopy (AFM)

**IN SILICO MOLECULAR DOCKING STUDIES OF AZOLES AGAINST LANOSTEROL-14-ÁDEMETHYLASE PROTEIN (ERG11P) FROM CANDIDA TROPICALIS**

**Apurva Chatrath, Anchal Sharma, Poonam Kumari, Rashmi Gangwar and Ramasare Prasad\***

*Department of Biotechnology, Indian Institute of Technology, Roorkee.  
E-mails: apurva.chatrath@gmail.com, anchalpriyansh@gmail.com,  
bpoonam15@gmail.com, rashmi22gangwar@gmail.com,  
\*Corresponding author: rapdyfbs@iitr.ac.in*

*Candida tropicalis* is an emerging opportunistic fungal pathogen in Asia-Pacific region, causing high mortality rate due to candidiasis. Azole drugs are enormously used in several antifungal treatments. The azoles inhibit fungal lanosterol 14- $\alpha$ -demethylase (ERG11) protein, a key enzyme of the ergosterol biosynthetic pathway, resulting in an altered fungal cell membrane. *C. tropicalis* isolates have shown azole drug-tolerance, which are attributed due to the point mutations in ERG11p. In the present work, the comparison of the molecular interactions of different azoles with ERG11p was evaluated. The 3D structure of ERG11p of *C. tropicalis* was prepared through homology modelling and validated through SAVES server. The best-generated model was further used for the molecular docking studies with the azoles. The binding energies and molecular interactions between the azoles and the ERG11p were compared and posaconazole exhibited the strongest binding in comparison to the other azoles. The molecular docking studies provide the insights of azole-ERG11p interactions, which may be helpful for further optimizing and development of other inhibitory analogues of azoles asserting the expansion of other proficient broad-spectrum antifungals.

**Keywords:** *Candida tropicalis*; ERG11p; azoles; homology modelling; molecular docking

**SUBSTITUENT STRUCTURE-SOLUBILITY RELATIONSHIP FOR PRODRUG DESIGNING WITH IMPROVED SOLUBILITY PROFILE**

**Nupur S Munjala<sup>a</sup>, Manu Sharmab , Chittaranjan Rout\***

*a Department of Biotechnology and Bioinformatics, Jaypee University of Information Technology, Waknaghat, Solan, Himachal Pradesh, 173234, India bCollege of Pharmacy, Maharishi Markandeshwar University, Mullana-Ambala, Haryana, India \*Correspondence Author, Email: chittaranjan.rout@juit.ac.in*

Paclitaxel (taxol), a western yew is a complex diterpene which provides antitumor activity against ovarian, breast, lung and prostate cancers. This drug's use is limited mostly due to poor aqueous solubility and bioavailability. Hence, prodrugs were developed to increase the solubility; however, no judicious direction is followed. The quantitative structure propertyrelationship (QSPR) models and data mining methods are efficient techniques to correlate molecular characteristics with physicochemical properties of molecules. In the current study a QSPR model is developed to correlate structural property of Paclitaxel substituents with solubility of prodrugs. Prodrugs with certain substitution group can improve solubility, therefore site directed substitution is important for determining solubility. Mainly 2'- and 7'- site substitutions were reported for Paclitaxel prodrugs. Current study aims to develop QSPR model which correlate structure of substituent (2'-site) with solubility. Various substituents data was collected literature. Geometry optimization of substituents was performed at b3lyp level using Gaussian software. Thirty groups of descriptors were extracted for each substituent using Dragon7 software. In order to find out the independent descriptors uniformly each group (in total 30 groups) is divided into eight subgroups. AIC (akaike information criteria) and VIF (variance inflation factor) multicollinearity indicators were applied to find independent descriptors in each subgroup then only independent descriptors in each subgroups were combined and the descriptors were further reduced which gave the final QSPR model. The selection of descriptors was also performed in MATLAB using 'stepwise fit'. After evaluating many combinations, only few descriptors from some groups provided good regression ( $R^2$ ) and correlation ( $Q^2$ ) coefficients and the QSPR model obtained with twenty three significant descriptors from Edge adjacency indices, 3D- MoRSE, WHIM, GETAWAY, Functional

group counts, Atom-centred fragments, 2D Atom Pairs, CATS 3D groups giving R<sub>2</sub> 0.97 and Q<sub>2</sub> 0.86 has been obtained from descriptors selected using MATLAB and twelve descriptors with R<sub>2</sub> 0.86 and Q<sub>2</sub> 0.76 has been obtained from decscriptors selected using AIC and VIF multicollinearity indicators. This approach can assist synthetic chemistry to make structural modifications in Paclitaxel that may improve solubility profiles of prodrugs. Keywords: QSPR, AIC, VIF, PM6, AM1, Paclitaxel, Drug solubility.

PP182

ICABB-175

## INDUCED PLURIPOTENT STEM CELLS- A STEP FORWARD IN STEM CELL THERAPY

Hitesh Bhardwaj, Aayushi Bhatnagar and  
Dr. Sujata Mohanty\*

Jaypee Institute of Information Technology, Sector 62, Noida,  
Uttar Pradesh

\*Corresponding author: sujata.mohanty@jiit.ac.in

Stem cell Biology attracts great attention due to the potential use of stem cells in cell based therapy as regenerative medicines. Although, human embryonic stem cells(hESCs) are pluripotent in nature and have maximum potency of giving rise to all most all type of cells, but under ethical debate. Furthermore, adult stem cells (ASCs) are found to have limited potency and also scanty in number. In 2006-2007, these issues have highly resolved with the knowledge that somatic cells have the ability to reprogram into pluripotent stem cells and are defined as induced pluripotent stem cells (iPSCs). Scientists have revealed that the differentiated somatic cells can be reprogrammed to generate induced pluripotent stem cells through the overexpression of particular set of transcription factors. To this respect, human iPSCs are anticipated to open enormous opportunities in the biomedical sciences in terms of cell therapies for regenerative medicine and stem cell modeling of human disease. Also induced pluripotent stem cells (iPSCs) technology is advancing in the field of genetics and cell- transplantation. These reprogrammed pluripotent cells are morphologically and phenotypically similar to embryonicstem (ES) cells. Inthis review, the main focus is on some of the important areas in which iPSC technology has been applied as cardiovascular medicine. This paper also discusses the future directions and ongoing challenges in the field of medicine. Stem cells are unique cells that have the capacity for self-renewal and are capable of forming at least one, and sometimes many, specialized cell types

**Keywords:** iPSCs, Pluripotent, Embryonic stem cells (ESCs), Regenerative medicine, Cardiovascular medicine.

PP183

ICABB-176

## RAS ONCOGENES AS EMERGING THERAPEUTIC TARGETS AND POTENTIAL BIOMARKERS FOR HUMAN CANCERS

Tanvi Shukla and Vibha Rani\*

Jaypee Institute of Information Technology, A-10, sector -62,  
Noida, Uttar Pradesh, India 201301

E-mails: tanvishukla2410@gmail.com, \*Corresponding author:  
vibha.rani@jiit.ac.in

The Ras oncogene family has been studied extensively over the last three decades. The members of the Ras GTPase family are crucial for a large number of signaling networks connecting a variety of upstream signals as well as to a wider number of downstream effector pathways linked to a number of cellular processes including cell cycle progression, growth, migration, cytoskeletal changes, apoptosis and senescence. Amongst the cellular signaling networks, RAS-RAF-MEK-MAPK pathway has been proven essential for control of cell proliferation, differentiation and survival. Oncogenic mutations in a number of upstream and downstream components of Ras signaling pathways at respective codons have been detected in more than 30% of all human cancers with the most common being lung, colon, and pancreatic cancer. Ras molecules have served as potential target for cancer therapeutics. Small molecule inhibitors to RAS-RAF-MEK-MAPK pathway have been validated as effective in therapy against a variety of cancers, and have gained wide application. AS pathway mutations may serve as a biomarker to identify patients eligible for targeted cancer therapy. As per the recent studies, RAS pathway mutations have been established as a predictive biomarker for treatment adaptation in pediatric B-cell precursor acute lymphoblastic leukemia. The presence of K-RAS and B-RAF mutations has been studied as biomarker for metastatic colorectal cancer. In summary, the Ras-Raf-MEK-ERK pathway is of major interest for new therapeutic strategies and biomarker evaluation.

**Keywords:** Ras family, Signaling Oncogene, mutations, Cancer, Therapeutics, Biomarker

## ASSOCIATION OF SEROTONIN (5-HT) WITH DRUGS/SUBSTANCE ABUSE ADDICTIVE BEHAVIOR

Anit Kumar<sup>1</sup> and Dr. Amit Kaushik<sup>1\*</sup>

1. Molecular genetics research lab, Amity Institute of Biotechnology, Amity University Uttar Pradesh, Noida, 201313, (U.P.)  
 \* Corresponding author: sshirodkar@amity.edu

Serotonin (5-HT), a monoamine neurotransmitter is a type of chemical that regulates mood, emotions, sleeping, eating, reward function, motor skills and many more by relaying signals from one area of brain to another. Mostly it is found in digestive system, also in blood platelets & throughout central nervous system. Serotonin is derived from an essential amino acid tryptophan. On the other hand, the use of psychoactive substances like opium is a wide spread behaviour in human societies. Here we focus on the role of the serotonergic (5-HT) system in the establishment of drug use-associated behaviours. Different levels of 5-Hydroxy tryptophan are found to associate with various kinds of addictive or antisocial behaviours. Serotonin system is found to be crucially involved in opioid drugs use compulsive behaviour. Studies suggested specific adaptations in serotonin system, which coincide with the establishment of controlled drug use-associated behaviours. These adaptations render the nervous system susceptible to the transition to compulsive drug use behaviours and often overlap with genetic risk factors for addiction. Serotonergic system possesses transporters, receptors, regulatory enzyme mono-amino oxidase which is found to contribute to the vulnerability to addiction and relapse in various situations & environmental conditions.

**Keywords:** Serotonin, Neurotransmitter, Addictive behaviour

## CHIKUNGUNYA POLYMERASE: A POTENTIAL TARGETS FOR INHIBITORS- IN SILICO STUDY

Ritu Ghildiyal<sup>1</sup>, Vandana Gupta<sup>2</sup>, Reema Gabrani<sup>1</sup>, Amita Gupta<sup>3</sup>, V.K. Chaudhary<sup>3</sup> and Sanjay Gupta<sup>1\*</sup>

1 Center for Emerging Diseases, Department of Biotechnology, Jaypee Institute of Information Technology, Noida, UP 201309, India. 2 Department of Microbiology, Ram Lal Anand College, University of Delhi South Campus (UDSC), Benito Juarez Marg, New Delhi 110021, India. 3 Department of Biochemistry, University of Delhi South Campus, Benito Juarez Marg, New Delhi 110021, India.  
 E-mails: ritu.ghildiyal03@gmail.com, vandanagupta72@rediff.com, reema.gabrani@jiit.ac.in, ag0907@yahoo.com, vkchaudhary@south.du.ac.in, \* Corresponding author: sanjay.gupta@jiit.ac.in

In the absence of any effective antiviral regime and/or vaccine, Chikungunya virus (CHIKV) has become a serious health concern as it remains the leading cause of massive epidemics of debilitating Chikungunya fever in tropical and subtropical countries worldwide. CHIKV is a positive sense single stranded RNA (11.8 kb) belonging to Alphavirus genus and belonging to Togaviridae family. The genome encodes 5 structural and 4 non-structural proteins (nsPs). Non-structural protein 4 (nsP4) of CHIKV possess RNA dependent RNA polymerase (RdRp) activity and plays a crucial role in genome replication and hence it can be a promising target for novel therapeutics. Though this protein is important in viral life cycle, but is less explored as antiviral target for the non-availability of crystal structure. nsP4 Polymerase comprises the catalytic core with conserved GDD motif which is observed not only across different CHIKV strains but also across other Alphaviruses. This emphasizes the uniqueness and importance of this motif in the functioning of this polymerase. Therefore, in this study we used a receptor created around GDD motif for docking of drugs. Herein, a model of nsP4 polymerase was developed using Swiss Model and validated by Ramachandran plot. Pocket comprising the catalytic triad was predicted using computational pocket finding module and was used with some modifications. Molecular docking was performed using LeadIT Flex-X flexible docking module with FDA approved drug molecule library. On the basis of binding energy, top 5 best leads with binding energies -33.7588, -30.2555, -29.6043, -28.916 and -28.5042 were selected. These leads could be promising inhibitor of CHIKV polymerase and will be further validated by in-vitro assays.

**Keywords:** Catalytic triad; Chikungunya Virus (CHIKV); Molecular docking; RNA dependent RNA polymerase.

PP186

ICABB-189

## BIOLOGY AND COMPARATIVE GENOMIC ANALYSIS OF ACENETOBACTER BAUMANNII: AN EMERGING NOSOCOMIAL PATHOGEN

**Khare A<sup>1</sup>, Pillai P<sup>1</sup> and Jain C<sup>1\*</sup>**

*1. Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201307, Uttar Pradesh, India*

\* Corresponding author: ckj522@yahoo.com

*Acinetobacter baumannii* is a gram negative bacteria that has recently emerged as an opportunistic pathogen which is responsible for various hospital acquired nosocomial infections that include bacteremia, pneumonia, meningitis, urinary tract infection, and wound infections. Studies on *A. baumannii* are gaining popularity because of its ability to acquire multidrug resistance very rapidly which makes it extremely difficult to deal with the infection it causes. To overcome these problems, comprehensive knowledge of the pathogenesis and antibiotic resistance mechanisms of *A. baumannii* is important. This paper discusses about the underlying biological knowledge of drug -target-drug interaction, the issue of antibiotic resistance and associated mechanism of *A. baumannii*, the issue of antibiotic resistance and presently available drugs with global epidemiology are also elaborated. The literature reveals about that *A. baumannii* gains its resistance against drugs via horizontal gene transfer and hence, the elaboration on comparative genomic analysis of the organism along with genetic variation has been discussed for the discovery of novel drug targets. The modern network biology / system biology along with modern bioinformatics analysis could be facilitate the new insight to establish the possible mechanism.

PP187

ICABB-191

## CHARACTERIZATION OF MIR-30 FAMILY MEMBER IN NOREPINEPHRINE INDUCED CARDIAC HYPERTROPHY

**Yashika Rustagi<sup>1</sup> and Vibha Rani<sup>1\*</sup>**

*1. Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201307, Uttar Pradesh, India*

E-mails: yashikarustagi@gmail.com,

\*Corresponding author: vibha.rani@jiit.ac.in

Cardiac hypertrophy, the most common cardiovascular disease is associated with heart failure and sudden death. microRNAs (miRNAs) are endogenously expressed 18-24nt noncoding RNAs that regulate gene expression at post-transcriptional level. Our previous stage specific microRNAs profiling identified miR-30 as a critical regulator of fetal cardiac gene program during development. In the present study, we investigated the *in silico* and molecular functions of miR-30d in h9c2 cardiac cell lines. miR-30d is a member of miR-30 family and is encoded within an intron of actin- $\alpha$ 1 (ACTC1), a fetal cardiac marker gene and essential for cardiac muscle contraction. miR-30d was found evolutionary conserved and differentially expressed in various stages of heart development. Overexpression of miR-30d was sufficient to suppress the upregulated fetal cardiac genes- actin alpha1, myosin7, alpha actin and GATA-4 in Norepinephrine induced *in vitro* hypertrophic model. miR-30d also repressed tumour necrosis factor-alpha gene expression. Our study demonstrated that miR-30d is conserved during heart development. Also, overexpression of miR-30d was sufficient to inhibit expression of a set of fetal cardiac genes in hypertrophied cardiomyocytes. Together, our study revealed that uncharacterized cardiac specific miR-30d modulates cardiac hypertrophy in h9c2 cardiomyocytes and could serve a potential molecule for miRNA based therapeutics.

**Keywords:** microRNAs, Heart Development, Gene Regulation, Cardiac Hypertrophy

## **STUDY ON DRUG FORMULATION FOR NEUROPATHIC PAIN**

**Akshay Jain<sup>1</sup>, Kuldeep nigam<sup>1</sup> Atinderpal Kaur<sup>1</sup> and Dr. Shweta Dang<sup>1\*</sup>**

*Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sec-62, Noida-201307, Uttar Pradesh, India*

\* Corresponding author: shweta.dang@jiit.ac.in

Neuropathic pain(NP) is a disease affecting the nervous system. Neuropathic pains(NP) are characterized by partial or complete somato sensory change in the innervations territory corresponding to peripheral or central nervous system pathology, and the paradoxical occurrence of pain and hypersensitivity phenomena within the denervated zone and its surroundings. It is vital disorder that clinicians are aware of the circumstances that increase the risk of Neuropathic Pain. This awareness will assist in early diagnosis, initiation of treatment and potentially a better outcome for the patient. These circumstances include acute and chronic medical conditions, surgery and trauma. The treatment progresses through first, second, and third line drug treatment, includes advice on antidepressant, anticonvulsants and opioids (in specific circumstances), and describes non-pharmacological approaches. Advances in NP diagnostics and therapeutics over the last few decades are largely responsible for this dramatic improvement. Nanoparticles (NPs) have been of significant interest from so many years as they offer great benefits for drug delivery to overcome limitations in Neuropathic pain. They can not only be formed in a range of sizes (1-1000nm) but also be made using a variety of materials. In addition, they can be tailored to simultaneously carry both drugs and imaging probes and designed to specifically target molecules of diseased tissues. The first nanoparticles had entered the pharmaceutical market in 1995. Since then, nanocarriers for neuropathic drug delivery have been developed are currently under development due to their many advantages including targeting to specific organs to be treated.

**Keyword:** Anticonvulsants, Antidepressant, Neuropathic pain, Nanoparticle, Opioids

## **EXPANDING THE REPERTOIRE OF AMINO ACID**

**Shreya Singh, Varun Thakur, Deepali Verma and Vibha Gupta\***

*Department of Biotechnology, Jaypee Institute of Information Technology, Sector-62, Noida-201309,*

*E-mails: Shreya.singh14414.ss@gmail.com, arun68060@gmail.com, deepali.biotechnology@gmail.com,*

*Corresponding Author: vibha.gupta@jiit.ac.in*

The recent developments in the field of genetic engineering allow the expansion of amino acids resulting in the production of several proteins in cells and animals. This has been possible by creating the orthogonal tRNA/aminoacyl-tRNA synthetase pairs and with the viability of artificial genetic code. It has already been reported that there are 20 natural or canonical amino acids in a standard genetic code. However, with the advancement in genetic engineering, it is possible to incorporate an unnatural or noncanonical amino acid (NCAA) into the genetic code of an organism. The incorporation of NCAA into the proteome of an organism can be done by stop ("amber")-codon suppression or reassignment of rare sense codon. Another approach includes usage of tRNAs with quadruple code. The applications of codon expansion includes the generation of proteins, bi-specific antibodies, etc. that hold promise for future therapeutics and would be difficult to obtain without NCAA incorporation. This review describes the strengths, technical considerations and challenges of current methods employed for incorporating modified amino acids into a protein of biotechnology relevance.

**Keywords:** Amino acid, noncanonical amino acids, aminoacyl-tRNA synthetase, amber codon suppression, four base codon

PP190

ICABB-216 PP191

ICABB-219

## **DRAMATIC INCREASE EXPRESSION IN THE EXPRESSION OF RECOMBIANT CysE FROM STREPTOCOCCUS PNEUMONIA BY CODON OPTIMIZATION**

**Deepali Verma and Vibha Gupta\***

*Department of Biotechnology, Jaypee Institute of Information Technology, Sector-62, Noida-201309, India*

*E-mails: deepali.biotechnology@gmail.com, \*Corresponding author: vibha.gupta@jiit.ac.in*

*Streptococcus pneumoniae* (Spn) is a causative agent of community-acquired pneumonia and meningitis in children and the elderly. This bacterium is also responsible for ear infections, sinus infections, and bacteremia. Though antibiotics are available for curing infections caused by this pathogen, the emergence of Multi Drug Resistance Spn strains necessitates the development of novel therapeutics. *De novo* cysteine synthesis pathway is essential for the survival of many pathogenic bacteria such as *M. tuberculosis*, *H. influenza*, *S. aureus* and *B. subtilis* in their hosts. As this pathway is absent in humans, it represents a unique target for therapeutic intervention. The first enzyme of this pathway, CysE (serine acetyltransferase), catalyzes the production of O-acetyl serine from L-serine and acetyl CoA. This study reports the molecular cloning of *cysE* from Spn in the pET21c expression vector and focuses on large scale production of recombinant CysE in the heterologous *E. coli* host. Further optimization of induction parameters in conventional *E. coli* BL21(DE3) cells did not yield any significant expression. But high level expression of recombinant Spn CysE could be attained in BL21-CodonPlus (DE3)-RIL cells demonstrating the effectiveness of codon optimization strategies for improving over expression in *E. coli*.

**Keywords:** *Streptococcus pneumoniae*, CysE, cysteine synthesis pathway, BL21-CodonPlus (DE3)-RIL, optimization

## **ROLE OF NANOTECHNOLOGY IN STEM CELL THERAPY**

**Akshay Amritanshu, Anushruti Bhardwaj and Sudha Srivastava**

*Department of Biotechnology, Jaypee Institute of Information Technology, A-10 Sector 62, Noida, U.P. India*

*E-mails: akshayamritanshu97@gmail.com, anushrutibhardwaj3@gmail.com, \*Corresponding author: sudha.srivastava@jiit.ac.in*

This review addresses role of nanotechnology in stem cell therapy. Advancements in stem cell therapy from isolation of embryonic stem cells in 1981 to establishment of induced pluripotent stem cells in 2007 for treatment of physical injuries, bone and tissue regeneration, cardiovascular disease to various degenerative diseases has been presented. The major hurdle of tracking and guiding stem cells has limited stem cell research to laboratory scale. Optical properties of nanomaterials overcoming the issue of imaging and tracking of stem cells via nanoparticles, quantum dots or magnetic nanomaterials have been discussed. Apart from labeling and tracking, size and morphology of nanomaterials mimicking natural systems has been impetus in tissue engineering for stem cell research. Nanofibers and nanocomposites employed for development of scaffolds in tissue engineering, for adhesion, migration, proliferation and differentiation have been discussed in detail.

**Keywords:** Stem cell, nanomaterials, tissue engineering, bone regeneration.

PP192

ICABB-226

## **ANALYSIS OF EXEMESTANE FROM LIPID-POLYMER HYBRID NANOPARTICLES**

**Md. Rizwanullah<sup>1</sup> and Saima Amin<sup>2</sup>**

*Department of Pharmaceutics, School of Pharmaceutical Education and Research, Jamia Hamdard, New Delhi 110062.*

*E-mail: mdrizwanullah54@gmail.com*

Breast cancer is a commonly occurring devastating and life threatening disease in women. One-third of human breast tumors are reported to be hormone dependent and estrogen is the most important hormone involved in the growth of these tumors. Exemestane (EXE) is an irreversible aromatase inhibitor used for the treatment

breast cancer. EXE is orally active but its bioavailability is about <10% due to its low aqueous solubility, expulsion from P-gp efflux pump, and extensive first pass effect. Conventional dosage forms exhibit low bioavailability due to extensive first pass metabolism and non-targeted delivery of anticancer drugs results in numerous side effects. Thus, it was aimed to develop lipid-polymer hybrid nanoparticles (LPHNPs) to improve aqueous solubility and oral bioavailability. LPHNPs made from building blocks of polymers and lipids that integrate the advantages of lipid-based nanoparticles and polymeric nanoparticles. The hybrid architecture provides advantages such as controllable particle size, surface functionality, high drug loading, tunable drug release profile, and improved stability in GIT. EXE loaded LPHNPs were developed by single step self-assembled nanoprecipitation technique and evaluated for particle size, entrapment efficiency, drug loading and drug content determination. A reverse phase HPLC method was developed to assess drug content in the prepared LPHNPs. The method was validated as per ICH guidelines for its sensitivity. The validation parameters showed sensitivity in the range 0.1–100 µg/ml with limit of detection and limit of quantitation 0.01–0.033 µg/ml. Therefore, it is concluded that the prepared LPHNPs will be assayed through the developed method.

**Keywords:** Lipid polymer hybrid nanoparticles, breast cancer, oral bioavailability, first pass metabolism, HPLC, drug content

PP193

ICABB-231

## PSYCHOBIOTICS: PIRATES OF GUT MICROBIOTA

Tanya Gupta, Akanksha Jain and Garima Mathur\*

Department of Biotechnology, Jaypee institute of information technology, A-10, Sec-62, Noida-201307, India  
 E-mails: tanyagupta9697@gmail.com, akanksha21096@gmail.com,  
 \*Corresponding author: garima.mathur@jiit.ac.in

The human gut provides shelter to the noteworthy number and species of microorganisms, constituting gut microbiota. The microbiota profile of an individual is acquired at the time of birth and is continually influenced by various factors including age, genetics, diet and lifestyle. Despite, the relative abundance and distribution of microbes is similar among healthy individuals. The bidirectional communication between central nervous system and gut microbiota, is referred to as gut-brain axis. The gut-brain axis has been of interest to investigate the modulations in microbiome

and role in various diseases. If the aberrant microbiota or dysbiosis develops in an individual, it results in imbalance in this bidirectional communication, ultimately leading to disease. Recent studies have elucidated that the dysfunction in the gut-brain axis is directly linked to various neuropsychological, metabolic, and gastrointestinal disorders. Providentially, the recognition of psychobiotics as an emerging therapy for mental health benefits mediated by gut microbiota is a growing area of research. Psychobiotics are the live bacteria (probiotics) or the support of such bacteria (prebiotics) that affect the gut-brain axis. Studies have proved that psychobiotics not only improves the behavioural problems but also enhances the gut microbiota which reduces the depression levels and various GI disorders like (IBS) Irritable Bowel Syndrome. Thus, psychobiotics are at the frontier of advancement in healthcare sector.

**Keywords:** Psychobiotics, Gut-brain axis, Gut microbiota, Dysbiosis, Probiotics

PP194

ICABB-242

## BIOINFORMATICS AND DRUG DISCOVERY

M Qasif Masis and Dr. Deepak Sharma

Meerut College, Meerut, Ch. Charan Singh University  
 E-mails: mqasif17@gmail.com, depshad@gmail.com

Bioinformatics analysis cannot only accelerate drug target identification and drug candidate screening and refinement, but also ease up characterization of side effects and predict drug resistance. High-throughput data such as genomic, epigenetic, genome architecture, cistromic, transcriptomic, proteomic, and ribosome profiling data have all made significant contribution to mechanism based drug discovery. Accumulation of protein and RNA structures, as well as development of homology modeling and protein structure simulation, coupled with large structure databases of small molecules and metabolites, built the way for more realistic protein-ligand docking experiments and more informative virtual screening. Drug discovery starts with diagnosis of a disease with well characterized symptoms that reduce the quality of life. Conventionally, a desirable drug is a chemical (which could be a simple chemical or a complicated protein) or a combination of chemicals that reduces the symptoms without causing severe side effects in the patient. Other properties of a desirable drug include affordability, low chance of drug resistance leading to dramatic decrease in the commercial value of the drug,

low deleterious effect on the environment, e.g., no reactivation by bacterial species after human use. Thus, a desirable drug is one that not only is efficacious with little side effects, but also has minimal long-term negative effect on the patient, the society and the environment. Bioinformatics is an interdisciplinary science spanning genomics, transcriptomics, proteomics, population genetics and molecular phylogenetics. Bioinformaticians in drug discovery use high throughput molecular data in comparisons between symptom-carriers (patients, animal disease models, cancer cell lines, etc.) and normal controls. The key objectives of such comparisons are to connect disease symptoms to genetic mutations, epigenetic modifications, and other environmental factors modulating gene expression, identify drug targets that can either restore cellular function or eliminate malfunctioning cells (e.g., cancer cells), predict or refine drug candidates that can act upon the drug target to achieve the designed therapeutic result and minimize side effects, and assess the impact on environmental health and the potential of drug resistance.

**Keywords:** Drug candidate, Genomics, Proteomics, Transcriptomics, Population genetics, Epigenetics, Phylogenetics.

PP195

ICABB-244

## NANO-CARRIERS FOR VACCINE DESIGNING -UPDATES & CONCERNS

**Neha Goyal<sup>#</sup>, Manavi Jain<sup>#</sup> and Manisha Singh<sup>\*</sup>**

Department of biotechnology, Jaypee Institute of Information Technology, A-10, Sector-62, Noida-201307, Uttar Pradesh, India  
E-mails: arshavinvanpersie@gmail.com, manavijain97@gmail.com,

\*Corresponding author: manisha.singh@jiit.ac.in

<sup>#</sup>Equal contribution

The limitations of traditional vaccines related with their stability, delivery and their biological effects have been a major challenge globally. Although the advances in immunological discoveries of many potential and advanced molecules for vaccine delivery has been reported extensively in last two decades but still an assured and effective strategy to secure there targeted delivery and stability remained a concern. The nanocarrier based vaccine designing has emerged as an effective way to address the same. Nanoparticles based carrier systems for vaccine delivery are opted, due to their numerous advantages of being biocompatible, non toxic and inert nature etc. Here, in this paper, the structure and immunological influences of the nano carrier based vaccines along with its

activation is discussed. It will also discuss about the various targeted routes for an efficient delivery of vaccine like -intranasal route of administration for PLA-PEG nanoparticles and its advantages over the other routes of administration. Their interaction can enhance the immune response and elicit the binding affinity of antigen to specific antibodies. Further, they can also eliminate the antigen from the body without showing any histopathological change in the body. But there are certain concerns related to the development and enforcement of nanoparticles drug delivery system and the reasons of not being fully adapted in today's world.

**Keywords:** Vaccines, Nanoparticles, Immunization, Drug delivery system.

PP196

ICABB-246

## FABRICATION, VALIDATION AND OPTIMISATION OF POLYMERIC NANOPARTICLES FOR ENHANCING NEURAL ACTIVITY.

Rishika Chaddha, Novis Srivastava,  
Prakhar Agarwal, Aishwarya Kashyap,  
Saurabh Srivastava, Akhil Kumar and  
Manisha Singh\*

Department of Biotechnology, Jaypee Institute of Information Technology, Sector-62, Noida

E-mails: rishika.chaddha@gmail.com, novissriv@gmail.com, aprakhar50@gmail.com, aishakashgr8@gmail.com, snsjr17@gmail.com, akhil27dec@gmail.com, \*Corresponding author:  
manisha.singh@jiit.ac.in

Today's modern day medicines although proves to be an efficient strategy to combat with the curtailing rise of neural disorders but due to their insufficient accessibility and impregnation in to the deeper cortical regions of the brain, limits their therapeutic index, apart from also limiting their specific and controlled therapeutic interventions. The formulations and delivery system for the same are not been impressive so far as most of them (~98%) small-molecule drug candidates unable to enter the brain due to the restriction by blood-brain barrier (BBB) or blood-cerebrospinal fluid barrier (BCSFB). So to overcome from these restricting barriers, varied strategies are developed using nanoparticles as a drug delivery / carrier system, out of which polymeric nanoparticles (PNPs) are reported to show long-term stability, biocompatibility and better impregnation in to deeper thalamic or cortical regions. Polymeric nanoparticles (PNPs) are solid colloidal carriers composed of organic

polymers, either natural or synthetic or semi-synthetic in origin and are the most common materials for constructing nanoparticle-based drug carriers. Their structural construction helps in providing a variety of ways in which drug could be attached. Drug could either be entrapped or dissolved or encapsulated or adsorbed at the surface of PNP. Along with drugs, they could be effectively used as a carrier system for transporting several classes of therapeutic agents including proteins and DNA to target cells. In our study we have used various polymers like Chitosan, polycaprolactone;  $\epsilon$ -carrageenan, poly vinyl alcohol etc., which are reported to enhance the neural activity, to fabricate polymeric nanoparticles and further, optimised them with respect to their ratio, volume, concentration and encapsulation of drug.

**Keywords:** Neurodegenerative diseases; Blood-brain barrier; Central nervous system; Carrier system.

PP197

ICABB-248

### APPLICATION OF NEXT GENERATION SEQUENCING IN DECIPHERING HUMAN GUT MICROBIOME

Drishti Mittal, Ishita Tiwari, Jasmine Pruthi,  
Isha gupta, Sharad Saxena and Vibha Rani\*

Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sector-62, Noida, Uttar Pradesh, India 201301  
E-mails: Itiawari233@gmail.com, mittaldrishti96.dm@gmail.com,  
isha123gagan@gmail.com, jasminepruthi09@gmail.com,  
s.a28@hotmail.com, \*Corresponding author: vibha.rani@jiit.ac.in

**Metagenomics** (also referred to as environmental and community genomics) is the genomic analysis of microorganisms by direct extraction and cloning of DNA from an assemblage of microorganisms. The human gastrointestinal tract harbors the most complex human microbial ecosystem (intestinal microbiota). Gut microbiota not only helps in digestion but also in making of robust and balanced immune system. The comprehensive genome of these microbial populations (intestinal microbiome) is estimated to have a far greater genetic potential than the human genome itself. Analysis of the human gut microbiome, collective genomes of over 100 trillion cells which form the complex bacterial community, has recently become more practical due to remarkable advances in next-generation sequencing technologies (NGS). Several studies using NGS-based metagenomic approaches have been conducted to comprehensively analyze genes/functions and species composition in the human gut microbiome. The 16S rRNA gene contains both

highly conserved regions for primer design and hypervariable regions to identify phylogenetic characteristics of microorganisms, thus is the most widely used marker gene for profiling bacterial communities. These NGS-based approaches have demonstrated that their ecological and biological features that have been rather difficult to pursue can now be characterized with relative ease and high-throughput. In this review analytical tools used in NGS-based techniques which provide the detection of human gut is discussed and also some guidelines that must be followed to aid the same.

**Keywords:** Metagenomics, Next generation Sequencing, microbiome, human gut.

PP198

ICABB-250

### DETECTION OF COPY NUMBER VARIATIONS THROUGH NEXT GENERATION SEQUENCING TO IDENTIFY GENETIC BASIS OF CANCER

Isha Gupta, Jasmine Pruthi, Drishti Mittal,  
Ishita Tiwari, Sharad Saxena and Vibha Rani\*

Department of Biotechnology, Jaypee Institute of Information Technology, A-10, Sector-62, Noida, Uttar Pradesh India -201301  
E-mails: isha123gagan@gmail.com, jasminepruthi09@gmail.com,  
mittaldrishti96.dm@gmail.com, itiawari233@gmail.com,  
s.a28@hotmail.com, \*Corresponding author: vibha.rani@jiit.ac.in

Copy number variations (CNVs) contribute significantly to human genomic variability, some of which lead to diseases such as cancer. CNVs are large genomic DNA segments ( $>1$  kb) with variable copy number among individuals. CNVs encompassing genes can potentially alter gene dosage, disrupt genes or perturb their expression levels, and are known to contribute to a number of disorders such as cancer. Accurate detection of somatic copy number variations (CNVs) is an essential part of cancer genome analysis, and plays an important role in onco-target identifications. Traditional methods for CNV identification include array comparative genomic hybridization (aCGH) and SNP array technologies. Recently, a popular method to analyse the copy number variations is Next generation sequencing (NGS). This review aims to provide a guide to the analytic tools used in NGS-based cancer CNV studies, and to discuss the important factors that researchers need to consider when analyzing NGS data for somatic CNV detections. We have also discussed the principles for data pre-processing, segmentation, interpretation, and discuss the challenges in somatic CNV detection

along with the list of current analytic tools used for CNV detection in NGS-based cancer studies. Tools such as SeqCNV, targeted high-multiplex PCR-based NGS panel (OncoMine Comprehensive Assay) coupled with highthroughput sequencing using Ion Proton sequencer for routine screening of solid tumors have been introduced in this review.

**Keywords:** Next Generation Sequencing, copy number variation (CNV), Cancer

PP199

ICABB-251

## IN SILICO STUDIES OF FDA APPROVED DRUGS AGAINST SALMONELLA TYPHI FTSZ CELL DIVISION PROTEIN

Muneera Mashkoor<sup>1</sup> Manoj Kumar<sup>2</sup> and Abdul S. Ethayathulla<sup>2\*</sup>

1. Department of Computer Science, Jamia Millia Islamia, New Delhi-110025 2. Department of Biophysics, All India Institute of Medical Sciences, New Delhi-110029

E-mail: muneera.mashkoor@gmail.com, manmath.manoj@gmail.com,

\*Correspondence author: ethayathulla@gmail.com

FtsZ is one of the important cell division proteins involved in cytokinesis and is responsible for making cell division plane through Z-ring formation via GTP-dependent self polymerization. It plays important role initiating cell division assembly making it an ideal drug target to design new antibacterial agents. The aim of this study is to screen potential ligands against FtsZ from *Salmonella Typhi* to design new drug leads for typhoid *Salmonella*. Based on reported studies, it is known that FtsZ inhibitors targets two major sites in the protein - a site near T7-loop which is responsible for self-polymerization activity while other site is a GTP-binding pocket. In this study, we targeted site near T7 loop in order to create structure based pharmacophore model. As the crystal structure of FtsZ from *S.Typhi* is not known, we developed a 3D model of FtsZ through homology modeling. The protein model was used to identify the essential pharmacophore features by structure based pharmacophore modeling approach to screen the FDA approved drugs for the identification of potential ligands for drug repurposing. The obtained hits were further subjected to molecular docking studies using LigandFit docking protocol with default parameters. The best ligands were selected based on highest docking score as well as maximum interactions with target protein. Out of the total identified hits, 5 compounds were showing good binding interactions with T7-loop site through hydrogen bond and

hydrophobic interactions. The docked complex of the best ligand from screening was subjected to refinement by MD simulation for 50ns using GROMACS simulation engine. Based on computational screening, we have identified potential inhibitors of FtsZ from *Salmonella Typhi*, a novel drug target. These inhibitors can provide lead compounds for the development of drugs against drug resistant Typhoid cases along with susceptible ones.

**Keywords:** Homology modeling, Molecular docking, Pharmacophore based screening, Molecular dynamics (MD) simulation, Drug repurposing.

PP200

ICABB-261

## STANDARDIZATION OF VIRTUAL-SCREENING AND POST-ANALYSIS PROTOCOLS RELEVANT TO IN-SILICO DRUG DISCOVERY

Sunita Gupta<sup>1</sup>, Andrew M. Lynn<sup>2</sup> and Vibha Gupta<sup>1\*</sup>

1. Department of Biotechnology, Jaypee Institute of Information Technology, Sector-62, Noida, UP-201307, India, 2. School of Computational and Integrative Sciences, Jawaharlal Nehru University, New Delhi-110067, India

E-mails: sunita.bio@gmail.com, andrew@jnu.ac.in

\*Corresponding author: vibha.gupta@jiit.ac.in

Structure based drug discovery has emerged as a powerful tool in computational drug discovery and has gained rapid acceleration due to development of better algorithms for high end computation in an affordable time period. Molecular docking and virtual screening methods have gained importance in estimating the binding poses using approximated scoring functions, but calculating the binding energies close to experimental values are still needed. MM-PBSA and MM-GBSA are commonly used methods for predicting the binding free energies of well equilibrated structures of ligand-receptor complexes sampled during explicit molecular dynamics simulations. Here, we have tested the Binding Energy After Refinement (BEAR) Algorithm, on docked complexes of *Plasmodium falciparum* DHFR with known sets of ligands and decoys (generated using DUD) using AutodockVina followed by free energy calculation and enrichment curve. Apart from routinely used MM(PB/GB)SA implemented in Amber, we used in-house g\_mmpbsa open-source tool for binding free energy calculations on refined complexes treated implicitly with three-tier MM/MD/MM protocol. To further reduce the computation time we also computed the relative

energies for AutodockVina generated docked poses and the energy minimized complexes. Surprisingly, a binding energy rescoring on the docked pose alone had a lower accuracy than the inherent scoring function of the docking method. However, encouraging results were seen after refinement both with only energy minimization and relaxation with molecular dynamics followed by re-minimization. MMPBSA calculations yielded better enrichment curve which proved to discriminate well between true and false binders and can be further intensified by longer molecular dynamics runs. g\_mmpbsa, implemented in Gromacs also gave satisfactory results and can be used as freely available open source tool for binding free energy calculations.

**Keywords:** Standardization, AutodockVina, BEAR Algorithms, MM(PB/GB)SA, g\_mmpbsa

PP201

ICABB-266

### IN SILICO STUDIES OF NATURAL COMPOUNDS AGAINST JAPANESE ENCEPHALITIS VIRUS NS3 PROTEIN

Mandeep Singh<sup>1</sup> and Munazzah Tasleem<sup>2\*</sup>

1. Department of Computer Science, Jamia Millia Islamia, Delhi-110025, India 2. Bioinformatics Infrastructure Facility, Jamia Hamdard, Delhi-110062, India

E-mails: mandeepraina333@gmail.com

\*Correspondence author: munazzah.t@gmail.com

Japanese Encephalitis, one of the several *Flavivirus* causative mosquito borne disease has become the major cause of central nervous system anomalies such as encephalitis and meningitis worldwide. As is the case with other vector borne diseases people, especially children of developing countries of Asia and Indian subcontinent are at a serious risk of infection owing to low standard of living, poor sanitation and inaccessibility of preventive vaccines to most of the population. The 11kb Japanese Encephalitis virus (JEV) RNA genome upon translation forms a single polyprotein which is processed by Non-structural protein 3 (NSP3) into three structural (C, M. and E) and seven non-structural proteins (NS1, NS2A, NS2B, NS3, NS4A- NS4B and NS5). The 619 residue long multifunctional NSP3 contains serine-protease activity domain at its N-terminus that is responsible for proteolytic cleaving of the viral polyprotein. It also possesses ATPase/helicase and RNA triphosphatase at its C-terminal end that are essential for RNA replication. Owing to these multifunctional properties of NSP3 it is being put forth as a promising drug target

against Japanese Encephalitis. As the crystal structure of JEV NS3 protein is not known we developed a 3D model of JEV NSP3 through various molecular modeling approaches (Swiss Model, Phyre2 and I-Tasser). Best validated 3D model was used to perform molecular docking (Autodock vina) and interaction studies (PLIP) on it with natural compounds previously known to possess antiviral properties in vitro and in vivo testing. Compounds Solophenol, Aloemodin and Flinderole showed essential binding affinity with NSP3 and best hydrogen and other bonding interactions. These were further evaluated for drug likeness, ADME and toxicity profiling. Thus, these natural compounds should further be studied both *in-silico* and clinically to validate them as potential lead molecule and for designing novel drugs for the treatment of JEV.

**Keywords:** ADMET, Japanese Encephalitis Virus (JEV), Molecular Modeling, Molecular Docking, Natural compounds.

PP202

ICABB-221

### IDENTIFICATION AND ANALYSIS OF MOBILE GENETIC ELEMENTS IN GIBBON GENOME

Kamal Rawal\*, Jaisri Jagannadhan, Chahat Kubba and Tanya Sharma

<sup>1</sup> Department of Biotechnology, Jaypee Institute of Information Technology, A10, sector62, Noida, Uttar Pradesh, India-201307\*

E-mails: jaisrij@gmail.com, chahatkubba@yahoo.com,

tanyasharma434@gmail.com, \*Corresponding author:

kamal.rawal@gmail.com

Recent sequencing of genome of northern white-cheeked gibbon (*Nomascus leucogenys*) has provided important insights into fast evolution of gibbons and signatures relevant to gibbon biology. It was revealed that the mobile genetic elements (MGE) play a major role in gibbon evolution. Here we report that most of the gibbon genome is occupied by the MGEs such as ALUs, MIRs, LINE1, LINE 2, LINE 3, ERVL, ERV-class1, ERV-class II and other DNA elements which include hAT Charlie and TcMar tigger. We have provided a detailed description and genome wide distribution of all the MGEs present in gibbon genome. Previously, it was reported that gibbon-specific retrotransposon (LAVA) tend to insert into chromosome segregation genes and alter transcription by providing a premature termination site, suggesting a possible molecular mechanism for the genome plasticity of the gibbon lineage. We show that insertion

sites of LAVA elements present atypical signals/patterns which are different from typical signals present at insertion sites of Alu elements. This suggests possibility of distinct insertion mechanism used by LAVA elements for their insertions. We also find similarity in signals of LAVA elements insertion sites with atypical signals present at Alus /L1s insertion sites disrupting the genes leading to diseases such as cancer and Duchenne muscular dystrophy. This suggests role of LAVA in premature transcription termination.

**Keywords:** Mobile genetic elements, LINEs, SINEs, ALUs, Gibbon, repeat masker, ELAN

PP203

ICABB-058

---

## EVALUATION OF BOSWELLIC ACID DERIVED FROM *BOSWELLIA SERRATA* AS ANTI-INFLAMMATORY AND ANTI-OXIDANT AGENT.

Lavina Rajput, Aditi Agarwal, Vipin Verma and Priyadarshini\*

Department of Biotechnology, Jaypee Institute of Information Technology, Noida

\*Corresponding author: priyadarshini@jiit.ac.in

---

Drugs derived from plants have major role in both traditional and modern medicine. Medicinal plants contribute directly as therapeutic agents and raw materials for manufacturing synthetic drugs. A number of traditional plant-derived medicines are being integrated into mainstream health systems for

the benefit of human population. Medicinal plants act as protective agents against damaging factors like reactive oxygen species. *Boswellia serrata*, well known by its common name Shallaki is known to cure various diseases like diabetes, arthritis and joint pains but it is still not explored well for all of its potential medicinal benefits. The main pharmacologically active ingredients of this medicinal plant are  $\alpha$  and  $\beta$  boswellic acid, and pentacyclic triterpenic acids. A detailed study about properties of its extract may lead to development of new therapeutic drugs with minimal side effects. For this purpose boswellic acid was extracted from *Boswellia* resin powder and its anti-oxidant potential (DPPH-assay), anti-inflammatory activity (protein denaturation method) and anti-microbial activity was studied. A significant increase in the percentage inhibition of the free radicals was observed when the extract concentration was increased. There was a significant inhibition of the albumin protein denaturation. With increase in the concentration of plant extract, there was an increase in percentage inhibition of protein denaturation for both plant extract and drug. The plant extract was showing anti-microbial potential through zone of inhibition assay. The extract was found to possess both anti-oxidant and anti-inflammatory potential and also showed antimicrobial properties at slightly elevated concentrations. Our study shows that boswellic acid extract obtained from *Boswellia* resin has anti-inflammatory, anti-oxidant as well as antimicrobial potential.

**Keywords:** Medicinal properties; *Boswellia serrata*; Anti-oxidant; Anti-inflammatory; antimicrobial; Drug development.