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“Role of Microbe-Plant-Animal Interactions in Human Health”

ABSTRACT E-BOOK

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Plenary Lectures
Evolution, diversity and development of multi-drug resistance in *Mycobacterium tuberculosis*

**Randeep Guleria**

All India Institute of Medical Sciences, Ansari Nagar, New Delhi-110029

**Presenting Author**
randeepguleria2002@yahoo.com

Tuberculosis, the disease that caused cachexia and death for centuries, has been referred by different names in various ancient literatures. Despite adequate anti tubercular drugs, tuberculosis still continues to be a major public health challenge especially in developing countries. *Mycobacterium tuberculosis* (MTB), the causative agent of tuberculosis, remains an important cause of morbidity and mortality worldwide. *Mycobacterium* species have survived a “population bottleneck”, and travelled across continents, human subspecies and animals to attain their current genotype and virulence. Studies favor the hypothesis of co-evolution between humans and certain MTB complex lineages. The exact duration of the association between humans and MTB complex is subject to intense debate, but irrespective of this, different phylogenetic lineages of MTB complex are associated with different geographic regions, and possibly adapted to specific human populations. In addition, some lineages seem to behave in a generalist way, while others appear to be specialists restricted to a smaller group of human host populations. Humans differ in their genetic susceptibility to TB. Genetic diversity in MTB complex is also increasingly recognized as a factor influencing the outcome of TB infection and disease. Recent studies have reported interactions between human and bacterial genetic diversity, reinforcing the view that in addition to environmental variables, TB susceptibility varies as a function of both the human and MTB complex genotype. Strains causing human disease, and more specifically the drug resistant MTB strains, can be traced back to a few genotypes. MTB continues to adapt to immunologic mechanisms of humans. Newer mutations in MTB were mostly governed by genetic drift, negative selection, and background selection. Other factors include improper or inadequate drug treatment and HIV co-infection. Identifying molecular loci of host pathogen interactions may help us in understanding pathogenesis of the disease, and identification of newer targets for antitubercular drugs.

Early diet and environment’s impact on microbiome and the development of allergies

**Ruchi Gupta**

SOAAR, Northwestern Feinberg School of Medicine, USA

**Presenting Author**
r-gupta@northwestern.edu

PL1

PL2
The human microbiome is a sum of bacteria, viruses, and fungi, their genomic elements, and their interactions. Changes in early life microbial exposure may alter the microbiome and can lead to the development of an atopic disease. There are many early life factors that can produce these changes in the skin, lung, and gut microbiota, including mode of delivery (vaginal vs. cesarean), antibiotic use, skin exposure, hygiene, food consumption, and geographic origin. Today, Dr. Ruchi Gupta will present on how early diet and the environment can impact the microbiome and furthermore, the development of allergies. Dr. Gupta will also expand on the importance of geographic origin and its effect on the microbiome and childhood food allergy. With India’s rich cultural heritage and varying diet as the 7th largest country in the world, there is a need to expand research on childhood food consumption in different regions of this country. To this end, Dr. Gupta will explain the FACE Study, or Food Allergy and Atopy Collaboration and Evaluation in India, whose goal is to examine the prevalence of food allergy in India in more detail. In addition, by collecting bio specimen samples and assessing early diet introduction and antibiotic use, researchers will also be able to examine the structures that impact the diversity and colonization of the microbiota. To conclude, Dr. Gupta will compare and contrast the common dietary and hygiene practices in urban India with current Western practices and their effects on microbiomes and the development of childhood food allergy.

**PL3**

**Discovery and Development of SIRTURO-A new drug for drug-resistant tuberculosis-Harnessing value of Innovation**

**Anil Koul**
Director, CSIR-IMTECH, Chandigarh, India

**Presenting Author**
director@imtech.res.in

**PL4**

**Metagenomic analysis of stressed bacteria and genes from the Hexachlorocyclohexane (HCH) dumpsite and Manikaran hot springs**

**Rup Lal**
Department of Zoology, University of Delhi, Delhi-110007

**Presenting Author**
ruplal@gmail.com

We have been using genomic and metagenomic approaches to analyse the selective evolution of bacteria and genes from two stressed sites: the HCH dumpsite and Manikaran hot water springs. Our research over the past ten years from these niches revealed that the stressed environments are highly
vibrant to force speedy evolution of bacteria and genes. The evolution of microbial diversity and genes and metabolic pathways that we observed during the course of our investigations will be discussed.

PL5

**Oral Microflora and Systemic Diseases – A Causal or Casual Relationship?**

**Mahesh Verma** and Priya Kumar  
Maulana Azad Institute of Dental Sciences, New Delhi  
**Presenting Author**  
dpmaids@gmail.com

The oral microbiome is a dynamic society of over 700 species of inter-communicating microorganisms and is amongst the most diverse in the body. It has become increasingly clear that the oral cavity can act as the site of origin for dissemination of pathogenic organisms to distant body sites, especially in immunocompromised hosts such as patients suffering from malignancies, diabetes, or rheumatoid arthritis or having corticosteroid or other immunosuppressive treatment. Oral opportunistic bacteria, particularly, *Porphyromonas gingivalis* and *Fusobacterium nucleatum*, have recently been deviated from their traditional roles and arguably ascended to key players based on their participations in complex co-dependent mechanisms of diverse systemic chronic diseases’ risk and pathogenesis, including cancers, rheumatoid-arthritis, and diabetes. Currently the links between the oral microbial consortia and their interactions with the host in the maintenance of homeostasis and in the pathogenesis of many diseases have taken center stage. This more novel concept attributes the observed systemic effects not to secondary dissemination and spread of specific microorganisms and/or their toxins, but to a dysbiotic change in the constitution and inter-microbial interactions of the healthy oral microbial community, leading to an immune response from the host, locally and systemically. The appreciation of the oral microbes for the well-being of the entire body, including even embryonic development is evolving rapidly with the newly forming knowledge on the human microbiome. Yet there is still much unknown about the inter-microbial dynamics as well as their complex interface within either healthy individuals or diseased mucosal sites. The accumulated evidence, although perhaps preliminary and not specific enough in some circumstances, consistently points that specific oral microbes expressively involve in increased risk of a number of chronic diseases, although the causal direction of these relations have not yet been entirely ascertained.

PL6

**Stable isotope fractionation concepts to track in situ degradation of HCH**

**Hans Richnow**  
Department of Isotope Biogeochemistry, Helmholtz Centre for Environmental Research- UFZ  
**Presenting Author**  
hans.richnow@ufz.de
Hexachlorocyclohexanes (HCH) from the former production of Lindane has spread around the globe and HCH are found in remote areas and accumulating in arctic food chains. The HCH are practically inert to chemical degradation under typical environmental conditions and only biodegradation processes leading to elimination of HCH in the environment. Thus it is interesting to characterise biodegradation processes directly in the environment and to link sources and sinks of HCH. During photo-chlorination of benzene, β, δ,ε and ε HCHs are formed of which α- appears asracemic mixture of 2 stereoisomers. γ-HCH is used as pesticide and other isomers are waste products mostly dumped in the vicinity to the production site. Anaerobic and aerobic microbial degradation of HCH has been shown. Anaerobic degradation of HCH leads to the generation of mixture of chlorobenzenes and benzenes from successive dichloro elimination and dehydrochlorination reactions as the major products which can subsequently mineralized completely under both aerobic and anaerobic conditions. We studied the stable isotope fractionation HCHs in order to characterise degradation processes in the environments. Reference experiments with cultures and enzyme assays were conducted with α-HCH for obtaining carbon isotope and enantiomer fractionation factors for developing a concept to analyse processes in field studies. The correlation of enantiomer and isotope fractionation have some diagnostic potential for characterising the mechanism of chemical and biological degradation processes. We selected Bitterfeld, Germany and Lucknow, India as the model site for to evaluate the potential to track degradation processes in the environment. Technical HCH mixtures and Lindane were produced in both areas for many years. Industrial wastes were buried in the site, eventually contaminating regional aquifers. Waste water were discharged to local rivers and the contamination were spread to agricultural soil due to storm water flooding, but also by airborne transport of dust from production sites. Reactive transport processes governing uptake for contaminated soils HCH into plants during plant, and HCH accumulated in food and wild animals. These processes can be characterised by enantiomer and isotope fractionation. We will provide a brief overview on our ongoing work with respect to evaluation of the degradation processes of HCH in soils, sediments and aquifers at the scale of a landscape. Further the transformation of HCHs in food webs using compound specific isotope analysis, enantiomeric fractionation and enantiomer specific isotope analysis starting with the reactive transport of HCHs from soils to plants, and from plants to higher organisms will be discussed.

Genome-based taxonomic framework for Bacteria

Jongsik Chun¹²

¹School of Biological Sciences, Seoul National University, Seoul 151-742, Republic of Korea

²ChunLab, Inc., JW Tower, 2477, Nambusunhwang-ro, Seocho-gu, Seoul 06725, Republic of Korea
Presenting Author
jchun@snu.ac.kr

Prokaryotic taxonomy has been benefited from new technologies in the field of molecular biology, notably DNA sequencing, PCR and nucleic acid hybridization. Next generation sequencing (NGS) provides affordable means of sequencing whole bacterial genomes and has great potential to enable the objective, robust and automated classification and identification system of Bacteria and Archaea. Since whole genome data is the ultimate information about an organism, introducing it to the taxonomic framework should also improve the stability of nomenclature. Recently, genome sequence-based bacterial species concept has been suggested, which seems to reach in conclusion among bacterial taxonomists that various types of pairwise overall genome sequence similarity, collectively called Overall Genome Relatedness Index (OGRI), can be used for defining species. Average Nucleotide Identity (ANI) is the most widely used algorithm, with several variations were proposed to improve the original algorithm. Supraspecific (from genus to phylum) classification has relied on phenotypic, chemotaxonomic and 16S rRNA gene phylogeny which have limitations resulting in inconsistent taxonomic scheme among different phyla. Methods designed to calculate OGRI have limited resolution therefore not suitable to confer the phylogenetic relationship at the genus or higher taxonomic levels. Here, I will introduce a new phylogenomic method, called BCG54 that allows the unified way of elucidating phylogenetic relationships of any bacterial phyla. It is clear that whole genome-based phylogeny should provide better accuracy and resolution at the species and supraspecific level taxonomy.

Bioinformatic tools:

- Average Nucleotide Identity (ANI) calculator (online): http://www.ezbiocloud.net/tools/ani
- OrthoANIu for large scale ANI calculation: http://www.ezbiocloud.net/tools/orthoaniu
- Software tools for Bacterial Core Gene-based taxonomy: http://www.ezbiocloud.net/tools/bcg54

Keywords: Genomics. Bacterial taxonomy. Bioinformatics. Phylogeny. Species concept.
Keynote Lectures
Importance of college level research and efforts in this direction

Yogendra Singh
Department of Zoology, University of Delhi, Delhi 110007

Presenting Author
ysinghdu@gmail.com

In the recent era of fast-growing scientific breakthroughs, many of the academic concepts available in the curriculum require regular amendment. This is only feasible when students get an exposure to scientific research right from the undergraduate level. This helps immensely in clarifying concepts and helps them to plan their future career in a better way. In our country, most of the students at undergraduate level are loaded with class room lectures and examination. While the teaching programs do give them excellent theoretical knowledge, practical aspects of course vary among different colleges and universities, and innovation is given little emphasis in the current set-up. One could give several reasons to this that includes huge syllabus, large number of students, lack of funding and motivation to think differently. Delhi University is supporting college level research by funding research in innovation projects. In addition, colleges can apply for grants to various funding agencies. We expect that with this infrastructural support provided by the university, there will be a positive change in the way of teaching, mentoring and creating a congenial atmosphere to brainstorm and translate ideas into useful outcome.

Role of potential microbes in bioremediation of hazardous waste

Tanu Jindal and Abhishek Chauhan
Amity Institute of Environmental Toxicology, Safety and Management, Amity University, Sector-125, Noida, Uttar Pradesh, India

Presenting Author
tjindal@amity.edu

Bioremediation is considered as one of the safer, cleaner, cost effective and environmental friendly technology for decontaminating sites which are contaminated with wide range of toxic waste. It uses biological agents, mainly microorganisms such as bacteria, fungi, yeast and algaeto degrade environmental contaminants into degradable form or get mineralized into CO$_2$ and H$_2$O. Bioremediation techniques such as *In situ* i.e. bioventing, biostimulation, bioaugmentation *Ex situ*, land farming, composting biopiles/biocells and bioreactors (slurry/aqueousreactors) are being used for the degradation of several toxic materials with aerobic or anaerobic microbes. Studies have been
carried out for the bioremediation of contaminated sites through heavy metal, organic waste material, wastewaters with recalcitrant organic compounds, pesticides, PAH, PCBs, textile waste effluent, tannery effluent, oil spills, dyes, detergents, dairy effluents, petroleum, radioactive waste, radionuclides, pharmaceuticals, electronic waste, plastic waste and many other xenobiotics nationally and internationally. One of the successful examples is the use of *flavobacterium* in biobeds for the removal of *coumaphos* in liquid waste from cattle dipping vats containing thousands of gallons of pesticides suspension along the US Mexican boarders. *Antarctic microorganisms (psychrophilic bacteria, fungi, yeast and algae)* possess a very good potential for bioremediation having ability to survive in extreme environment. Screening studies for novel strains is in progress. The on-going microbial genomics studies will deliver more robust technologies for the bioremediation of toxic material. Exciting developments in the use of microorganisms for the recycling of metal waste, with the formation of novel biominerals with unique properties are also predicted in the near future. Certainly, bioremediation holds great promise for dealing with toxic waste contaminated sites in ecofriendly and cost effective manner, however much of it is yet to be realized in field conditions.

**Keywords:** Microbial Bioremediation, hazardous waste, Cost Effective, Environmental friendly Technology

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**Research within the College and the University: Our Experience**

**Rup Lal**

Department of Zoology, University of Delhi, Delhi

Presenting Author

ruplal@gmail.com

The experience of research in a college as well as in the University of Delhi has been a very rewarding experience for us. We initiated the establishment of a small research laboratory in Sri Venkateswara College in 1982, at a time when very few others were doing research in the colleges of the University of Delhi. This was due to the foresight and persuasion of the college principal, Dr. V. Krishnamoorthy and colleagues. We attempted to supplement our humble beginnings by applying for funding from the Department of Environment (now Ministry of Environment, Forests and Climate Change, Govt of India), and our hard work was rewarded. We were fortunate to receive funding and sourced it into initial research and purchase of instruments, supplanted with long research hours and late nights spent at the laboratory. With this background, I applied at the Department of Zoology, University of Delhi, in order to be able to supervise and guide Ph.D. students independently. Fortune was in our favour, and we established a good lab from scratch and began research. During times of deadlocks with results from research, we focussed on writing review articles and books. Soon, I got the opportunity to become a Fellow of the prestigious Alexander von Humboldt Fellowship, and after a stint as postdoctoral researcher in Germany in 1992, I moved from Sri Venkateswara College to the
Department of Zoology, University of Delhi in 1992. The experience of carrying out research within an environment of minimum research facilities and tight funding conditions, attracting brilliant and top ranking students to carry out research, establishing long-term collaborations nationally and internationally, applying and getting funds and grants from National and International agencies, and motivating and mentoring bright students (more than 60 Ph.D. students and 100 UG and PG summer trainees) to explore emerging areas of biological sciences helped us to carry out good research. In this presentation, the model that we followed over the past four decades in teaching and research will be presented.

PLFA and soil analyses using MIDI system

A. M. Deshmukh
Dr. Babasaheb Ambedkar Marathwada University, Aurangabad
Presenting Author
amdeshmukh1@rediffmail.com

MIDI Inc. is a private biotechnology business which developed three rapid Microbial Identification Systems (MIS). It was founded in 1991 by Dr. Myron Sasser, former professor in plant pathology at University of Delaware and based in Newark, DE, USA. Sherlock MIS is used in Agri-biotech labs, Bio/Pharmaceutical Microbiology QC, Public health labs/ Bio defence, Environmental Labs, and Clinical Hospital Labs/ Private Clinical Labs. MIDI Sherlock MIS technology uses the fact that each organism has a unique fatty acid pattern which can be used as a fingerprint for identification and tracking purposes. Fatty acids are extracted from microbes and are converted to their respective Fatty Acid Methyl Esters (FAME), then analysed on Agilent GC, this gives GC-FAME profile of that microbe. Sherlock utilizes its automated pattern recognition software to match the unknown samples GC-FAME profile with stored patterns of known microbial species and assigns a Similarity Index (SI) which is a statistical measure of closeness. Sherlock calibration standards are used to adjust the chromatography so that Sherlock can name the fatty acids with great precision. Sherlock has Electronic Records and Signatures (ERS) which allows compliance with FDA 21 CFR part 11 and ensures data security. Sherlock has software like 2D, Dendogram and Tracker which can be used for tracking strains. These are used as a visual tool to show relationship between unnamed samples, common in pharma QC environments, and in tracking a contamination source. Sherlock MIS for Agri-biotech is the fastest growing market for MIDI because, it is an accepted method for plant protection and soil science, a required method for all new species in the International Journal of Systematic and Evolutionary Microbiology (IJSEM), contains more than 2,000 bacterial species, and identifies both bacteria and PLFAs (biomarker fatty acids in the soil). Phospholipid Fatty Acids (PLFAs) are essential components of microbial cell membranes which give an estimate of living microbial community composition and biomass size. Changes in PLFAs act as early warning indicator to
changes in a soil ecosystem’s health or point to a microbial contamination problem in a food source. Using GC, Sherlock software identifies all the fatty acids in the sample and converts the data into percentages of fatty acid types (Mono and Poly unsaturated, Straight chained fatty acids, cyclo etc.) and microbial types (Gram negative, Gram positive, Fungi, Yeast, Eukaryote etc.) based on signature fatty acids. In conclusion, Sherlock MIS is an established technology with extensive libraries and low consumable cost (less than 5$ per test). It is a high throughput system which can identify a sample from pure culture in as little as 25 minutes with a powerful software and technical support from microbiologist, software and instrumentation experts. It is a multi-use system which can be used for microbial identification, as well as fatty acid analysis from any source (e.g. food, soil, bio fuel feedstock, etc.).

KL5

Current infection problems and prospective solutions in stem cell based therapies and research

Shibashish Giri

Department of Cell Techniques and Applied Stem Cell Biology, Centre for Biotechnology and Biomedicine, Medical faculty, University of Leipzig, Deutscher Platz 5, D-04103 Leipzig, Germany.

Presenting Author

Shibashish.giri@bbz.uni-leipzig.de, +49-341-9731353 (phone), +49-341-9731329 (fax)

Stem cell based therapies have been routine clinical approaches for treatment of several diseases which greatly improve the survival and quality of life to millions of patients around the world. But the bacterial, viral, fungal infection and several more health complication including poor patient satisfactory outcomes are negative factors in stem cell treatments. We have developed new stem cell therapy concept to overcome those existing limitations with high patient satisfactory outcomes. We have tested the clinical benefits of our approach in diabetic wounds, burned skin, spinal cord injuries, cosmeceutical approaches for anti-aging and other cases in human clinical setting as well as in preclinical models. Moreover, our bioreactor approaches for various tissue engineering products are highlighted here especially to avoid the infection issues in clinical oriented approaches for newest and safest clinical investigation for new drug discovery approach. Nonhuman models are routinely used for disease modeling in the drug discovery process, but the human response is not to predict from these models. Patient-derived induced pluripotent stem cell technology is a low cost and high quality new drug discovery process, which could replace millions of animals currently sacrificed in preclinical drug development process. Toxicity assessments and clinical efficacy of drug candidates using patient-derived induced pluripotent stem cell technology is an efficient frontier approach to save money and time before moved into costly and lengthy preclinical and clinical trials, eventually,
provide a impeccable route to new safer pharmaceutical products. These above approaches which are in current clinical development that have the potential to impact clinical benefits in near future.

Soil and freshwater ciliate biodiversity: an India report; emphasis on extremophilic habitats

1Komal Kamra, 1Harpreet Kaur, 1Shashi, 2Santosh Kumar, 3Jasbir Singh, 4Rup Lal, 5Alan Warren

1Ciliate Biology Lab, SGTB Khalsa College, University of Delhi, Delhi, India
2Zoological Survey of India, Prani Vigyan Bhawan, New Alipore, Kolkata, India
3Department of Zoology, SGTB Khalsa College, University of Delhi, Delhi, India
4Department of Zoology, University of Delhi, Delhi, India
5National History Museum, London, UK

Presenting Author
komalkamra@gmail.com, Ph:9871771417

The Indian Subcontinent is rich in biodiversity as it has diverse ecosystems. The ciliated protist communities show richness as well as uniqueness. This is true both for aquatic and soil ciliates. In our laboratory, we have been working with several regions including niche segments such as The Silent Valley in state of Tamil Nadu, The Eastern Himalayas and the Silent Valley in the state of Uttarakhand. The richness and uniqueness of these regions in terms of their ciliate diversity have been documented. Some important features are the presence of several species of the same genus in the same soil sample, the presence of ciliates in hot water springs and in lakes where the temperature can go below 0°C. At zero point in Sikkim, which is covered with snow for 10 months a year, and which has just rocks sparsely laden with lichens, also had ciliate species. Some of these ciliates had an affiliation with those reported from Nepal and China. Currently, species diversity and abundance correlation with soil and water quality are being assessed from the river Yamuna flowing through Delhi, India. More studies are needed to fill gaps and assess geographical distribution of ciliated protists in India. The ciliate community from different regions will be shared during the presentation.
Invited Lectures
L1.1

Understanding the host *Mycobacterium tuberculosis* interaction

**Nisheeth Agarwal**

Translational Health Science and Technology Institute, Faridabad

**Presenting Author**

nisheeth@thsti.res.in, Ph: 0129-2876304

*Mycobacterium tuberculosis* (Mtbt), one of the most ancient human pathogens known so far, stands today as greatest threat to human civilization by virtue of centuries of an evolutionary advantage. Remarkably Mtbt has succeeded in crossing over every checkpoint and has latently infected more than one third of world’s population. The prolonged association of Mtbt with humans eventually results in a deadly infectious disease known as tuberculosis (TB). At the molecular level, it remains to identify and completely understand the chain of physiological events induced upon host-*Mycobacterium* interaction that promote either the active disease or result into the asymptomatic latent infection. In this meeting, I will primarily discuss some of our findings on how the host cells and the TB pathogen crosstalk to each other which eventually decides the course of infection.

L1.2

Biting the hand that feeds: host lipid metabolism in TB infection

**Sheetal Gandotra**

Institute of Genomics and Integrative Biology, Delhi

**Presenting Author**

sheetal.gandotra@igib.in

Pathogenic organisms rely on the host environment for their survival and often manipulate it to suit their preferred lifestyle. The pathogen responsible for the largest number of deaths worldwide, *Mycobacterium tuberculosis*, is capable of utilizing a variety of host lipids. It is not surprising that it creates an environment rich in lipids during active disease. If we understand how this environment is created, which particular lipid species provide nutrients to the bacilli, and whether lipids are also involved in the immune response to the bacilli, perhaps we can attain a handle to reduce morbidity, mortality, and thus burden of the disease in the human population. My talk will touch upon aspects of host lipid metabolism in TB infection and what we and others in the field have shown using various model systems.
**L2B.1**

**Cost effective bioethanol production from biodegradable municipal solid waste with zero waste technology**

**S.K. Soni**
Department of Microbiology, Panjab University, Chandigarh-160014, India  
**Presenting Author**  
sonisk@pu.ac.in

The world is facing dual problem of energy crisis and climate change due to the continuous escape of green house gases from the landfill sites of biodegradable municipal solid waste (BMSW). As the biodegradable municipal solid waste chiefly consists of food waste residues rich in various carbohydrates including cellulose, hemicelluloses, starch and pectin, the same be hydrolyzed into simple sugars by using a cocktail of hydrolytic enzymes for biotransformation into a wide range of desired products and thus can save the environment by diverting the BMSW from landfill. Keeping this in mind we have developed a biorefinery for valorization of zero value municipal solid waste residues by using as a resource for the low cost production of ethanol. The process involves the i) production of a cocktail of multiple carbohydrases comprising CMCase, FPase, β-glucosidase, Xylanase, Xylosidase, Mannanase, mannosidase, galactomannanase, α-amylase, glucoamylase, pullulanase, pectinase by solid state fermentation of BMSW with suitable strain of *Aspergillus niger*, ii) thermal pretreatment of BMSW residues, iii) hydrolysis of pretreated BMSW using the in-house produced enzyme cocktail into fermentable sugars comprising glucose, xylose, galactose, mannose etc and iv) fermentation of released sugars with a consortium of hexose and pentose fermenting yeasts into ethanol. The complete processing is a zero waste technology as the solid residue left after the fermentation may be used as a biofertilizer. The process has yielded 150-175 ml of ethanol from 1 Kg of BMSW on dry weight basis in addition to 200 g of biofertilizer which is quite encouraging.

**L2B.2**

**Microbes as cell factory for clean fuel production through biological route**

**Sanjukta Subudhi**  
Environmental and Industrial Biotechnology Division (EIBD), The Energy and Resources Institute  
Darbari Seth Block, Habitat Place Lodhi Road, New Delhi - 110 003, India  
**Presenting author:**  
ssubudhi@teri.res.in, sanjuktasubudhi@yahoo.com, Ph: 91-11-24682100 and +91-11-41504900

Currently more than 80 % of global energy demand is being fulfilled by conventional fossil fuel sources. Further, with increase in global energy demand, global energy reliance on fossil fuel based energy sources is rising concomitantly. This has raised a great concern for the nations globally for
energy security and for environmental protection, due to the increase in Green House Gas (GHG) emissions, associated with use of fossil fuel resources. These issues triggered the worldwide effort to focus on development of non-polluting and alternate energy production processes from renewable energy sources. In this context, energy production from environment friendly renewable sources; solar, hydro, wind, and biofuels, got substantial global attention. Among various renewable energy forms, biofuel production through the use of microbes, algae, from alternate sources, offer promising approach for clean energy generation owing to their carbon neutral nature and low input energy requirement. Biofuels include liquid (such as bio-ethanol, bio-butanol, bio-diesel) and gaseous fuel forms (bio-hydrogen, bio-methane) produced from non fossil sources. Initially feed stocks that have traditionally used as food (first generation feedstock) were used biofuel. Eventually use of these feed stocks for biofuel production (first generation biofuel) raised the concern for food security and competition with land area. Food security issues made the nations to advocate for policies for use of non feed competitive feedstock (second generation feedstock) for biofuel production. Hence, subsequently the priority bio-energy research areas shifted towards production of advanced biofuel from non feed competitive feed stocks. Several microbes encompass unique pathway(s) for production of different fuel forms from renewable sources and have great potential to serve as cell factory for production of clean biofuel, in a sustainable manner. This presentation will focus on leads obtained at TERI (The Energy and Resources Institute) on microbial production of clean biofuel from first and second generation feedstock. Prospects and challenges of these processes will be highlighted.

L3B.1

**Computational approaches in probiotic interactions, novel platform designs and its impact on human health**

Pratyoosh Shukla

Enzyme Technology and Protein Bioinformatics Laboratory, Department of Microbiology, Maharshi Dayanand University, Rohtak-124001, Haryana, India

**Presenting author:**

pratyoosh.shukla@gmail.com

It has become easy to identify and select an appropriate microorganism with the advancement in various molecular biology and analytical techniques. Here, we have highlighted on various tools and techniques viz. 16S and 23S ribosomal DNA sequencing, RNA analysis by reverse transcriptase (RT-PCR), fluorescent in situ hybridization (FISH), quantitative analysis by real time PCR (RT-PCR or qPCR) and fluorescent activated cell sorting (FACS) used for effective screening and selection of a better candidate bacterium for probiotic applications. Further, bile salt hydrolase (BSH) is an enzyme that catalyses the deconjugation of bile salt, so it has enormous potential toward utilizing such capability of *Lactobacillus plantarum* RYPR1 toward detoxifying through BSH enzyme activity. We have also evaluated the prebiotic utilization, catalytic interactions and molecular docking from the isolate *Lactobacillus plantarum* RYPR1, an indigenous fermented beverage
Raabadi, consumed during summers in Haryana and Rajasthan regions of India. Furthermore, we have also described a unique protein engineering strategy with novel platform technology using metabolic engineering, use of strong promoters, novel vector elements such as inducers and enhancers, protein tags, secretion signals, high-throughput devices for cloning and process screening as well as fermentation technologies. The prominent studies in these areas are inspired towards process optimization and control on such processes. A meticulous perceptive of these areas is crucial in understanding of microbial interactions and its further impact on human health.

L3B.2

Comparative metagenomic analysis of functional and microbial diversity in two different pesticide contaminated soil microbiome

Raj Kumar Regar\textsuperscript{1,2}, Vivek Kumar Gaur\textsuperscript{1}, Nivedita Singh\textsuperscript{2}, Mohan Kamthan\textsuperscript{1} and \textbf{Natesan Manickam}\textsuperscript{1}\textsuperscript{*}

\textsuperscript{1}Environmental Biotechnology Laboratory, Environmental Toxicology Group, CSIR-Indian Institute of Toxicology Research, Vishvigyan Bhawan, Lucknow-226001, India.
\textsuperscript{2}Department of Biochemistry, School of Dental Sciences, Babu Banarasi Das University, Lucknow-226028, India

Presenting Author
nmanickam@iitr.res.in

Shotgun metagenomic sequencing based microbiome profiling was performed using two soil samples from 1. Hindustan Insecticides Ltd., Cochin and 2. India Pesticides Limited, Lucknow, India as these sites were found to have high contamination with hexachlorocyclohexane, DDT and endosulfan and at least 6 polycyclic aromatic hydrocarbons. An insight into the metagenome analysis revealed presence of both Archaea and Eukaryota of bacterial kingdoms in these contaminated sites. As compared to control samples, a significantly reduced abundance of bacterial phylum such as Actinobacteria, Bacteroidetes, Gemmatimonadetes, Chloroflexi, Planctomycetes, Nitrospirae and Verrucomicrobia was recorded from the industrial dump sites. However Proteobacteria, Terrabacteria and Protostomia were in abundance in the contaminated samples. ARDRA-based bacterial community profiling resulted in identification of 17 different phylotypes having genus \textit{Planococcus}, \textit{Planomicrobiium} and \textit{Psychrobacter} in high abundance in test soil samples which matched the results derived from microbiome based analysis. Genes encoding enzymes for halogenated compound degradation such as haloacid dehalogenase and haloalkane dehalogenase were found in the metagenome data indicates existence of microbial communities involved in biodegradation. A total number of 77 different monoxygenases and dioxygenases, encoding key transformations of diverse persistent compounds were found to be occurring in both the contaminated soils. For example nitronate monooxygenase, homogentisate 1,2-dioxygenase, phenol 2-monooxygenase, catechol 2,3-dioxygenase, cyclohexanone monooxygenase, hydroxyquinol 1,2-dioxygenase and biphenyl 2,3-dioxygenase were found in the metagenome. In hazardous ecosystem, as an adaptive response, the bacteria were found to harbor large number of plasmids and other mobile genetic elements. These includes the genes sequences for
bacteriophages, viruses and catabolic plasmids reported for naphthalene, toluene, phenol, benzoate and biphenyl were also found, indicating presence of well studied microorganism in biodegradation of these compounds. Occurrence of mobile genetic elements, metal resistant and multi drug resistant bacteria were also found indicating the function versatility of the soil which may help in bioremediation of the chemical contaminants.

Microbial Biodiversity Explorations of Estuarine Chilika Lake: Insights into development of sustainable technology and Climate change

Vishakha Raina

Environmental Biotechnology Laboratory, School of Biotechnology, KIIT University, Bhubaneswar, Odisha-751024

Presenting Author

vishakha.raina@gmail.com

Estuarine habitats are among the most biodiverse and productive natural habitats in the world as they lie midway between freshwater and saline water possessing a unique microbial biodiversity. Chilika Lake (nearly 1,100 sq. km), the largest brackish water lagoon in Asia and the second largest lagoon in the world, situated on the east coast of India gets primary inflow acquired by nearly 35 river streams, which outflow through the mouth at Satpada to merge into the Bay of Bengal. The lake is known for its rich flora and fauna biodiversity. A large salinity gradient across the lake also contributes to rich populations of macro and microalgae, marine seaweeds, marine sponges and sea grasses. However, the microbial diversity until recently was virtually unexplored and an attempt has been make to study the same. Studying complex microbial communities by using conventional methods can be very slow, hence we use a combination of culture dependent and culture independent (metagenomics) approaches by which the microbial communities can be explored and their role in maintenance of the ecosystem and the environment can be understood. Isolation, identification and inventory of cultivable bacterial strains with high biological activities have been done from the lake. Besides this potential isolates have been identified for biotechnological and industrial uses. An exploration of complete spatial and temporal dynamics of phylogenetic distribution and relative abundance of bacterial community from four zones (north, south, central and outer channel) and three seasons (summer, rainy and winter) in Chilika Lake was conducted. Micro-organism communities in the lake are constantly evolving by interacting among themselves, other organisms, lower or higher and even with inorganic elements of nature. During their interactions they contribute immensely to functioning of ecosystems and running of several biogeochemical cycles (especially carbon and nitrogen) for maintenance of the environment. A caused a major disturbance, which also impacted distribution of microbial communities leading to impacts on climate change. Effects of ecological disturbances and changes in distribution of microbial communities in the event of a recent severe cyclonic storm PHALLIN was studied using non culturable methods. The results and major leads from the study giving information on novel genes and pathways will be discussed with future perspectives.
**L3B.4**

**Metabolomics as an emerging tool to understand interactions of xenobiotics with model organisms**

*Mohana Krishna Reddy Mudiam*

Chromatography Unit, Analytical Chemistry & Mass Spectrometry Division, CSIR-Indian Institute of Chemical Technology, Tarnaka, Uppal Road, Hyderabad – 500007

**Presenting Author**

mmudiam@iict.res.in; mmudiam8@gmail.com

The environmental metabolomics is a sub-discipline of metabolomics to measure the phenotypic changes in the intracellular system of any organism due to environmental stressors. The metabolomics is of post genomic tool helps to identify the mode of action of xenobiotics. The advancement in spectrometric and spectroscopic techniques and their hyphenation with separation techniques have revolutionized this area of research due to its vast applications in human and environmental health. Nuclear Magnetic Resonance (NMR) and Mass Spectrometry (MS) are the most widely used techniques to perform metabolomics experiments. MS based metabolomics has gained promising interests owing to its high sensitivity, resolution and availability of mass spectral libraries. In the present talk, I will illustrate the overview of general experimental protocol, extraction methods, instrumental conditions and statistical methods to be used for metabolomics studies. I will also illustrate about the use of metabolomics to identify differential metabolites as an early indicators for metabolic changes in organism due to xenobiotics exposure. In conclusion, I will emphasize on the use of environmental metabolomics as a routine tool for characterizing the organism response to xenobiotics.

**L4.1**

**Prediction of species-specific biotransformation of xenobiotic/drug molecules by human gut microbiota**

*Vineet K. Sharma, Ashok K. Sharma, Shubham K. Jaiswal*

IISER, Bhopal

**Presenting Author**

vineetks@iiserb.ac.in

The population-specific differences in human microbiome due to diet, geographical location, age, etc. play a key role in determining human health and metabolism. Out of all anatomical sites, the vast microbial diversity found in our gut is involved in several roles such as the breakdown of the complex polysaccharides and stimulation of our immune system. The microbial species residing in the human gut also harbour an enormous metabolic potential, which can alter the metabolism of orally administered drugs leading to individual/population-specific differences in drug responses. The investigation of species-specific contribution to xenobiotic/drug metabolism by experimental studies is a challenging task considering the large heterogeneous pool of human gut bacteria and their
metabolic enzymes. Therefore, we have developed a novel computational approach ‘DrugBug’ to predict the metabolic enzymes and gut bacterial species, which can potentially carry out the biotransformation of a xenobiotic/drug molecule. A substrate database was constructed for metabolic enzymes from 491 available human gut bacteria. The structural properties (fingerprints) from these substrates were extracted and used for the development of Random Forest models, which displayed excellent accuracies of up to 98.61% and 93.25% on cross-validation and blind set, respectively. After the prediction of EC subclass, the specific metabolic enzyme (EC) is identified using a molecular similarity search. The performance was further evaluated on an independent set of FDA-approved drugs and other clinically important molecules. Further, a tool ‘ToxiM’ was developed to predict the toxicity of metabolites. A few selected DrugBug predictions such the metabolism of amphetamine and digoxin drugs, were validated using structural and experimental methods. To our knowledge, this is the only available approach implemented as ‘DrugBug’ tool for the prediction of xenobiotic/drug metabolism by metabolic enzymes of human gut microbiota.

L4.2

Genomic Approach to Segregate Friends and Foes
Vipin Chandra Kalia
Microbial Biotechnology and Genomics, CSIR - Institute of Genomics and Integrative Biology (IGIB), Delhi University Campus, Mall Road, Delhi-110007, India.

Presenting Author
vckalia@igib.res.in, vc_kalia@yahoo.co.in

Bacteria are an integral part of the ecosystem. These organisms have unique abilities to adapt to ever changing environmental conditions. The range of bacterial association with plants, animals and human beings has been found to be beneficial to some extent and pathogenic on the other. Bacteria in the human gut and skin are more beneficial than dreadful. The general perception about bacteria is their pathogenicity to living beings. The ones which cause deadly infectious diseases are the focus of most studies. The issue is to find methods to quickly identify these bacteria, diagnose the disease and start the treatment. The task of bacterial identification has been made easy by sequencing their ribosomal gene -16S rRNA (rrs). The trouble starts when a single genome possesses multiple copies of rrs. It makes the identification a tricky job. Some of the gene copies show exact homology to those present in other species of the same genus. In order to circumvent this issue, novel approaches have been developed. This strategy relies upon specific genes, which are present in all the species but still have unique characteristics such as restriction endonuclease sites. This feature results in certain patterns which can be used as biomarkers to distinguish friendly bacteria such as Bacillus, Lactobacillus, from pathogens such as Clostridium, Yersinia, Vibrio, Staphylococcus, and Streptococcus.
Phytoplasma: the trans-kingdom hitchhiker - a potential guide to plant development

Suman Lakhanpaul
Department of Botany, University of Delhi, Delhi-110007, India

Presenting Author
sumanlp2001@yahoo.com

Phytoplasma, the plant pathogenic and insect vectored Mollicute affect more than 100 economically important crop plants and their allies worldwide. Spread and severity of Phytoplasma associated plant diseases is increasing at fast pace that is often attributed to the climate change. Phytoplasma is also gaining attention due to its unique properties such as minimum genome size, fastidious nature, trans-kingdom existence, unusual symptoms etc. The peculiar symptoms associated with Phytoplasma diseases include virescence, phyllody, fasciation, witches’ broom, little leaf etc. Sesame or til (Sesamum indicum L.), an ancient oil seed crop of immense importance and nutraceutical value suffers significant yield losses due to Phytoplasma associated diseases in India and other sesame growing countries. Thorough understanding of this pathogen and the mechanism of disease development leading to severe reduction or complete loss of flower and fruit formation are needed to develop the control measures. Phyllody affected sesame plants were subjected to detailed investigations at morphological, anatomical and molecular level to identify the precise processes involved in development of the peculiar symptoms. Differential expression of the putative genes involved in the processes such as leaf and flower development, indeterminacy, cell division, hormone signaling etc was investigated in symptomatic and asymptomatic sesame plants. Upregulation of leaf development (SeKNOTTED) and indeterminacy (SeHAIRYMERISTEM) pathway genes and downregulation of floral meristem (SeLEAFY), carpel identity (SeTOUSLED) and floral asymmetry genes (SeDIVARICATA) was revealed. Upregulation or statistically insignificant downregualtion of genes involved in floral development such as SeSQUAMOSA, SePLENA, SeSEPALLATA and SeCONSTANS indicated their post transcriptional inhibition or redundancy of the genes involved. In addition, comparative microRNA profiling of healthy and phyllody affected plants revealed that unique miRNAs seem to have a more significant role in development of phyllody than the differentially expressed miRNA. Further, inaccessibility of shoot apical meristem to Phytoplasma, the site of differentiating cells getting modulated, suggests the involvement of effector molecules that are secretary in nature and are directly or indirectly interacting with the genes involved in plant development or their downstream products. Further studies on the delineation of symptom development based on these leads will be helpful in developing disease control measures and also to unravel the molecular mechanisms underlying some of the basic plant developmental processes.
Student Lectures
Comparative genomics of *Thermus* species highlights natural competence as a vital evolutionary decision within this genus

Charu Tripathi, Komal Kamra and Rup Lal

Molecular Biology Laboratory, University of Delhi, Delhi – 110007, India

Presenting Author

charutripathi89@gmail.com, Ph. No: +91-11-27666254

Thermophiles have played a pivotal role in research by providing biotechnologically relevant processes, enzymes and insights which have led to paramount advances in microbial research. The genus *Thermus* has been placed at the forefront of studies related to thermophilic organisms. The ubiquity, small genome size and extreme amount of shuffling are intriguing characteristics of the group. With an aim of deciphering the genetic basis of heterogeneity and strain level conservation, 17 genomes of *Thermus* were analyzed in this study. The phylogenetic relationships within this genus were better resolved with whole genome methods such as average nucleotide identity, 400 conserved marker genes, tetra nucleotide frequency, pan genome and digital DNA-DNA hybridization. Strain level conservations were evident through the elucidation of metagenomic islands and core-pan genome characteristics. A significant factor responsible for the plasticity of *Thermus* genomes is the highly efficient transformation system which enables the uptake of foreign DNA from the environment. Uptake of DNA serves an important role in both conditions of nutrient limitation and introduction of novel components in the genome. Through the evaluation of the gene locus pivotal in imparting natural competence in *Thermus*, we were able to highlight the predominance of signatures associated with horizontally transferred regions. Additionally, we found evidence for high incidence of viral signatures wide these genomes. Type IV pilin system responsible for natural transformability also plays a role in phage infection in *Thermus*. Thus, the evolution and diversification of natural competence in *Thermus* paves the way for additional opportunity for introduction of genomic variability by means of transduction, but at the same time makes them susceptible to phage invasions. This leaves the genus with a crucial choice between viral predation versus natural transformation. The intricate balance between the two is a significant survival choice for this genus.

Insights into the diversity and functional potential of microbial community resident of gastrointestinal tract of fish *Tor putitora* (Ham.)

Himani Khurana, Rup Lal and Ram Krishan Negi
The gut microbiota of fish is constituted by trillions of bacterial cells who live in close symbiotic association with the host and play important roles in digestion, development of effective immune system and nutrient cycling. Although fish represents the greatest biodiversity among all vertebrates, there are important gaps in our present understanding of their resident gut microbiome and the varied genetic and metabolic attributes conferred by them. Until recently, the research on fish focussed only on pathogenic organisms and importance of microbiome to host health and physiology were of little interest. The concept of manipulation of microbiome for novel therapeutic approaches has largely shifted the focus. *Tor putitora*, commonly known as Golden mahseer is one of the largest sport fish of the Indian freshwater system and serves as angler’s delight. Besides being an important fish from the view of aquaculture, its population is under severe threat due to anthropogenic activities. The main reason for its lesser numbers is the construction of dams which inhibit the migration of this fish species, which is necessary for spawning. Therefore, we undertake a study to investigate the microbial diversity present in the gut of this species and also determine the functional potential of the community. This will be a pioneering study to understand the role of such communities in the growth and survival of this fish. It has widespread occurrence in the Himalayas, therefore fish samples were collected from Gobindsagar reservoir, Himachal Pradesh and pooled samples were directly sequenced to obtain shotgun metagenomic data. Also, as the art of culture-dependent approach augments culture-independent approach, culturable diversity was also deciphered.

**Keywords:** *Tor putitora*, Microbiome, Metagenomics, Culturable diversity

**SL 3.B.5**

**Comparative genomics of Genus *Deinococcus*: Insights into adaptation to harsh conditions**

**Nitish Kumar Mahato, Roshan Kumar, Shekhar Nagar, Ram Krishan Negi, Yogendra Singh and Rup Lal**

Department of Zoology, University of Delhi, Delhi-110007

Presenting Author

nitishyayati.du@gmail.com, Ph: +91-11-27666254

Bacteria belonging to the genus *Deinococcus* are highly radiation, temperature and desiccation resistant representing life’s outer limits. Available evidences indicate efficient DNA repair systems,
manganese import and high DNA copy number play pivotal role in acquiring extremophily. The natural habitat of these extremophiles has not been defined as different deinococci have been isolated from a variety of habitats worldwide from organic nutrient rich environments to dry, nutrient-poor, UV-exposed extreme surroundings. Using a comparative genomic approach, we investigated 31 bacterial genomes (11 complete and 20 draft) of genus Deinococcus to unravel adaptations of these extremophiles to lethal DNA damaging agents. Phylogeny based on 16S rRNA gene sequences revealed habitat-specific clustering of phylotypes. Preliminary analyses revealed that genome size within genus varied from 2.8 Mbp to 6.6 Mbp with %G+C content variation from 67.4 to 70.8%. A comparative analysis of genome features can unravel adaptations of deinococci to extreme harsh conditions.

**Role of Type VI secretion system (T6SS) in shaping plant growth promoting potential of *Pseudomonas fluorescens*: A comparative genomics perception**

**Princy Hira, Utkarsh Sood, Rup Lal and Mallikarjun N. Shakarad**

Department of Zoology, University of Delhi, Delhi-110007

**Presenting Author**

princy.hira@gmail.com, Ph: 011-27666254

*Pseudomonas fluorescens* sp. are ecologically significant microorganisms well known for soil decontamination, phosphate solubilization and plant growth promotion. They are widely deployed as plant growth promoting rhizobacteria (PGPR) by the inoculant industry. They synthesize a remarkable array of secondary metabolites which directly enhance plant growth and protect them against broad spectrum of phytopathogens as biocontrol agents. Bacterial systems possess notable multiprotein complexes classified as Type I to VI secretion systems for regulated transport of various effector molecules across its cell membrane. Type VI secretion system in gram negative bacteria analogous to T3SS and T4SS possess upturned phage like injectisome machinery to directly inject effectors into host cells. Fluorescent pseudomonads employ this machinery to outcomplete several phytopathogens by secreting Hcp (Haemolysin co-regulated proteins) and VgrG proteins as piercing device. In the present study, we isolated and sequenced a novel isolate of *Pseudomonas (P. fluorescens)* PsChi) from chilli rhizosphere in Lakhimpur, Assam and conducted comparative analysis with its available complete genome sequences in Pseudomonas database. Our findings suggest that PsChi is clustered within the SBW25 clade with average nucleotide identity of 87.16% with SBW25. Interestingly, all the strains in the study possessed complete cluster of T6SS except strain UK4. Further, genes coding for Hcp and VgrG proteins are present in multiple copies in strains Pf0-1 and NCIMB 11764 suggesting better competitive potential and adaptation as compared to other strains.
Genetic manipulation of the rifamycin B polyketide synthase gene cluster in
*Amycolatopsis mediterranei* S699

Priya Singh, Rashmi Kumari, Rup Lal

Molecular Biology Laboratory, Department of Zoology, University of Delhi, Delhi-110007, India

Presenting Author

priya.impulse@gmail.com, Ph. 011-27666254

Rifamycin B is an antibiotic produced by *Amycolatopsis mediterranei* S699. It’s semi-synthetic derivatives (rifaximine, rifampicin, rifalazil, rifabutin and rifapentine) are used worldwide for the treatment of tuberculosis (TB) and other mycobacterial infections. Multi Drug Resistant-TB (MDR-TB) strains are resistant to all these antibiotics. Thus, there is need to develop novel rifamycin B analogs and its corresponding derivatives to combat drug-resistant strains. All the possible chemical modifications for the production of semi-synthetic derivatives have already been done. Therefore, an alternative to this approach is to modify the rifamycin B chemical structure by genetically manipulating the Rifamycin Polyketide Synthase (*rif*PKS) gene cluster. The biosynthesis of rifamycin is catalyzed by the *rif* gene cluster which includes ten modules of polyketide synthase (PKS) genes organized into five closely packed open reading frames. Each module is primarily responsible for the polyketide chain elongation. The acyltransferase (AT) domain select the precursors. Based on the proof of concept for the production of a novel rifamycin B analog, the present study was designed wherein the acyl transferase domain of *rif*PKS (adds propionate unit) was swapped with the acyl transferase domain (adds acetate unit) of rapamycin polyketide synthase gene cluster (*rap*PKS). The two-step homologous recombination events involved in this process produces a hybrid PKS gene cluster leading to the production of a novel rifamycin B analog.

Evolution of virulence factors of *Pseudomonas aeruginosa*

Utkarsh Sood, Rup Lal and Mallikarjun Shakarad

Department of Zoology, University of Delhi, Delhi-110007

Presenting Author

utkarsh.sood@gmail.com, Ph: 011-27666254

The pathogenic potential of a bacterium is deciphered by the arsenal of virulence factors produced by it. The genomic analysis of an outlier strain of *Pseudomonas aeruginosa* CR1 showed that there is continuous evolution undergoing particularly at the genomic repertoire coding for virulence factors. As already known, these outliers are deficient in type III secretion system and therefore thought to be less pathogenic. But the analysis of our strain shows that the phenomenon of losing and acquiring new genes at the pathogenic loci is highly dynamic. The analysis revealed that CR1 being the first
environmental isolate of the outlier clade has acquired various virulence factors which are specific to plant interacting microbes. The prominent differences include a novel plasmid bearing a VirB/D4 complex (similar to plant pathogenic species of Pseudomonas syringae) associated with trimeric auto-transporter (TAA) bearing a yadA like domain, variation at flagellin biosynthetic locus (particularly at flab gene), a shorter LPS-O antigen and the newly reported exolysin (exlA) toxin characteristic of the outliers was present. Interestingly, strain CR1 lacks both haemolytic phospholipase C (plcH) and phospholipase D (pldA). Therefore, we can conclude that these organisms are renewing and selecting virulence factors according to their environment.

**Keywords:** Pseudomonas aeruginosa, outliers, virulence factors, plasmid, VirB/D4 secretory system

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**Comparative genomics of outbreak associated Croatian Acinetobacter baumannii clones CRO1, CRO2 and CRO3 using phylogenomics, core-pan dynamics, antimicrobial resistance and host pathogen interaction approach**

Vipin Gupta, Rup Lal, Yogendra Singh

Department of Zoology, University of Delhi, Delhi 110007

Presenting Author

vipingupta@zoology.du.ac.in

*Acinetobacter baumannii* has gained immense attention in scientific community and always been in forefront of because of its antibiotic drug resistance determinants. Recently WHO has enlisted this species as a critical pathogen because of its penchant to intensive care units (ICU). ICU serve as the most hostile conditions for *A. baumannii* species, as admitted patients have multiple deceives insertion and several antibiotic prescriptions. We have performed a prospective study with three *A. baumanii* clinicals isolates (CRO1, CRO2, CRO3) from Croatia outbreak to investigate the pathogenesis using *in-silico* methods. We have compared the genomes of these three strains with 39 American isolates and predicted their resemblance on functional basis. Using 400 marker genes based phylogenetic analysis with 119 validly maintained species we have predicted the core-Pan genomic dynamics with novel Genomic Island responsible of antibiotic resistance. Two of the isolates (CRO1 &CRO3) belong to *A. baumannii* International Clone type-II (IC-II) and one isolate CRO2 belongs to International Clone Type-I (IC-I). Using in-silico Host Pathogenic Interactions Modelling, we have predicted and explained the role of pathogenic gene PurL from pathogen (*A. baumannii* CRO stains) playing the most influenceable role for its pathogenesis in various diseases and NF-kB1 from the host to be most influenced gene from pathogen. Study has provided a deep insight in to the genomics of *A. baumannii* species.
Oral Presentations
Innovative Sciences
Complete genetic repertoire of a hexachlorocyclohexane degrading bacterium, *Sphingobium indicum* B90A

Helianthous Verma$^{1,2}$ and Rup Lal$^1$

$^1$Molecular Biology Laboratory, Department of Zoology, University of Delhi, Delhi 110007

$^2$Department of Zoology, Kirorimal College, University of Delhi, Delhi 110007

**Presenting Author**

helianthousverma@gmail.com

*Sphingobium indicum* B90A is predominantly known for its role in degradation of hexachlorocyclohexane (HCH) isomers. The bacterium was isolated from HCH treated rhizospheric soil, Cuttack and identified initially as the first microorganism to metabolize all the HCH isomers ($\alpha$, $\beta$, $\gamma$, $\delta$- and $\varepsilon$-HCH). Previous biochemical and genetic studies on the bacterium has revealed that enzymes called as Lin enzymes, catalyzes the HCH degradation. But their precise location in the genome sequence of the strain has not been determined yet. In this study, the whole genome of strain B90A was sequenced using Single Molecule Real Time Sequencing (SMRT) (~230X) and assembled into a complete sequence using Overlap layout consensus method using Hierarchical Genome Assembly Process (HGAP). This revealed that strain B90A consists of one chromosome and three plasmids which were designated as pSRL1, pSRL2 and pSRL3. The location of *lin* genes was determined as *linA*$_2$, *linB*, *linDER*, *linF*, *linGHIJ* and *linKLMN* were annotated on the chromosome, *linA*$_1$, *linC* and *linF* were annotated on pSRL1 and *linDEbR* on pSRL3 while pSRL2 did not contain any *lin* gene. In addition, multiple copies of *lin* genes such as *linA*, *linD*, *linR*, *linGHIJ* and *linF* with two variants of *linE* were present which supports that strain has efficient lower and upper HCH degradation pathway. Among these, duplication of *linA* gene between the replicons of strain B90A is proposed via homologous recombination. 26 copies of insertion sequence IS6100 were found which are earlier demonstrated as the drivers of *lin* gene evolution among sphingomonad. Further, incomplete tyrosine metabolism pathway and accumulation of homogentisic acid is identified as the reason behind the prominent brown pigment production by the strain B90A using both in-silico and laboratory experiments. This study opens up to elucidate the regulatory mechanisms which regulate the acquisition and transfer of *lin* genes with the other fellow HCH degraders inhabiting HCH contaminated sites.

Isolation, screening and characterization of protease and lipase producing thermotolerant bacteria from Gujarat, India

Leena Ambasana

Biotechnology Department, Shree M. & N. Virani Science College, Rajkot, Gujarat
Thermophiles are microorganisms that live and grow optimally in temperature range of 45 to 70°C. The enzymes produced by these organisms have great potential in industrial process due to their stability at high temperatures. Isolating bacteria from their natural source and their identification are important in terms of discovering novel industrial enzymes. A preliminary investigation was performed about the presence of industrially important thermophilic bacteria in the hot springs and in its vicinity within Gujarat, India. Around 30 bacterial isolates were isolated from different regions of Gujarat and were further screened for industrially important lipase and protease producing strains. The screened isolates were identified based on morphological and biochemical characteristics. The conditions for growth and enhanced enzyme production were optimized. The temperature range for growth at a pH of 7 was between 50-55°C with optimum growth at 50°C after 42 h of incubation. The crude enzyme exhibited highest activity over a wide temperature (37°C to 80°C) and alkaline pH (6.0-8.0) range with fermentation period of 24-120 hr. Crude extract of enzymes were efficient in removal of blood stains from clothes. The enzymes will be purified for further applications.

IPL3

Comparative genomics of Dengue virus: Conserved epitopes and CPG Island analysis

Mansi Verma*1, Nidhi Mittal1, Kavita Kaler1, Jyoti Bodwal1, Yugal Sandilya1, P.S. Dhanaraj1, Rup Lal2

1Sri Venkateswara College, University of Delhi, New Delhi, India
2Molecular Biology Laboratory, University of Delhi, Delhi, India

Presenting Author
mansiverma20@gmail.com

Dengue is one of the most severe emerging arthropod born viral diseases globally. Member of the genus Flavivirus and family Flaviviridae, DENV is a positive stranded RNA virus composed of three structural proteins which forms the components of virion and seven non-structural proteins which control various functions like viral replication, immunity and pathogenesis. There are five different serotypes of virus namely DENV-1 to DENV-5. So far, no vaccine with higher efficacy has been known for treating all serotypes of dengue. In the present study, comparative genomics of Dengue virus was conducted to explore potential candidates for novel vaccine targets. Simultaneously, comparative analysis of CpG islands was also conducted. Methods: All ten proteins of all four serotypes of dengue virus were downloaded and analysed for conserved motifs using MEME software. Several B-cell epitopes were predicted using Immune Epitope Database B-cell prediction tool & Bepipred. Overlapping epitopes sequences were analysed for surface accessibility and
conservancy. For CpG island prediction, genome sequences of DENV serotypes were downloaded and CpG islands were obtained using methprimer 2.0. Based on our studies, we could find several conserved epitopes which are antigenic in nature. Genome analysis revealed presence of conserved CpG islands in serotypes DENV-1, 3 and 4. Using in silico analysis, we could successfully obtain many conserved epitopes common to all serotypes of dengue virus, which seems promising for designing novel vaccine targets. Also the conserved CpG islands may shed light on the epigenetics of Dengue.

IPL4

Evaluation of circulating cell free DNA (CCFDNA) for P53 gene mutations as a novel strategy for liquid biopsy in eyelid sebaceous gland carcinoma

Perumal Jayaraj1, *, Anita Verma1, Rajendra Phartyal1, Sarika Yadav2, Srishti Rangarajan2, Abhilasha Gahlawat2, Neelanjana Ray3, Reema2, Kirtana Vasu3, Cheshta Jain4, Charu Jain4, Kriti Negi4, Aanchal Trikha4, Mrigya Kaushik1, Seema Sen5

Department of Zoology1 Sri Venkateswara College, University of Delhi, Department of Biochemistry2 Sri Venkateswara College, University of Delhi,
Department of Biological Sciences3 Sri Venkateswara College, University of Delhi,, Department of Life Sciences4 Sri Venkateswara College, University of Delhi,
Department of Ocular Patholog5, R. P. Centre, AIIMS, New Delhi

Presenting author
jay.aiims@gmail.com

Eyelid sebaceous gland carcinoma (SGC) is an aggressive tumor with increased chances of recurrence and metastasis. The treatment varies from local excision to orbital exenteration. The p53 gene is expressed upon cellular stress signals mediating antiproliferative responses. Sestrins serve as one of the downstream effectors of P53, and expresses in response to DNA damage (by Gamma or UV radiation). Circulating cell free DNA (ccfDNA) are fragments of nucleic acid ranging from 18-200bp released by apoptosis. Since ccfDNA is known to possess similar mutation signatures as that of the primary tumor, it is assumed that it has originated from the tumor tissue and thus, it might potentially serve as a prognostic marker in the absence of clinically detectable metastases. In our study we try to correlate the expression of p53 and Sens2 in SGC. Further, ccfDNA was sequenced for P53 mutations. ccfDNA from 20 Sebaceous gland carcinoma was extracted from the plasma and tumour DNA was isolated by QIAamp tissue DNA midi Kit. The Quality of the DNA was estimated by ALU PCR (Arthrobacter Luteus Polymerase chain reaction). The amplified DNA was sequenced for analyzing P53 gene mutations using the Sanger’s Method and analysed using Bioedit software. Immunohistochemistry (IHC) using mAb was performed to detect tissue level expression of P53 and Sestrin2. IHC evaluation revealed nuclear expression of P53 in 55% of cases studied. The plasma ccfDNA [17.45 ng/µl (12.76–19.66)]yield was sufficient to perform downstream assays (PCR for p53). Direct sequencing analysis revealed mutations in SGC patients (25%). A C > T transition in
exon-6 (R196X) was identified in two patients in both tumor and ccfDNA. Sesn2 expression was also found to be significantly reduced in P53 mutated SGC patients and cases with P53 immunostaining. In addition to P53 mutations, downregulation of P53 mediated Sestrin expression was found to be of biological significance in the development of SGC. The potential clinical use of ccfDNA as a diagnostic measure will allow non-invasive assessment, screening, disease classification and monitoring of cancer.

IPL5

Degradation of environment pollutant dye, methyl orange using silver nanoparticles synthesized by green approach

Poonam Dwivedi* and Marut Jain

*Department of Chemistry, Ramjas College, University of Delhi, Delhi-110007

Presenting Author

poonam8971@gmail.com

Green synthesis of nano materials is the most emerging method, as this is simple, cost effective, eco-benign, energy efficient, relatively reproducible and often results in more stable materials. Physical and chemical properties of metal nanoparticles are significantly different from those of the bulk materials. Silver nanoparticles (Ag NPs) among all metal nanoparticles, have been paid more attention due to their specific electrical, thermal, optical and electromagnetic properties. Furthermore, having a high surface to volume ratio, Ag NPs can dramatically enhance the interaction between reactants and catalysts. Greensynthesis of metal nanoparticles involves using microorganisms, enzymes, fungus, and plant sources. One pot synthesis of Ag NPs using plant source involves reduction of silver salt with plant source in aqueous medium. This method has advantage over chemical/physical methods as plant source functions both as reducing as well as capping agent. Formation of Ag NPs can be easily monitored visually from the change in colour of the reaction mixture. Very recently, Anacardiumoccidentale, Hyphaenethebaica, Abutilon indicum, Solanumtricobatum, Erythrina indica, beet root, mangosteen and olive etc., have been reportedly used to synthesize Ag NPs. Silver NPs have been characterized by many physicochemical and morphological techniques. Dyes are the major effluents from various industriesthat require better and improved wastewater-treatment measures. A representative dye, Methyl Orangeis a major effluent from textile and food industry and is also a well-known carcinogen. It has already been reported that, reduction of methyl orange by NaBH₄ only is thermodynamically feasible, but kinetically not, but in presence of Ag NPs, reduction reaction becomes thermodynamically as well as kinetically feasible as Ag NPs reduces the activation energy. The degradation kinetics has been studied using UV-visible spectroscopy.
**IPL6**

**Reporter Gene Technology and Biosensing: A boon in Environmental Pollution Management**

**Rekha Kumari**

1st and Jan Roelof van der Meer

1. Miranda House, University of Delhi, Delhi 110007.
2. Department of Fundamental Microbiology, University of Lausanne, 1015 Lausanne, Switzerland.

**Presenting Author**
rekha.kumari@mirandahouse.ac.in

Whole cell microbial biosensors or bioreporters are chosen over chemical analysis methods to monitor a pollutant due to its cost-effectiveness and being amenable to genetic manipulations to tweak the detection levels. Fluorescent protein molecules are fused to the regulatory elements like promoters which are induced by the pollutant. *Alcanivorax borkumensis* is a marine bacterium found to use hydrocarbons as sole carbon source for its growth in the presence of oil. Oil spills pose a very high risk to the marine life and fauna. Surface layer of the oil gets evaporated soon after the spills but long-chain hydrocarbon compounds of the oil are persistent and cause damage. Detection of long-chain hydrocarbons like tetradecane and their bioavailability to the organism is an important issue to be addressed as it may help in designing specific strategies to clean up the area. In this study egfp was fused with the regulatory AlkS and the alkB1 promoter from *A. borkumensis* SK2. The gene cassette was introduced into *A. borkumensis* after confirmation through conjugation. The gel patch diffusion assays were performed to check the bioavailability and/or bioaccessability and accumulation of signal over period of time. Imaging was used to calculate Average Grey Value (AGV) as a measure for increasing or decreasing signal from the oil source. Cell- culture suspended flask reported assays using fluorimetry helped in measuring signal from biosensor in a direct contact conditions. At the end alkane analysis was used to check the extent of oil biodegradation with bidimensional gas chromatography. The biosensor can be used to assay long-chain alkane accessability to measure efficacy of oil degradation. The fluorescence test in the flasks can be of particular use to in case of onsite tests during oil spills.

**IPL7**

**Application of Punica granatum extract for antibacterial textile finishing:**

**Development of health care textile**

**Simran Jit**

1st, Jyoti Arora, Prerna Agarwal, Gunjan Gupta

1. Department of Zoology, Miranda House, University of Delhi, Delhi 110 007
2. Department of Genetics, University of Delhi 110021
3. Department of Biotechnology, Manav Rachna International University, Haryana 121004

**Presenting Author**
simranjit@mirandahouse.ac.in
Natural dyes and herbal extracts are known to possess antimicrobial, antifungal and antiviral properties and hence there is growing consideration for application of these bioactive molecules for the production of functionalized textiles. Products from these finished textiles are not only environment friendly but also offer health benefits to the wearer. In this study, rind of pomegranate (*Punica granatum*) was used as a source of bioactive molecules and tested for its antibacterial properties on organic cotton. The efficacy of the bioactive extract was estimated against *Escherichia coli* MTCC 82; *E. coli* ATCC 25922 (gram negative) and *Staphylococcus aureus* MTCC 96; *S. aureus* ATCC 25923 (gram positive). Three cross-linking agents viz., Citric acid, Glyoxal and Glutaraldehyde were tested both in the absence and presence of mordant (Alum). Qualitative assessment of the antibacterial property was made against the indicator strains by disc diffusion method and parallel streak method (AATCC 147) while bacterial reduction method (AATCC 100) was performed for the quantitative estimation. The result showed the extract to be effective in inhibiting the growth of indicator strains while mordant did not have a significant effect on impact on finishing. The AATCC 147 method proved glyoxal to be the most suitable cross-linking agent with 11.41 mm for *S. aureus* MTCC 96 and 9 mm for *E. coli* MTCC 82. The pomegranate extract completely inhibited the growth of indicator strains as observed by AATCC 100 method. Thus, we conclude that rind of pomegranate, a bio waste from food industry can be used for antibacterial textile finishing for use in health care apparels. It is recommended to isolate and purify the bioactive compounds responsible for this antibacterial activity using advanced scientific techniques.

IPL8

**Qualitative estimation of phytochemicals and insecticidal activity of plant extracts against *Tribolium* sp.**

*Suman Sharma*¹, *Sandeep Kaushik*², *Charu Dogra Rawat*³

¹Department of Botany, Ramjas College, University of Delhi  
²Department of Environmental Science, IGNTU, Amarkantak  
³Department of Zoology, Ramjas College, University of Delhi

**Presenting Author**  
suman_s18@yahoo.co.in

Plants harbor a varied group of phytochemicals commonly known for medicinal and insecticidal properties. Different parts of the plants possess diverse set of metabolites (alkaloids, flavonoids, tannins, saponins etc.) varying in concentration. Biotic and abiotic factors especially regulate the temporal and spatial variability of composition and concentration of the secondary metabolites among various plant taxa. These secondary metabolites though not much necessary for the metabolism of the plant unlike primary metabolites may act as attractant (pollination) or deterrent (defence mechanism) to other fauna. Stored pests are known to cause an immense economic loss to
the food grains across the world thus affecting the quality and quantity of various edible products. Among various stored pests *Tribolium* sp. (Insect: coleoptera: Tenebrionidae) commonly known as confused flour beetle is a notorious insect of oriental origin. In the present scenario on a larger scale, economically costlier, environmentally hazardous, non-biodegradable, non-specific chemical agents that too in larger quantities turn capable of causing health and environment hazards are rampant used to control these insects ultimately hampering the micro-ecosystems. With an objective to substantiate the harmful and costly synthetic pesticides and insecticides present investigations were carried out to ascertain the bio-efficacy of various biodegradable and environment friendly plant extracts against *Tribolium* sp. Qualitative phytochemical analysis and bioassays for locally available seven plant taxa was performed against *Tribolium* sp. Insect repellant activity for the same plant extracts substantiated the phytochemical results as the aqueous extracts showed more repellency to *Tribolium* adult beetles as compared to the methanolic ones. Interestingly, aqueous extracts of *Datura* and methanolic extracts of *Withania* showed a comparatively higher repellant activity wrt *Azadirachta indica* extract, a potent and well known insecticidal plant.

**IPSOP1**

**Assessment of pigment system and biochemical response of hydroponically grown *Vigna radiata* under heavy metal stress**

*Aishwarya Karelia, Janki Ramani, Praveen Gupta*

Shree M. & N. Virani Science (Autonomous) College, Rajkot, Gujarat

**Presenting Author**

aishwarya.okha@gmail.com

With the expansion of the world population, the environmental pollution and toxicity by heavy metals is increasing continuously. Heavy metals including Lead, Nickel, Cadmium, Copper, Cobalt, Chromium and Mercury are hazardous heavy metal pollutants that cause toxic effects to plants as well as animals; they act as stress to plants and affect the plant physiology and cause severe health problem in animals. Pb(NO₃)₂ has been taken as a source of lead at the 300 μM, 600 μM and 900 μM concentration and *Vigna radiata* has been grown hydroponically in Hogland solution along with control plant. With increasing level of lead were reduced in germination and growth compared to control plants. Expected result from this project is that the possibilities hyperaccumulation of lead can be observed in root, stem and leaf. But in stem and leaf the amount of accumulation would be less compared to root. Study would also provide the better insight in phytoremediation and development of heavy metal tolerant plant in future.
Virtual screening of potential inhibitors against rar protein for treatment of acne

**Dhruv Kumar Patel, Khushbu Rabadiya, Nutan Prakash***

Shree M. & N. Virani Science (Autonomous) College, Rajkot, Gujarat

**Presenting author**

dhruvp.patel@avm.edu.in

Acne is a common disease of the teenage population causing cosmetic disfigurements as well as many psychological problems in the affected persons. Isotretinoin is the drug which is used for the treatment of acne. Isotretinoin inhibits the sebaceous gland function and keratinization, so it is used for the treatment of dermatological diseases. The drug has teratogenic and other considerable side-effects. In the current work, we conducted a virtual screening of 58 lead-like compounds retrieved from PubChem using a virtual screening approach with an experimental structure of retinoic acid receptor protein. Isotretinoin has shown binding affinity of $-4.8$ kcal/mol and it is binding around the active site region of the receptor. Based on the properties of Isotretinoin, more similar compounds were retrieved and a structure-based virtual screening was carried out by AutoDockVina in PyRx 0.8. Drug like properties and ADME properties were checked, best 5 novel drug-like compounds were identified. Observations made in this study may extend an assuring platform for developing competitive inhibitors against Retinoic acid receptor protein.

Studies on optimization of glucose concentration on exopolysaccharide production by *Bradyrhizobium japonicum*

**Maheshwaryba Jadeja** and **Praveena Bhandari**

Shree M&N Virani Science (Autonomous) College, Rajkot, Gujarat

**Presenting Author**

mkjadeja0014@gmail.com

Effect of different glucose concentration on Exopolysaccharide production by *Bradyrhizobium japonicum* was analyzed. For the *Rhizobium* mannitol is generally used as carbon source. But instead different concentrations of glucose were added. 12.5mM, 25mM and 50mM concentration of glucose were taken as carbon source for EPS production. To prepare a standard curve, glucose is taken as
standard sugar. EPS extracted from these sugar sources were analyzed. Maximum EPS was found in glucose having 50mM concentration and minimum EPS was found in glucose having 12.5mM concentration. However the above information can be used to study varied applications of EPS such as scaffolds or matrices in tissue engineering, drug delivery and wound dressing etc in medical sciences. Also in food industries the novel EPS may bring improvement in the cost, hydration of food products, and production of low calorie foods.

IPSOP4

Influence of plant extracts on the reproductive behaviour and development of *Aedes aegypti*

Namrata Sharma<a>, Nisha Chauhan<a>, Akash Kataria<b>, Ranjana Seth<c> and Varsha Baweja<sup>a</sup>

<a>Department of Zoology, University of Delhi, New Delhi, 110007, India

<b>Guru Jambeshwar University of Science and Technology, Hisar, Haryana, 125001

<c>Department of Zoology, Deshbandhu College, University of Delhi, Kalkaji, New Delhi-19, India

Presenting Author

namrata28ish@gmail.com

Due to development of resistance against a large number of insecticides, the control of dengue fever mosquito, *Aedes aegypti* has now becomes a challenge for the researchers. *A. aegypti* is ubiquitous and causes many deadly diseases like, dengue fever, dengue haemorrhagic fever, chikungunya and yellow fever. Use of phytochemicals to control insect pests/vectors is known since ages as a part of indigenous and traditional knowledge. Many plant products decrease insect longevity, and interfere with their reproductive bioactivities. In view of this ethanol and hexane plant extracts of three plants *Ocimum*, *Nerium* and *Citrus* peel were evaluated at different doses, viz., 100ppm, 200ppm and 400ppm with respect to reproductive behaviour and development of *Aedes aegypti*. All tested concentrations of plant extracts were observed to act as ovipositional deterrent, showing negative values of oviposition activity index. The hexane extract of *Ocimum* at 400ppm showed maximum (98.7%) ovipositional deterrence. The studies on larvicidal activity of these plant extracts revealed that at 400ppm, *Citrus* (orange peel) had maximum larvicidal activity (72.5%) followed by *Nerium* (52.5%) and *Ocimum* (40%). The plant extracts impaired behavioural responses of *Aedes* larvae too. The treated larvae deviated from their normal wriggling, swimming and resting pattern. The extract of orange peel exhibited maximum metamorphic inhibition at 400ppm, only 26.7% fourth instar treated larvae could metamorphose into pupae. These results suggest that the phytochemicals extracted from common Indian plants and plant waste can be employed in an effective vector control program against *A. aegypti*. Further detailed research is needed to identify the active ingredients present in the extracts and to get more conclusive results.
Tuberculosis (TB) has become a major health problem in the world and ranks alongside HIV as a leading cause of death. One of the major concerns associated with TB is its latency which helps Mycobacterium tuberculosis (M.tb) to survive in host cell under stress conditions. There are evidences of many bacterial pathogenic factors which target host mitochondria and make host cell a safe niche for intracellular pathogens. Thus, we hypothesised that M.tb DosR proteins may target host mitochondria and this interaction may regulate the latency. Protein sequences of DosR regulon genes of M.tb strain H37Rv and their orthologs in avirulent strain H37Ra, clinical isolate CDC1551, M. bovis BCG Pasteur strain and M. smegmatis were analysed by various Bioinformatic tools(MitoProt II and PsortII) for mitochondrial targeting. The Mitoprot II score of above 0.6 and PsortII score of above 30% was set as criteria for selecting proteins being targeted to mitochondria. We observed that Rv2003c, Rv1736 and Rv1737c and their orthologs in M.tb H37Ra, M.tb CDC1551 and M. bovis showed high probability of mitochondrial targeting under the selected criterion. The orthologs of Rv2003c and Rv1736 were absent in avirulent M. smegmatis, whereas Rv1737c ortholog in M. smegmatis did not show mitochondrial targeting. DosR regulon proteins Rv2003c (conserved hypothetical protein), Rv1736 (nitrate reductase) and Rv1737c (nitrate/nitrite transporter) and their orthologs in virulent Mycobacterium species show mitochondrial targeting and may have key role in regulating host cell survival. The absence of orthologs of these genes in avirulent M. smegmatis or the inability of M. smegmatis orthologs to be targeted to mitochondria further emphasize the relevance of these genes in virulent M.tb. These proteins may help virulent M.tb to adapt and persist in stressful microenvironment of host cell. The role of these proteins in regulating apoptosis needs to be validated experimentally to understand the pathogenesis of latent TB.
The plastic waste is one of the major issues in a developing country like India. The increasing environmental problems arising due to dumping of plastic, needs to be replaced by something eco-friendly and also not compromising the basic needs of people. The whole mindset needs to be improved in devising formation of plastics from Agricultural waste byproduct, which possess properties like the conventional plastics and in addition even acquire the unique property of ‘Biodegradability’. Starch, which is a basic component of the agricultural plants is used as the key element in bioplastic production. A protocol has been devised for incorporating the use of residual potato starch and converting it into plastics, which are biodegradable in nature, therefore known as bioplastics. As potato starch, contains refined starch, with minimal level of fat and proteins, it is a primary aspect to be used in the production of bioplastic. In present project, we procured the waste potato starch from Balaji Wafers private limited, Rajkot to make bioplastics. The quality of bioplastics was analyzed through various physical and chemical parameters like tensile strength, melting temperature, acid base resistance test, Glass transition temperature ($T_g$), fibre formation test, floatation test, solubility in different solvents etc. The basic glucose units makes it prone to easy biodegradation by amylase producers, whereas its non-solubility in various number of solvents including water, ends the quest of replacing the oil-based plastics to the starch based ‘Bioplastic’
Oral Presentations
Young Scientist Colloquium
Genome based insights into the biosynthetic pathways in bacteria isolated from chemically contaminated soil

Abhay Bajaj, Yogendra Singh and Rup Lal

Molecular Biology Laboratory, Department of Zoology, University of Delhi, Delhi-110007
Bacterial Pathogenesis Laboratory, Department of Zoology, University of Delhi, Delhi-110007

Presenting Author
abhaybajaj@gmail.com

Bacteria posses various survival strategies to adapt in every kind of environment that exist. Recent advances in genome sequencing and analysis has provided metabolic clues for identification of genetic signatures which plays elemental role in developing such survival strategies. Various secondary metabolites like pigments, surfactant molecules have been implicated to play critical role in survival and growth of organisms in different environment. In the present study, metabolic pathway reconstruction was performed for synthesis of secondary metabolites using the whole genome based information. Preliminary chemical and functional analysis studies have suggested these as the potential metabolites which can be used for human and environmental health application. Comparative genome analysis studies were performed to analyze the distribution and evolution of metabolic traits and draw genus level functional and phylogenetic associations. The study highlights the advances in genome based tools for inferring potential bacterial functions for bio-synthesis of microbial products.

Systems biology approach based on host-pathogen protein-protein interactions to uncover the host cell mechanisms

Kalaiarasam Ponnusamy, Shazia Haider, RK Brojen Singh, Pawan K Dhar, RNK Bamezai

Synthetic Biology Lab, School of Biotechnology, Jawaharlal Nehru University, New Delhi, India
School of Computational and Integrative Sciences, Jawaharlal Nehru University, New Delhi, India
School of Life Sciences, Jawaharlal Nehru University, New Delhi, India

Presenting author
kalaiarasan@jnu.ac.in
Infectious diseases are the result of protein-protein interactions between the pathogens and host. The host-pathogen protein-protein interactions (HP-PPI) play an important role in infections and they may favor the pathogens or their clearance. In order to understand the molecular mechanisms of pathogenicity it is necessary to identify the host proteins targets by pathogenic proteins. Here we used the network theory methods, using pathogenic proteins and identified important protein for pathogenic regulation, which demonstrated a hierarchical scale-free fractal HP-PPI network. The key regulators were also individually found to control highly clustered modules and play an important role in the stability of the overall network. The feedback loop regulation motif was identified among these crucial motif topologies were also reflected in high frequency. The propagation of the perturbed signal from the hubs was found to be active. Hamiltonian energy analysis was used with network properties approach and found significantly contributing to the understanding of stable and self-organized HP-PPI system. Finally, the key hubs were observed to regulate the host by influencing motifs, propagation of signals, module regulation, which was validated through removal of hubs, signifying their key regulation of biological process.

**Microbial ecology of aquaculture-based sewage treatment system at Cuttack, Odisha, India**

**Priyambada Patri and S. Ayyappan**

Bharati College, University of Delhi, Delhi

**Presenting Author**

priyambadapatri@rediffmail.com

To understand the relationship between chemical and microbial community structure in a duckweed and fish-based Aquaculture sewage treatment system, a study on microbial ecology was conducted at a aquaculture-based sewage treatment system at Matagajputr receiving from a major drainage system of Cuttack, Odisha (Lat 20° 028’; Long 85° 52’ E). The bacterial communities like aerobic heterotrophs, total coliforms, faecal coliforms, faecal streptococci, Salmonella, Yeast and moulds, amylolytic bacteria, cellulolytic baceteria, nitrogen fixing bacteria, nitrifiers, denitrifier and phospho-solubilising bacteria involved in Carbon, Nitrogen, Phosphorus and sulphur cycle at various stages of treatment/depuration were correlated differently with the physico-chemical parameters. The system reduced the microbial pollution effectively by removing the organic pollutants, pathogenic bacteria and algal blooms for which the effluents were in the permissible limit and are allowed to enter into the nearby Kathojodi river. This biological treatment process highly influenced the bacterial and plankton composition which leads to water quality improvement.
Effect of inoculation with *Aspergillus tubingensis* on growth and yield of wheat plants grown at two different agro-climatic regions

Rachana Jain¹, Anumegha Gupta³, Jyoti Saxena² and S.N. Naik¹

¹Centre for Rural Development and Technology, Indian Institute of Technology, Delhi, Hauz-Khas, New Delhi 110016, India
²Biochemical Engineering Department, BT Kumaon Institute of Technology, Dwarahat, Uttarakhand 263653, India.
³Department of Bioscience & Biotechnology, Banasthali University, Distt.Tonk, Rajasthan 304022, India.

Presenting Author
rachana_nbs@yahoo.co.in, Ph- 09694756975

For sustainable agriculture, substitution of chemical fertilizers with eco-friendly biofertilizers is the prime requirement. Intensive research on Phosphate solubilizing fungi (PSF) is currently underway worldwide for developing biofertilizers. PSF, *Aspergillus tubingensis* S33 isolated from rhizospheric soil has a great potential to be developed as bioinoculant. It was able to solubilize different inorganic forms of phosphorus (P) viz. dicalcium phosphate, tricalcium phosphate, ferric phosphate and Udaipur rock phosphate. This isolate were evaluated for improvement of wheat crop with and without tricalcium phosphate (TCP) fertilization under 2 different agro-climatic conditions viz., Banasthali, Rajasthan (26.38°N 75.87°E, 315 m above the sea level, semi arid climate) and Dwarahat, Uttarakhand (29.78°N 79.43°E, Himalayan hilly terrain, 1467 m above the sea level, subtropical). Both sites has harsh environment. Application of the fungal strain as bioinoculants showed significant effect on wheat growth, yield, nutrition uptake and available P in soil. Improvement in crop yield and soil fertility at 2 different sites was more pronounced when TCP was supplemented along with fungal inoculation as compared to uninoculated control. The results suggested that *A. tubingensis* S33 have the potential to play important role in wheat growth promotion and increase in soil available phosphorus (P) in different agro-climatic conditions.

Comparative Bacterial Genomics: An Environmental Perspective

ªRoshan Kumar, bInderjit Singh and aRup Lal

ªDepartment of Zoology, University of Delhi
bCentre for Environmental Management of Degraded Ecosystems, University of Delhi

Presenting Author
roshanzhc@gmail.com
Comparative genomics reveal comprehensive analysis of genomes to decipher the characteristic attribute(s) that differentiate different species or genera. These features are acquired by the organisms in the due course of time, thus these unique features are restricted to few organisms or group of organisms. Through comparative genomic analysis, we have analyzed the genetic divergence of *Sphingobium* strains in the light of hexachlorocyclohexane (HCH) degradation potential. The analysis reported the evidence of genus-level horizontal gene (HGT) transfer in *Sphingobium* spp. The study was further extended to genus *Novosphingobium*, where we characterized habitat specific gene diversity between the isolates of contaminated soil, rhizosphere, marine and fresh water using protein-protein interaction. The study revealed the amino acid preferences by these *Novosphingobium* strains based on their respective habitats. In environmental adaptation, the aerotolerance is an important parameter for organism’s survival. In a novel genus *Parapedobacter*, we analyzed the bacterial aerotolerance (BAT) operon known to provide protection against the oxidative stress and also reported the signal propagation to study the expression pattern of this operon. Thus, comparative genomic tools provided insight into the environmental adaptability of these organisms using genome sequences.

**Keywords:** Comparative Genomics, *Sphingobium*, *Novosphingobium*, *Parapedobacter*, BAT operon

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Co-existence of *Wolbachia* and its associated phage in lac insect

**Sandeep Kaushik¹, Suman Lakhanpaul²**

¹Department of Environmental Science, Indira Gandhi National Tribal University, Lalpur-Amarkantak, Annupur-484887 Madhya Pradesh

²Department of Botany, University of Delhi, Delhi-110007

Presenting author

sskaushik2002@igntu.ac.in

Eukaryotes do not live alone. They harbour cells of bacteria (Eubacteria and Archaea), and often other eukaryotic microorganisms, on their surfaces and internally in symbiosis or without any ill effect. *Wolbachia* are the most widely spread intracellular endosymbionts mostly reported from arthropods and is known to cause various sexual alterations such as cytoplasmic incompatibility, parthenogenesis, male killing etc. on their hosts. Molecular and histological investigations have indicated the occurrence of *Wolbachia* and YLS in *Kerria lacca*-Lac insect. Lac is secreted by the females of lac insect [*Kerria lacca* (Kerr)] which forms a protective covering through the surface of the insect. It is the only natural resin of animal origin and has diverse uses with immense industrial value. The present study deals with the detection of *Wolbachia* in *Kerria lacca* populations across India. A total
of 43 *Kerria lacca* insect lines belonging to kusumi and rangeeni strains from different geographical locations across India were tested for the presence of *Wolbachia* and *Wolbachia* Phage (WO). Co-existence of *Wolbachia* phage associated with *Wolbachia* infected *Kerria* accessions have been divulged for the first time. Phylogenetic analysis of WO sequences put the *Kerria lacca* insect lines into two distinct clades, with one clade representing predominantly rangeeni strain and the other with kusumi strains. Potential role of WO in species divergence and use of its sequences (orf 7) in strainal identification of the hitherto morphologically indistinguishable two economically important strains of *Kerria lacca* is revealed. The present study will prove to be a direction driven work in harnessing the potential role of endosymbionts in host manipulation with an ultimate objective of increasing the lac production.

**YSL7**

### Comparative genomic analysis of novel *Acinetobacter* symbionts: A combined systems biology and genomics approach

**Shazia Haider**, Vipin Gupta, Utkarsh Sood, Jack A. Gilbert, Meenakshi Ramjee, Ken Forbes, Yogendra Singh, Bruno S. Lopes and Rup Lal

1 Department of Zoology, University of Delhi, Delhi-110007, India
2 School of Medicine, Medical Sciences and Nutrition, University of Aberdeen, Aberdeen, AB25 2ZD, UK
3 Department of Surgery, University of Chicago, Chicago, 60637, USA

*Corresponding authors

Presenting Author

shaziahaidert@gmail.com

The increasing trend of antibiotic resistance in *Acinetobacter* is a matter of global concern as it drastically limits the range of therapeutic agents required to treat multidrug resistant (MDR) infections. This study focused on analysis of novel *Acinetobacter* strains using genomics and systems biology approach. Here we used the network theory method in *Acinetobacter* spp. (pathogenic and non-pathogenic) and identified the key regulatory proteins (hubs) in each strains. We identified nine major key regulatory proteins (hubs), guaA, guaB, rpsB, rpsI, rpsL, rpsE, rpsC, rplM and trmD which have functional roles demonstrating a hierarchical scale-free fractal protein-protein interaction network. Two unique key hubs, i.e., guaA and guaB played an important role in *Acinetobacter* sp. isolated from insect gut. The hub guaA was comparatively more important than guaB as it helped in effective module regulation. The rpsI gene was important in all the studied novel strains of *Acinetobacter* spp. The rplM protein was specific only to strains isolated from sheep gut. We also discovered that three hubs, rpsM, rpsB and rpsI, were involved in the regulation of overall network
topology across all Acinetobacter strains in this study. Further investigation into these hubs will investigate their usefulness as drug targets for treating infections caused by Acinetobacter spp.
Poster Presentations
Session A
(Microbe-Microbe Interactions)
Insights into the environmental stress response linked genome content of *Paracoccus* sp. novel strain AK26 isolated from chemically contaminated environment

Akshita Puri\textsuperscript{a,b}, Abhay Bajaj\textsuperscript{a}, Yogendra Singh\textsuperscript{b} and Rup Lal\textsuperscript{a}

\textsuperscript{a}Molecular Biology Laboratory, Department of Zoology, University of Delhi, Delhi-110007
\textsuperscript{b}Bacterial Pathogenesis Laboratory, Department of Zoology, University of Delhi, Delhi-110007

Presenting Author
akshita.du@gmail.com

The complete genome of *Paracoccus* sp. novel strain AK26 isolated from Hexachlorocyclohexane contaminated environment was analyzed for environmental stress response linked genome signatures. The strain AK26 contains a single circular chromosome and four extrachromosomal replicons. Nearly 87\% of annotated putative sequences were assigned to COG functional categories and were used for predicting their role in strain AK26 metabolism. Nearly 23\% of the proteins involved in metabolic processes were identified on the extrachromosomal replicons, suggesting functional importance of multireplicon architecture. The genome encodes for different types of sigma factors (\(\sigma^{24}\), \(\sigma^{32}\), \(\sigma^{54}\)) which are responsible for adaptation to environmental changes by globally regulating the gene expression, overall cellular metabolism and secondary metabolites production. Apart from this, transcriptional factors acting as global regulators belonging to CRP/FNR, Lrp families and local regulators belonging to LysR, LuxR, TetR, GntR, families were also identified. Interestingly, nearly 32\% of these genes encoding transcriptional regulators are present on extrachromosomal replicons highlighting their role in regulating overall gene expression. Being a soil isolate, genome analysis for identification of signatures for aliphatic and aromatic compounds utilization/degradation was performed which revealed presence of homogentisate pathway for compounds degradation. Interestingly, genes for homogentisate catabolism \textit{hmgABC} genes were annotated on extrachromosomal replicon. Beside this, as soil is usually a source of organic compounds especially herbicides like paraquat which are mechanistically toxic by inducing superoxide mediated oxidative stress. The defense response genes induced in the presence of paraquat and other superoxide generators present in the soil were analyzed. Genes encoding paraquat inducible proteins \((\text{pqi})\) in addition to genes encoding superoxide dismutase, catalase and peroxidases were annotated in multiple copies in the genome suggesting evolution of efficient stress management strategy in this strain. Also, chemotaxis genes were annotated which have been reported in other gram negative bacteria as upregulated during prolonged exposure of paraquat and other superoxide generators. Thus in the present study, genomic features conferring various stress response were annotated highlighting the efficient adaptability of this strain to counter stressed environment. Also, the analysis reveals that genomic content is effectively maintained and replicated via the multireplicon architecture of strain AK26 genome.
Paracoccus sordidisoli sp. nov., isolated from hexachlorocyclohexane (HCH) contaminated soil

Amit Kumar Singh, Puneet Kohli, Nitish Kumar Mahato and Rup Lal
Molecular Biology Laboratory, Department of Zoology, University of Delhi, Delhi-110007
Presenting Author
amit.k.singhbhu@gmail.com, Ph: 011-27666254

A Gram-stain-negative, non motile, cream coloured, short rod or coccoid bacterium, designated as LP91T was isolated from hexachlorocyclohexane contaminated soil (Lucknow, India). Phylogenetic analysis based on 16S rRNA gene revealed that the isolate formed a cluster within the genus Paracoccus in the phylum Proteobacteria ranging from 93.4% to 96.9%. DNA-DNA hybridization of strain LP91T with bacterial species more than 97% 16S rRNA gene similarity was performed. The values so obtained were much lesser than 70% i.e., P. aestuarivivens GHD-30T (51.2 ±0.64), P. laevigulosivorans 43PT (49.5 ±0.73), P. limosus NB88T (36.5 ±0.86) and P. marinus KKL-A5T (34.6 ±0.94). The major polar lipids in this bacterial strain were diphosphatidylglycerol, phosphatidylglycerol, phosphatidylcholine and phosphatidylethanolamine. Ubiquinone (Q-10) was the only isoprenoid quinone identified. Spermidine was the major polyamine along with the minor amount of putrescine. Major fatty acids were C18:0o7C/C18:0o6C and C16:0. The DNA G+C content of the strain is 67.2 mol%. Based on the result of genotypic, phenotypic and chemotaxonomic characteristics strain LP91T represent a novel species of the genus Paracoccus, for which the name Paracoccus sordidisoli sp. nov., is proposed. The type strain, LP91T (KCTC 42938T =CCM 8696T =MCC 3128T), was isolated from an HCH contaminated soil at Ummari village, Lucknow, Uttar Pradesh, India.

Study of Mycobacterium CRISPR-Cas system by comparative genomic analysis

Anoop Singh1, Mohita Gaur1, Shashank Gupta2, Rup Lal1, Debasis Dash2*, Yogendra Singh1*, Anupam Kumar Mondal2*, Richa Misra1,3*

1Department of Zoology, University of Delhi, Delhi-110007
2CSIR-Institute of Genomics and Integrative Biology, Mathura Road, Delhi-110020
3Sri Venkateswara College, University of Delhi, Delhi-110021

Presenting Author
anoop1792@gmail.com
CRISPR-Cas (clustered regularly interspaced short palindromic repeats–CRISPR-associated proteins) systems are now known to regulate processes like gene regulation, group behavior, and virulence in prokaryotes apart from providing adaptive immunity against invading foreign genetic elements including viruses. CRISPR-Cas systems are divided into two classes based on effector module composition. Each class is further characterized into three types which can have different subtypes. *Mycobacterium* genus constitutes a number of pathogens including *Mycobacterium tuberculosis* and many environmental bacteria, suggesting diverse genome evolution and adaptability. Although CRISPR-Cas system has been identified in *M. tuberculosis* complex (MTBC), we are at a nascent stage to understand the implication of its presence in them. We performed a comparative genomic analysis of 149 mycobacterial genomes obtained from NCBI repository by two popular tools for CRISPR detection, CRISPR-finder and CRISPR recognition tool (CRT). This dual approach highlighted the influence of algorithm differences in these tools on the final results. Our analysis revealed three types of CRISPR-Cas system belonging to class I characterized by the presence of multisubunit effector-complex. Based on 16S rDNA and *cas* gene profile, two clusters emerged, with MTBC strains forming the dominant one. The presence of type III-A system, characterized by the signature *cas10/csm1* gene, was unique to MTBC. Furthermore, two additional CRISPR-Cas systems, type I-E and IV-A, were identified in some of the nontuberculous mycobacteria and *Mycobacterium* sp. JS623 possess both these types. Though *Mycobacterium marinum* and *Mycobacterium leprae* are closely related to MTBC, we did not find the presence of CRISPR-Cas system in them. We speculate that acquisition of the CRISPR-Cas system has occurred independently in MTBC after the divergence of these three from their last common ancestor, which is supported by the results of the 16S rDNA based phylogenetic analysis. In view of the proposed role of CRISPR system in other organisms, more detailed work can provide us valuable insights about the evolutionary advantage conferred to mycobacterial strains by retention of CRISPR-Cas system in their genomes.

**Characterization of nickel tolerant bacteria isolated from heavy metal polluted glass industry for its potential role in bioremediation**

**Anubha Sharma and Akash Chaudhary**

Amity Institute of Biotechnology, Amity University, Noida, UP, India

Presenting Author
asharma10@amity.edu

Heavy metal contamination of the environment is a serious concern because of their deleterious effects on biological systems. To the best of our knowledge, this is the first investigation on isolation of heavymetal resistant bacteria from contaminated sites of glass industrial area. The study focused on isolation and characterization of Ni$^{2+}$ resistantbacteria from these sites and analysis of their Ni$^{2+}$ accumulation potential. Out of 38 different bacterial isolates 3 bacteria were able to tolerate up to 24
mM Ni2C concentration. These bacterial strains were identified as *E. coli* (AS17b), *Escherichia coli* (AS21) and *Microbacterium* sp. (AS33) by 16S rRNA (16S ribosomal RNA) sequencing and their basic local alignment search tool search analysis. Growing cell of *E. coli* and *Microbacterium* sp. revealed accumulation of 0.12, 0.08 and 0.06 mg of Ni2+ per mg dry weight of cells, respectively, by 72 hr. Similarly resting cell of these strains showed accumulation of 0.27, 0.11 and 0.08 mg of Ni2+ per mg dry weight of cells by 150 min, respectively. These results reveal that strain *E. coli* (AS21) shows maximum accumulation efficiency for Ni2+ among different isolates studied under shaking as well as starving conditions. Hence, *E. coli* (AS21) could serve as an efficient and promising bacterium for bioremediation of nickel contaminated sites.

**Key words**: Heavy metals; bioaccumulation; efflux pump; nickel; bacteria

**MMI5**

**Comparative genomic analysis of predatory bacteria of genus *Bdellovibrio***

**Chandni Talwar, Rup Lal and Ram Krishan Negi**

Department of Zoology, University of Delhi, Delhi-110007

**Presenting Author**

talwar.chandni556@gmail.com, Ph: 011-27666254

The genus *Bdellovibrio* consists of very small, motile, gram-negative bacteria belonging to class Delta-proteobacteria. The genus represents a remarkable group of predators that feed on other gram negative bacteria. To date the genus comprises two species that differ in their mechanism of predation. *B. bacteriovorus* exhibit an intra-periplasmic growth where it invades into the prey cell to form a bdelloplast and replicates at the expense of prey’s constituents. *B. exovorus* attaches to the outside of the prey cell and consume its contents while replicating itself also referred to as epibiotic predation. The only available *B. exovorus* genome is relatively smaller than that of *B. bacteriovorus*. Despite a very small size, their genomes are very large ~3.5Mb and are known to be rich in genes coding for lytic enzymes while being deficient in amino acid biosynthetic pathway genes. This corresponds with their obligate predatory nature although rare host-independent (HI) forms are also known to arise from mutations. Recent studies have also suggested for lateral gene transfer occurring in *Bdellovibrio* which was previously thought to be absent in the genus due to degradation of prey DNA upon predation by lytic enzymes. The study is aimed at comparing all the nine *Bdellovibrio* genomes available till date in the NCBI database that would provide crucial insights and reveal the peculiarities of their predatory mechanisms.
Genome analysis of *Sphingopyxis flava* R11H<sup>T</sup>: An overview of genetic attributes

**Gauri Dhingra, Helianthous Verma and Rup Lal**

Molecular Biology Laboratory, Department of Zoology, University of Delhi,
Delhi - 110007, India

Presenting Author
gaurigargdhingra@gmail.com

A HCH tolerant strain, R11H<sup>T</sup> was isolated from the soil sample of HCH dumpsite located at Ummari village, Lucknow, Uttar Pradesh, India. On the basis of 16S rRNA gene similarity, the strain was identified as the member of genus *Sphingopyxis* with highest identity with *Sphingopyxis indica* DS15<sup>T</sup> (97.85%). In addition, three more strains were identified with similarity >97%. The pairwise DDH analysis revealed that the strain R11H<sup>T</sup> belongs to a separate species. Further biochemical and chemotaxonomic studies confirmed the novelty of the strain and thus designated as *Sphingopyxis flava* R11H<sup>T</sup>. Due to the HCH tolerance ability, strain R11H<sup>T</sup> was selected for genome sequencing using Illumina Hiseq technology. It has a genome size of 4.15 Mbp, with G+C content of 63.75% and 90.40% coding potential. The strain was found to code for 4185 protein coding sequences. The number total RNA coded by the strain is equal to 58 with a single copy of 5S, 16S and 23S rRNA and 46tRNAs. The pfam analysis revealed 3219 protein sequences engaged in variety of metabolic functions, dominated by amino acid transport and metabolism, energy production and conversion, lipid transport and metabolism, replication, transcription and translation. The strain was also found to harbor five biosynthetic gene clusters including terpene and ectoine. The KEGG pathway genes include degradation pathways for number of compounds including amino-benzoate, benzoate, bisphenol, caprolactlam, chloroalkene, chlorohexane but *lin* genes which are known HCH degradation were not annotated in the genome. It will be interesting to further analyze the probable metabolic pathways of strain R11H<sup>T</sup> which helps the strain to withstand in such high concentration of HCH.

Purification of ε-HCH (Hexachlocyclohexane) and Role of Enzymes LinA (HCH Dehydrochlorinase) and LinB (HCH Haloalkane Dehalogenase) in its Biotransformation

**Kiran Bala, Hans Peter Kohler, Thomas Poiger, Christof Holliger and Rup Lal**

1Molecular Biology Laboratory, Department of Zoology, University of Delhi, Delhi-110007, India.
2Swiss Federal Institute of Aquatic Science and Technology, Eawag, Dubendorf, Switzerland.
3Swiss Federal Research Station, Agroscope ChanginssWadenswil, Wadenswil, Switzerland.
4Laboratory of Environmental Biotechnology, EPFL, ENAC-ISTE, Lausanne, Switzerland.

Presenting author
γ-HCH (Hexachloreclohexane) had been used as a pesticide for several decades. Technical HCH comprising of a number of other unused isomers α-, β-, δ- and ε- besides γ-HCH was also used for economic reasons. The extraction of γ-HCH, consists of isomers that were usually discarded in open areas constituting regions with high-level of HCH contamination resulting in dumpsites. These isomers are not only highly toxic but also are highly persistent in the environment. Most studies that were done so far concentrated on the degradation pathways of γ-, δ - and β -HCH and very little emphasis was given to the fate of ε isomer. This could be as ε -HCH isomer constitutes a mere 1-2% of the technical mix. However, in view of the high amounts of technical HCH dumped, the fate of ε -HCH needs to be considered for proper risk assessment. The study was conducted to get detailed information on the fate of ε -HCH. For this, ε -HCH was purified from technical HCH. The purification was carried out by preparative normal-phase HPLC on an instrument that was fitted with a refractive index detector. The purified ε -HCH was analysed by means of NMR and GC-MS and was shown to be ≈90% pure with a heptachlorocyclohexane isomer, a known minor constituent of technical HCH as main impurity. The toxicity of the purified compound was determined with the yeast estrogen screen as well as with the *Vibrio fischeri* biolumincence test. The purified ε -HCH was then used for enzymatic degradation study by employing 6x His tagged HCH dehydrochlorinase (LinA1/A2) and HCH haloalkane dehalogenase (LinB). Formation of trichlorobenzenes (TCBs) by the action of LinA1/A2 was demonstrated by GC-MS. The hydroxylated metabolites (E1 and E2) formed by the action of LinB were identified by NMR and GC-MS analysis. Enzyme kinetic studies were performed to confirm which enzyme would have the better capability to degrade this isomer. The turnover number of ε -HCH was found to be highest for LinB in comparison to LinA2 and LinA1. The order followed for ε -HCH was LinB>LinA2>LinA1.

**MMI8**

Utility of nucleic acid amplification method for molecular detection of abdominal tuberculosis

Mohita Gaur1, Anoop Singh1, Anil Chaudhry2, Yogendra Singh1*, Richa Misra1*

1Department of Zoology, University of Delhi, Delhi-110007.
2Rajan Babu Institute of Pulmonary Medicine and Tuberculosis, Kingsway Camp, Delhi

Presenting Author
m.mohitagaur@gmail.com

Smear microscopy remains the cornerstone of diagnosis of tuberculosis (TB) across the globe. The most frequently used clinical sample for detection of *Mycobacterium tuberculosis* by this method is sputum obtained from patients with pulmonary TB. However, difficulty in sputum expectorationin
many patients, especially children and human immunodeficiency virus-positive cases, hinders the ease of the method. Moreover, extra-pulmonary TB, the rapidly-emerging manifestation of *M. tuberculosis* infection, is not accompanied with coughing or any other symptomatic features commonly seen in pulmonary TB cases, which makes the clinical diagnosis extremely difficult. Furthermore, collection of extra-pulmonary material requires invasive procedure, and the paucibacillary nature of these specimens makes the smear microscopy and microbial culturing extremely difficult in many cases. The advent of nucleic acid amplification based GeneXpert® system proved to be a major advancement in diagnostics with more sensitive and faster results. This technique has boosted the diagnostic accuracy of extra-pulmonary TB cases apart from knowing their drug-resistant profile. The most commonly used specimens for detection of extra-pulmonary TB are excisional biopsy or fine needle aspiration from tissue samples, ascitic fluid, pleural fluid, pericardial fluid, cerebrospinal fluid, urine and blood. Among the non-respiratory, non-invasive samples, stool remains a relatively under-utilized sample for detection of *M. tuberculosis*. Stool is mostly collected in paediatric TB patients, where children mostly swallow sputum and so DNA is easily detectable by stool-PCR. A major hindrance in use of stool as a potential specimen is the sensitivity of the PCR-based assay since stool has rich microbial diversity and DNA cannot differentiate live and dead bacteria. The present study aims to study the utility of stool as a specimen for abdominal TB patients, which constitutes 10% of extra-pulmonary cases in India. Since *M. tuberculosis* is known to survive highly acidic gastric fluid, we aim to utilize a two-pronged approach wherein PCR assay will be carried out for selected genomic targets as well as detection of bacteria in Bactec MGIT 960 system and Lowenstein Jensen medium. This diagnostic technique offers a good alternative approach for detection of *M. tuberculosis* in a sensitive and non-invasive manner.

**MMI9**

**Genome based species identification of *Bacillus* strain RL isolated from cattle feaces**

*Monika Sharma, Himani Khurana, Helianthous Verma, R. K. Negi and Rup Lal*

Department of Zoology, University of Delhi, Delhi-110007

**Presenting Author**

monikagaur1494@gmail.com

The genus *Bacillus* constitutes gram-positive bacteria that are widely distributed in the natural environments like soil, marine habitat, food products and gut of the organisms. Member of genus *Bacillus* are very well known for their virulence ability, secondary metabolite production, antifungal and antimicrobial properties that make them valuable for the applied purposes. It is difficult to classify them into distinct species of genus *Bacillus* based upon 16S rRNA gene sequence as there is
no significant difference in their 16S rRNA sequence. Here, we used genome wide approach in order to get a true classification of *Bacillus sp.* RL isolated from cattle faeces. Genome based distance phylogeny (GBDP) deciphered the phylogenetic position of *Bacillus sp.* strain RL showing that *Bacillus thermotolerans* and *Bacillus andreraoultii* are its closest species. We also get insight into the secondary metabolite production of strain RL, which determined its ability to produce terpene and T3pks that are generally found in plants. We predict that these clusters might acquire through horizontal gene transfer as strain RL isolated from cattle faeces.

MMI10

**Taxonomic study of extracellular enzyme producing Actinomycetes from varied ecological habitats**

Monisha Khanna Kapur*, Munendra Kumar, Payal Das, Prateek Kumar, Renu Solanki

Acharya Narendra Dev College, University of Delhi, Govindpuri, Kalkaji,

New Delhi-110019

Presenting Author

sanchalwire110@gmail.com

Actinomycetes secrete various types of extracellular enzymes which have numerous applications in industry and agriculture. Traditional industrial microbiology has merged with molecular biology to yield improved recombinant processes for the industrial production of proteins, biopharmaceuticals and industrial enzymes. In a previous study, actinomycetes were isolated from diverse ecological habitats and screened for their ability to produce extracellular enzymes. Based on the results of primary and secondary screening, colonies 194 (Dumping site soil, Sarai Kale Khan Delhi), 51 (Agricultural soil, Dhanaura, U.P) and 157 (Agricultural soil, Dhanaura, U.P.) showed maximum cellulase activity; colonies 169 (Sugar plant soil, Dhanaura, U.P.), 126 (Lake soil, PuranaQuila, Delhi) and 202 (Chemical plant soil, Faridabad, Haryana) showed maximum xylanase activity; colonies 130 (Chemical plant soil, Faridabad, Haryana), 194 (Dumping site soil, Sarai Kale Khan, Delhi) and 184 (Sugar plant soil, Dhanaura, U.P.) showed maximum chitinase activity and colonies 165 (Agricultural soil, Kashipur, Uttarakhand), 122 (Agricultural soil, Nainital, Uttarakhand) and 242 (Great Himalayan National park soil, Teerthan Valley) showed maximum phosphatase activity. The highest xylanase and chitinase producers, colonies 169 and 130 were further analysed to determine the type of protein and its 3D structure. In the present study, two tests (Biochemical and Morphological) of polyphasic characterization of above strains was done. Spore chains of colonies 51, 157, 122 and 126 were of Retinaculiaperti type, colonies 130, 184, 202 and 242 possessed Spirales type of spore chains and in colonies 165, 169 and 194 Rectiflexibles type of spore chain was

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observed. Biochemical studies were performed to check the metabolic status of strains. Colony 169 was found efficient in utilizing L-arabinose, D-fructose, L-arabinose and degrading urea, casein, tween, hypoxanthine. Similarly, colony 130 was found efficient in utilizing D-mannitol, meso-inositol, D-fructose and degrading urea and hypoxanthine. From the results of biochemical and morphological tests it was concluded that the strains from different ecological habitats belongs to genus *Streptomyces*.

**Keywords**: Actinomycetes, Extracellular enzymes, Primary and secondary screening, Protein type and structures, Spore chain morphology, Biochemical studies

**MMI11**

**Biotransformation of hexachlorocyclohexane (HCH) by genetic variants of HCH dehydrochlorinase (LINA)**

Neha Niharika*a,b#, Thomas Fleischmannb, Hans-Peter E. Kohlerb and Rup Lal*c*

aDaulat Ram College, University of Delhi, Delhi-110007

bDepartment of Environmental Microbiology, Eawag, Überlandstrasse 133, 8600 Dübendorf, Switzerland

cMolecular Biology Laboratory, Department of Zoology, University of Delhi, Delhi-110007

**Presenting Author**

nehaniharika3006@gmail.com

Hexachlorocyclohexane (HCH) is a lipophilic polyhalogenated hydrocarbon pesticide which has been used indiscriminately in the last half of the twentieth century. It exists primarily in four isomeric forms, α-, β-, γ- and δ-HCH. The HCH isomers are carcinogenic, highly toxic and have water low solubility. Enzymatic bioremediation for HCH has never been attempted, but it seems feasible as the enzymes responsible for degradation of HCH isomers have been identified. Herein, enzyme HCH Dehydrochlorinase (LinA) can be a potential target for enzymatic remediation as it has broad substrate specificity and several variants of LinA are available with varying HCH degrading capability. The solubility of HCH isomers is less than the K_M-value for the LinA enzyme. In the present study, specificity constant (k_cat/K_M) of LinA- a HCH converting enzyme was determined. The Michaeli’s constant (K_M) reflects how well the enzyme and substrate interact while the catalytic constant (k_cat) reflects the maximum rate of product formation. Specificity constant expressed as M^-1 s^-1 for three LinA variants (LinA1, LinA2 and LinAγ1-7) on α-, γ-, δ- and β-HCH was determined. The result confirmed that undoubtedly both LinA2 and LinAγ1-7 are the enzyme variants possessing fastest dehydrochlorinase activity. These two LinA variants, LinA2 and LinAγ1-7 differ from each other only at two amino acid positions (110 and 111) where alanine from LinA2 is replaced by threonine at 110 position (A110T) and alanine at 111 position of LinA2 is replaced by cysteine (A111C). Hence, two site directed clones (A110T and A111C) were synthesized and their
catalytic efficiency was also determined and compared. These mutations led to a decrease in the catalytic efficiency of the enzymes and suggested that replacement of alanine with amino acids like threonine and cysteine individually could not lead to increase in catalytic activity but presence of both these amino acids together is essential for enhanced activity.

**MMI12**

**Laboratory and field scale bioremediation of hexachlorocyclohexane (HCH) contaminated soils by means of bioaugmentation and biostimulation**

*Nidhi Garg¹, Pushp Lata¹, Simran Jit¹, Naseer Sangwan¹, Amit Kumar Singh¹, Vatsala Dwivedi¹, Neha Niharika¹, Jasvinder Kaur¹, Anjali Saxena¹, Ankita Dua¹, Namita Nayyar¹, Puneet Kohli¹, Birgit Geueke², Petra Kunz², Daniel Rentsch³, Christof Holliger⁴, Hans-Peter E. Kohler² and Rup Lal¹*

¹- Department of Zoology, University of Delhi, Delhi 110007, India  
²- Swiss Federal Institute for Aquatic Science and Technology (Eawag), U¨ berlandstrasse 133, 8600 Dubendorf, Switzerland  
³- Laboratory for Functional Polymers, Swiss Federal, Laboratories for Materials Science and Technology, (Empa), 8600 Dubendorf, Switzerland  
⁴- EPFL-ENAC-ISTE-LBE, Station 6, 1015 Lausanne, Switzerland

**Presenting Author**

nidhigarg1804@gmail.com

Hexachlorocyclohexane (HCH) is an organochlorine pesticide that was used extensively for the control of agricultural pests and vector borne diseases. HCH was marketed in two formstechnical HCH and Lindane. Technical HCH contains a mixture of five isomers α- (60–70 %), β- (5–12 %), γ- (10–12 %), δ- (6–10 %) and ε-HCH (2–3 %) which was in use until the 1950 ties. Lindane consisting mainly of γ-HCH (99 %) and it was used worldwide from about 1950 to 1980. Among all the isomers, only γ-HCH possesses insecticidal properties. Purification of one ton of γ-HCH resulted in the formation of 8–12 tons of ‘HCH muck’ that mainly consisted of the remaining isomers. This HCH muck was discarded in the vicinity of industrial units that produced γ-HCH, creating many HCH dumpsites. In the present study HCH contaminated soils were treated for a period of up to 64 days *in situ* (HCHdumpsite, Lucknow) and *ex situ* (University of Delhi) in line with three bioremediation approaches. The first approach, biostimulation, involved addition of ammonium phosphate and molasses, while the second approach, bioaugmentation, involved addition of a microbial consortium consisting of a group of HCH degrading sphingomonads that were isolated from HCH contaminated sites. The third approach involved a combination of biostimulation and bioaugmentation. The efficiency of the consortium was investigated in laboratory scale experiments, in a pot scale study, and in a full-scale field trial. It turned out that the approach of combining
biostimulation and bioaugmentation was most effective in achieving reduction in the levels of $\alpha$ and $\beta$-HCH and that the application of a bacterial consortium as compared to the action of a single HCH degrading bacterial strain was more successful. Although further degradation of $\beta$- and $\delta$-tetrachlorocyclohexane-1,4-diol, the terminal metabolites of $\beta$- and $\delta$-HCH, respectively, did not occur by the strains comprising the consortium, these metabolites turned out to be less toxic than the parental HCH isomers.

**Keywords:** Hexachlorocyclohexane, Biostimulation, Bioaugmentation, Consortium and Toxicity

**The Binding affinities as well as interaction of rifamycin analogues with RNA polymerase**

*Nirjara Singhvi, Rup Lal and Yogendra Singh*

Department of Zoology, University of Delhi, Delhi-110007

**Presenting Author**

nirjara20@gmail.com, Ph: 011-27666254

Rifamycin produced by *Amycolatopsis mediterranei* can easily diffuse to tissues, living cells, and bacterial cells. The drug impairs metabolism of *Mycobacterium tuberculosis*, the causative agent of tuberculosis. This is due to its specificity for bacterial RNA polymerase. Of all the RNA polymerase subunits, the $\beta$ subunit is the second-largest subunit, and is encoded by the rpoB gene. The $\beta$ subunit contains active center responsible for RNA synthesis. Rifamycin binds in the pocket of $\beta$ subunit of RNA polymerase with high affinity thus inhibiting initiation of RNA synthesis. For this objective, Surface Plasmon Resonance technique can be used that is based on the principle of detection of label free interactions between two different molecules i.e the immobilized ligand attached to the metal surface on the sensor chip and the mobilized analyte present in the solution. In our case, the mobile analyte will be the purified Rifamycin analog and the immobilized ligand will be RNA polymerase. With the increasing binding of analog with RNAP the shift in the sensogram peak will be observed. Different mutants of RNAP will be used to check for the affinity with wild type rifamycin B as the control.

**Taxonomical Characterization of Pedobacter sp. nov., isolated from hexachlorocyclohexane contaminated soil.**

*Pooja Rani*, *Nitish Kumar Mahato*, *Komal Kamra*, *Yogendra Singh* and *Rup Lal*
A Gram-stain-negative, light brown pigmented, aerobic, short-rod shaped bacterial and non-motile strain PR1\textsuperscript{T}, isolated from the hexachlorocyclohexane contaminated soil was subjected to taxonomical characterization using polyphasic approach of bacterial taxonomy. 16S rRNA gene sequence based phylogenetic analysis delineated strain PR1\textsuperscript{T} to the genus *Pedobacter* showing highest sequence similarity with strain *Pedobacter zeaxanthinifaciens* TDMA5\textsuperscript{T} (96.5%). Range of pH and salinity at which strain PR1\textsuperscript{T} can grow was 6-10 and 0-3%, respectively. Strain PR1\textsuperscript{T} was catalase, oxidase negative and did not hydrolyze gelatin. Growth of strain PR1\textsuperscript{T} has shown sensitivity towards tetracycline, oxytetracyclin, gentamycin, kanamycin, ciprofloxacin, vancomycin, chloramphenicol and rifampicin while resistance to gentamycin, penicillin, ampicillin, polymixin B, nalidixic acid and amikacin. Phosphatidylethanolamine, phosphoaminolipid and phospholipid were detected as major polar lipids present in strain PR1. C\textsubscript{15} : 0, iso-C\textsubscript{17} : 0, summed feature 3 were detected as major fatty acids in the cell membranes of strain PR1\textsuperscript{T} while menaquinone-7 and sym-homospermidine were present as the major respiratory quinone and polyamine, respectively. Genotypic, phenotypic and chemotaxonomic analyses demonstrated that strain PR1\textsuperscript{T} is a novel member of genus *Pedobacter*, for which the nomenclature *Pedobacter sordidisoli* sp. nov. has been proposed. *Pedobacter sordidisoli* PR1\textsuperscript{T} (=KCTC 52496\textsuperscript{T} =CCM 8720\textsuperscript{T} =MTCC 12546\textsuperscript{T}) is the type strain.

**MMI15**

**Phylogenetic characterization of antibiotic producing Actinomycete strains from diverse ecological habitats**

Monisha Khanna Kapur\textsuperscript{1*}, Prateek Kumar\textsuperscript{1}, Payal Das\textsuperscript{1}, Munendra Kumar\textsuperscript{1}, Renu Solanki\textsuperscript{1}

\textsuperscript{1}Acharya Narendra Dev College, University of Delhi, Govindpuri, Kalkaji, New Delhi-110019,

Presenting Author

prateekzoologist@gmail.com

Actinobacteria are major producers of important biomolecules, accounting for 70-80% of secondary metabolites available commercially. Its various genera are known for production of different classes of antibiotics. Polyketides and non-ribosomal peptides produced by actinomycetes represent a large group of antibiotics. Microbial pathogens however, are developing resistance to existing antibiotics. There is an urgent need to discover and develop new therapeutic compounds with unique modes of action. In the current study, actinomycete strains representing diverse ecological
habitats were selected. These strains have been screened in a previous study for production of antibiotics. B.69 (agricultural soil, Pachmarhi, Madhya Pradesh) showed activity against *Bacillus cereus* and tentative structure of its compound was found similar to Mycinamycin III, L3.41 (HCH pesticide contaminated soil, Lucknow, Uttar Pradesh) against *Bacillus cereus* and *Fusarium oxysporum* and its compound had similarity to Actinomycin D, L3.46 (pesticide contaminated soil, Lucknow, Uttar Pradesh) against *Bacillus cereus*, *Candida albicans*, and *Fusarium oxysporum* and tentative structure of its compounds had similarity to Mycinamycin and Xantholipin. Antibiotic activity of some other strains was also investigated simultaneously. In the current investigation, the morphological, biochemical and 16S rRNA gene studies of these strains was done. Spore chain type was Retinaculiaperti in RI.24, S.4A, S.43, SL.4, and 51, Rectiflexibles in B.69 and RI.30 and Spiral in L3.41, L3.46 and 196. Biochemical studies were performed to check the metabolic status of the strains. Comparison of 16S rRNA gene sequences of strains with database indicated that these belong to genus *Streptomyces*. Clade member of B.69 is *Streptomyces atriruber* (99.78% similarity), for L3.41 the clade member is *Streptomyces parvulus* (100% similarity), while for L3.46 it is *Streptomyces samsunensis* (99.85% similarity). Based on the results of morphological, biochemical and 16S rRNA gene studies it was concluded that antibiotic producing bacterial strains isolated from different ecological habitats belongs to genus *Streptomyces*.

**Key words:** Actinobacteria, Antibiotic activity, Polyketides, Non-ribosomal peptides, Structural analyses, Morphological, Biochemical and 16S rRNA gene studies.

**MMI16**

**Comparative genomic analysis of the genus *Tessaracoccus* revealing niche specific adaptations.**

Rashmi Kumari, Priya Singh and Rup Lal

Molecular Biology Laboratory, Department of Zoology, University of Delhi, Delhi-110007

**Presenting Author**
rash21289@gmail.com, Ph: 011-27666254

Genus *Tessaracoccus* consists of gram-positive, facultative anaerobic bacteria isolated from diverse environment. With only eight published species and only 5 sequenced genomes, the genus *Tessaracoccus* remains underrepresented in the NCBI database. In this study, the draft genome sequence of *T. flavus* RP1ᵀ, a strain isolated from the drainage system of a lindane producing factory situated in Lucknow, India was obtained, annotated, and described giving comprehensive insights into the basic metabolic features of the organism followed by comparative genomic analysis with three other available genomes of the genus *Tessaracoccus*. Phylogenetic analysis of family *Propionibacteriaceae* revealed genus-specific clustering wherein *T. flavus* RP1 was found to be closer to *T. lapidicaptus* IPBSL-7 followed by *T. massiliensis* SIT-7 and *T. oleiagri* GCMCC 1.9159. *Tessaracoccus* species are reported to be facultative anaerobe, the enzyme complexes involved in
anaerobic respiration: DMSO reductase complex, nitrate reductase gene cluster, anaerobic glycerol-3-phosphate dehydrogenase and arsenic mediated anaerobic respiration Ars operon were found to be present in all the four genomes, depicting their role in the survival of these organisms under anaerobic condition. Presence of large number of mobile genetic elements, CRISPR elements, prophages and genomic islands (GIs) in the genome reflected horizontal gene transfer (HGT) events. A complete tad locus (tight adherence) was found to be acquired by *T. oleiagri* from the environment through HGT, which might help it to adhere to solid substrate or translocate across surfaces in a flagellar-independent manner. Protein-coding sequences of all the genomes clustered into 5,377 orthologous groups of which subset of core genes contained 1,368 genes. An “open” pan-genome was predicted for the genus, where new genes will be added for each newly sequenced genome. Thus, this study provides an evidence for niche specific adaptations these organisms have developed to cope up with stressed environment.

**Soil ecosystem - an insight into ciliate diversity from Delhi**

Renu Gupta¹, Seema Makhija², Jeeva Susan Abraham², Sripoorna Somasundaram² and Ravi Toteja²

¹Zoology Department, Maitreyi College, University of Delhi, Delhi, India.

²Ciliate Biology Lab, Acharya Narendra Dev College, University of Delhi, Delhi, India.

**Presenting Author**

guptar17@gmail.com; Ph: 8800188515

The soils of India inhabit unexplored microbial abundance. Preliminary investigations of soil ciliate biota have shown the availability of a vast number of soil ciliates. The complexity and unrecorded diversity is baffling. The objective of the present study was to characterize the ciliate community and assemble and disseminate relevant observational data on the diversity and identification of soil ciliates from in and around Delhi region. Random sampling was done and the soil samples collected contained plant roots and litter of leaves and algal material. All collections were analysed for ciliates by inspecting about 2 ml of the run-off on days 2, 7, 14, 21, and 28. Detailed morphological and morphogenetic characterization was performed after culturing the cells *in-vitro*. Ciliates found belonged majorly to three different groups, viz., oxytrichids, amphisiellides and stichotrichines. The oxytrichids showed the most abundant distribution. 17/21 genera belonged to Oxytrichidae, 2 to Amphisiellidae and 2 to Stichotrichines with each genus comprising of more than one species. In addition, colpodids and spathidids were also present in almost all the soil samples and were excysting quickly. This speaks about the adaptability and survival of these ciliates in different ecological niches. The huge Indian soil ciliate biodiversity, their survival strategies and resilience are worth further exploration.
Framing the diversity and functional dynamics of sulphur contaminated site Kheer Ganga in Northern Himalayas, Himachal Pradesh, India by using metagenomic approach.

Shekhar Nagar, Nitish Kumar Mahato, Roshan Kumar, Utkarsh Sood, Vipin Gupta, Mallikarjun N. Shakarad, Yogendra Singh, Rup Lal, Ram Krishan Negi

1 Fish Molecular Biology Lab, Department of Zoology, University of Delhi, Delhi, India
2 Molecular Biology Lab, Department of Zoology, University of Delhi, Delhi, India
3 Evolutionary Biology Lab, Department of Zoology, University of Delhi, Delhi, India

Presenting Author
nagar.shekhar90@gmail.com

The hotspring at Kheer Ganga, Himachal Pradesh, India represents an example of extremophilic conditions through continuous accumulation of sulphur and mesothermophilic environment. Due to these adverse conditions, it is probable that the site might harbor a diverse group of microbial community. Therefore, our focus was to explore the distinct genus, community relationships and the evolutionary changes by using metagenomic approach. This includes the recognition of archeal and bacterial diversity and determining the habitat specific minimal metabolism through examining three different habitats (microbial mat, sediment, water) from an open source of Kheer Ganga hotspring. For this, the extraction of metagenomic DNA (metaDNA) was performed using both crude method and kit method. The metagenomic DNA was further sequenced using Illumina platform, Hiseq 2000. The data obtained is further in process of analyzing the microbial diversity and functional aspects in hotspring, or more generally in mesophilic habitats. We hope that this will unravel the hidden potential of microorganisms inhabiting at such extreme niches and consequently, we are able to consider that those microorganism exists, due to its survival ability as an emerging trait and mutation as a potentially biased adaptation.

Potential role of phages in applications of microbial inoculation technologies for improving soil fertility

Sirawung Raiping and Radhey Shyam Sharma*

Bioresources & Environmental Biotechnology Laboratory, Department of Environmental Studies University of Delhi, Delhi-110007, India

Presenting Author
radheyss26@gmail.com
Biofertilizers have been proposed as an environmentally friendly option to chemical fertilizers. However, the efficacy of selected microbes for biofertilizers has been a major concern. Microbes, such as mineral solubilizers, nutrient mobilizers, phytohormone producers and antagonistic microbes serve as potential biofertilizers. However, the population density, colonization ability and genetic stability after inoculation affect their efficacy in the environment. The inoculated microbes (biofertilizers) need to compete with the native microbes and maintain their effective viable population to perform the desired ecological functions. To achieve this goal, they need to combat several abiotic and biotic stresses prevalent in the targeted soil. Being selected for their abiotic tolerance, the microbes face biotic stresses as the most important challenge for their performance in the environment. Bacteriophages are one of the important biotic stresses, which affect the ecology and evolution of bacterial communities. Being lytic, they serve as selection pressure and determine the species diversity and population size of the bacterial community, however, as temperate they influence the ecological fitness of individuals and influence the genetic diversity of the bacterial community. The phages have been widely used as a biocontrol agent to control the spread of harmful bacteria. However, the role of phages to engineer the bacterial community has not been visualized. Therefore, we have isolated and purified a plant growth promoting rhizobacteria (PGPR) from a wild grass. The bacterial strain was characterized for selected PGPR traits. The bacteriophage of the selected bacterium was also purified, and its relationship with selected bacterial strain was analyzed. Based on the study, we suggested the potential application of the phage for influencing the soil fertility. The study would serve as a step towards converting the ecological potential of phages into a reality for achieving sustainable soil health through improved microbial technology.

MMI20

Use of ciliates in biomonitoring heavy metal pollution

S. Sripoorna1, Jeeva Susan Abraham1, Swati Maurya1, Ravi Toteja1, Seema Makhija1* and Renu Gupta2

1Ciliate Biology Laboratory, Acharya Narendra Dev College, University of Delhi
2Maitreyi College, University of Delhi

Presenting Author
spoorna4@gmail.com

Heavy metals are widely distributed on the earth’s crust, and are present in the structure of various minerals which occur in the environment. Anthropogenic activity elevates the concentration of such elements, mainly in aquatic systems. Therefore, heavy metal pollution is of major concern these days. Due to heavy metal induce stress there is induction of stress proteins like Heat Shock Proteins (HSPs) and Metallothioneines (Mts). Heavy metal induced stress response has been reported in several multicellular organisms but this study is first of its kind from India where we are using ciliates to
assess heavy metal toxicity because of their small size, easy to cultivate, short generation time and absence of cell wall. In the present study, ciliates were exposed to varying concentrations of heavy metal under laboratory conditions. Induction of genes like hsp 70 and metallothionein was evaluated by qPCR. Preliminary studies suggests that the gene expression increased significantly in metal treated ciliates against the control cells indicating that this gene can be used for biomonitoring toxic effects of heavy metals in the aquatic or terrestrial ecosystem. Also, hsp70 gene has been sequenced and characterized.

**MMI21**

**Correlation of HCH Residues and Metagenomic Lin protein sequences at contaminated sites**

_Vivek Negi, Pooja Rani, Amit Kumar Singh and Lal R_

Molecular Biology Laboratory, Department of Zoology, University of Delhi, Delhi - 110007

_Presenting Author_

viveknegi2006@gmail.com

The metagenomic profiling of a complex community in pond sediment and it’s correlation with the hexachlorocyclohexane (HCH) residue levels was performed to highlighted the functional profiles of contaminated sites. The residue level of hexachlorocyclohexane (HCH) at HCH contaminated dumpsites were compared with the other nearby or related sites. Sediment and water samples were collected from different hexachlorocyclohexane (HCH) contaminated sites for residue analysis. These different sites include dumpsite (DS), solexa data of dumpsite (SolexaDS) and two samples from the pond sediment near the pesticide industry (PS1 and PS2). The study also included the previous analysis sites i.e., 1Km and 5Km away from the DS i.e., 1KM and 5KM respectively. The residue analysis of HCH contaminated sites correlates well with the degree and distribution of LinA and LinB proteins. Further, a gene-centric approach was used to investigate the prevalence of LinA and LinB protein sequences in the metagenomes of sites with different level of HCH contamination. The study showed that LinA and LinB sequences from the metagenomes were found to cluster in HCH stressed niches, thereby providing evidence in support of the proposed evolution of these proteins in the HCH-contaminated environment.
Session A
(Microbe-Plant Interactions)
Occurrence and distribution of G-quadruplexes in Phytoplasmanomes

Amrita Singh¹, Neetu Tyagi², KV Bhat² and Suman Lakhanpaul¹

¹Department of Botany, University of Delhi, Delhi-110007
²National Bureau of Plant Genetic Resources, Delhi-110012

Presenting Author

amrita.botany@gmail.com, Ph: 9717949561

Phytoplasmas (genus ‘Candidatus Phytoplasma’) are phytopathogenic bacteria belonging to the class Mollicutes. They are obligate parasites of plant phloem tissue and are transmitted by phloem sap sucking insects. Different strains of Phytoplasma have been associated with considerable damage in an array of economically important plants worldwide. So far, genomes of four phytoplasmas have been completely sequenced. They include ‘Ca. P. asteris’ strains OY-M and AY-WB, ‘Ca. P. australiense,’ and ‘Ca. P. mali’. G-quadruplexes are non-canonical secondary structures that form within guanine-rich DNA and/or RNA sequences. Several studies have indicated the role of G-quadruplexes in important biological functions including virulence in case of pathogens. Identification and distribution patterns of G quadruplexes in the genomes are increasingly gaining importance. However, no studies on the presence and the role of G-quadruplexes in the phytoplasma genome are available. This study was aimed at detecting putative G-quadruplex sequences in the genomes of four phytoplasmas using QGRS mapper software. The parameters were optimized for number of Gs, loop length and the maximum length of the quadruplex sequence. Preliminary studies have revealed non-uniform distribution of putative G-quadruplexes in the phytoplasma genomes. However, different patterns of correlation between the number of genes in a specific region and putative G-quadruplexes in the corresponding sites could be detected. Of all the four phytoplasma genomes used in this study, most distinct pattern was observed in the genome of Candidatus Phytoplasma mali, which is the smallest genome among the taxa analysed and has a linear chromosome as compared to circular in the other three genomes.

Bacterial diversity and genotypic analysis of heavy-metal resistance gene(s) from glass industrial soil of North-Central India

Akash Chaudhary, Ritvesh Gupta and Anubha Sharma*

Amity Institute of Biotechnology, Amity University Uttar Pradesh, Noida- 201313

*Corresponding author

Presenting Author
Isolation and characterization of bacteria from glass industrial soils of North-Central India to determine their diversity and presence of heavy metal resistance gene(s). Microbiological standard media (SLP with nickel) was supplied for enumeration and selection of heavy metal resistant bacteria. The most abundant genus out of 37 bacterial strains comprising of 15 genus, belonged to Microbacterium sp. (10 isolates). Five isolates belonging to different genera were found to be nickel tolerant (24mM) whereas other strains were capable of tolerating upto ~12 mM of other heavy metals e.g. Cd, Co, Zn and Cr. The phylogenetic relationship of the bacterial isolates has been investigated through 16S rRNA gene analysis and the presence of czc, ncc or/and cnr genes confirmed the metal tolerance properties of these bacterial species. Bacterial isolates AS15, AS28 and AS30 exhibited highest metal tolerance and they may be used for eco-toxicological and bioremediation studies.

Key words: Heavy metals, Bioaugmentation, czc gene, nccA gene, cnr gene, Efflux pump, Nickel, Diversity

MPI24

Growth performance, anti-microbial and phytochemical analysis of oil from Jatropha curcas grown on fly-ash soil amendments

Vijay Bharath V, Akshita Chhabra, Seema Raj, Sumedha Mohan, Praveen Dahiya

1 School of Basic and Applied Sciences, K.R Mangalam University, Gurgaon, India
2 Amity Institute of Biotechnology, Amity University, Noida-201303, Uttar Pradesh, India

Presenting Author
akshitachhabra34@gmail.com, vijayvel29@outlook.com, pdahiya@amity.edu, smehta1@amity.edu

Fly-ash is an important combustion residue and the most conversant industrial byproduct. It is a source of plant’s macro nutrients and micro nutrients. It is known to increase the soil pH, promote plant growth, improve the agronomic properties of the soil and cause a significant increase in soil nutrients such as- Na, K, Ca, Mg, and Fe. The striking variations towards the sensitivity of fly ash are observed in the growth performance and biochemical factors of plants. Jatropha curcas (Euphorbiaceae) is a biodiesel plant grown in various parts of India and other tropical countries. Its oil is used for the treatment of sciatica dropsy, paralysis, rheumatism, dysentery, diarrhoea and certain skin ailments. An attempt was made to examine the growth performance, physicochemical constituents and antimicrobial activity of Jatropha curcas plants oil extracts using various concentration of fly ash and soil (100%soil, 25% fly ash+ 75% soil and 50% fly ash+ 50% soil). In the present investigation, the oil extracts were evaluated for phytochemical constituents, antimicrobial activity and TLC bio-autography assay. From the phytochemical studies, it was
concluded that it contains the secondary metabolites such as alkaloids, saponins, flavonoids, anthraquinone, tannins, terpenoids, reducing sugar, cardiac glycosides etc. The oil extracts obtained from leaf samples grown on 25% and 50% fly ash-soil amendments showed broad antimicrobial activity against *Staphylococcus aureus, Escherichia coli* and *Klebsiella pneumonia* using disc diffusion method. Thus, this suggests that fly ash which contains certain heavy metals may prompt the production of bioactive components thereby increasing the medicinal potential of the plant.

**Keywords-Jatropha curcas**, Fly-ash-soil amendments, Physico-chemical analysis, Antimicrobial activity.

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**MPI25**

**Dynamics of soil nifH community structure and function in the cotton rhizospheres**

Sandhya Rai¹*, D.K. Singh² and K. Annapurna³

1 Department of Zoology, Deshbandhu College, University of Delhi, New Delhi-110 019  
2 Department of Zoology, University of Delhi, New Delhi-110 007  
3 Division of Microbiology, Indian Agricultural Research Institute, New Delhi-110 012, India  

**Presenting Author**  
sandhvarai1901@gmail.com

Microbial community structure and diversity have significant effects on soil health and processes. Numerous microorganisms mediated biogeochemical processes are crucial in maintaining soil ecology. Biological Nitrogen fixation is indispensable in maintaining the nitrogen budget of the soil ecosystem as it catalyzes the reduction of atmospheric nitrogen (N₂) gas to biologically acceptable ammonium. The relationship between diazotrophic community structure and functioning has not yet been investigated much and thus, there are lacunae in the existing knowledge which need to be addressed. Rhizospheric soils of cotton at different growth stages was examined for changes in diazotrophic community structure and functioning through traditional assays and molecular tools. Soil samples were analyzed for nitrogenase assay through ARA. Community DNA was subjected to PCR amplification targeting ~370bp fragment of the *nifH* gene. RFLP (Restriction Fragment Length Polymorphism) and T-RFLP (Terminal Restriction Fragment Length Polymorphism) of *nifH* amplicons were carried out for abundance, distribution and divergence of diazotrophic community. Twelve distinct TRF's and two dominant TRF’s viz: 56bp and 88bp were identified in all the samples. However, there was a marked difference in the relative abundance of these two TRF’s. A significant temporal shift of diazotrophic community structure was observed by the change in the relative abundance of TRFs 31, 35, 187 and 355 bp in length with least percentage shown by first sample (C0) and maximum percentage observed in the last sample (C180). Thus, the study highlights the changes in relative TRF abundance to the existence of temporal dynamics of diazotrophic community structure and diversity corresponding to crop growth stages. Interestingly, the pattern of
diazotrophic activity (nitrogenase activity) and the diazotrophic community structure could not be correlated.

Effect of biostimulation and impact of mixed microbial consortia on biodegradation of Chlorpyrifos by microbes isolated from agricultural field
Tanmaya Nayak, Tapan Kumar Adhya, Mrutyunjay Suar, Vishakha Raina*
Environmental Biotechnology Laboratory School of Biotechnology, KIIT University, Campus-11, Bhubaneswar, Odisha-751024
Presenting Author
tanmaya.nayak@kiitbiotech.ac.in

Organophosphorous Pesticides (OPs) are commonly used pest control agents in many countries. Widespread use of these compounds resulted in accumulation in various ecosystem like agricultural soil, water source ultimately affecting insects and humans. Chlorpyrifos (CP), a broad-spectrum pesticide has been used for controlling termites, beetles on agricultural fields & vegetable crops to get rid of termites & beetles by inhibiting acetyl-cholinesterase in the nervous system. Degradation of CP results in the formation of a metabolite TCP (3,5,6-trichloro-2-pyridinol) which is classified as mobile, toxic compound having antimicrobial property. Present study showed bacterial isolates from agricultural soil amended with CP. Three strains Ochrobactrum CPD-03, Microbacterium CPD-20 and Bacillus CPD-33 were identified based on 16s rRNA approach. Effect of biostimulation on the CP degradation in stimulated and non-stimulated conditions were performed resulting 88% CP degradation in stimulated condition and 66% degradation in non-stimulated condition respectively. This suggested that CP degradation is stimulated upon addition of nutrients which had provided a suitable indigenous environment for CP degradation. Corncob acted as an efficient carrier material for CPD-03 viability in soil for degradation. It was also found that, the consortia MC-1 had shown enhanced degradation efficiency in liquid media (80% degradation efficiency in 24 hours) and in presence of carrier material (60-65% degradation efficiency in 8-10 days). Moreover, plant growth promoting abilities of CPD-03 strain offer great promise for increased and sustained crop productivity even under pesticide contaminated environment. This can be potential for in situ bioremediation of contaminated soil ecosystem.

Key Words: Chlorpyrifos, TCP (3,5,6-trichloro-2-pyridinol), Resting cell assay, Degradation efficiency, Biodegradation, Biostimulation, DGGE
Microbial fertilizers helping plants to reduce insect induced oxidative stress

Garima Sharma and Vartika Mathur

Animal-Plant Interactions lab, Department of Zoology, Sri Venkateswara College, University of Delhi, Benito Juarez Marg, Dhaula Kuan, New Delhi, India

Presenting Author

vmathur@svc.ac.in

Under insect attack, plants induce various responses that are manifested as chemical and morphological changes. One of these responses causes the increase in synthesis of reactive oxygen species (ROS) which causes oxidative stress condition in local plant tissues. This leads to the triggering of a systemic response throughout the plant. To stabilize the oxidative damage, plant cells produce antioxidant enzymes. However, these responses utilize a substantial share of plant nutrition, which are diverted from growth to defence response. Use of microbial fertilizers is emerging as a promising plant growth promoting strategy for farmers. However, it is not known whether these microbial fertilizers boost both plant growth and immunity or is microbial fertilizer-facilitated growth compromised as a trade-off for immunity. We therefore evaluated the effect of phosphate solubilizing bacteria (PSB) on three antioxidant enzymes (superoxide dismutase, SOD; peroxidase, POD and glutathione reductase, GR) of Indian mustard (Brassica juncea) and tomato (Lycopersicum esculantum) after 3h and 9h of damage by the generalist insect Spodoptera litura. In both crops, antioxidant activity increased from the initial hour itself. In tomato, PSB supplemented plants, higher activity was seen in SOD and GR irrespective of insect damage. However, non-supplemented damaged plants displayed higher POD level at 3h which remained 3.5 times higher even after 9h. In the same set of plants, GR levels also increased 5 times by 9h, indicating increase in oxidative stress in plants upon insect damage. In mustard, SOD levels in PSB supplemented plants remained significantly lower than control plants at 3h and decreased subsequently by 9h. Although at 3h, POD and GR activity in damaged plants was significantly different from undamaged plants irrespective of PSB supplementation, by 9h its level were decreased to baseline indicating no oxidative stress. In light of the above results, it can be concluded that PSB, which is a well-known plant growth promoter, also helps in reducing oxidative stress. However, before spontaneously equating better growth to better immunity, fitness of PSB-supplemented plants must be compared in an environment that includes herbivores.
Session A
(Microbe-Animal Interactions)
Role of serine/threonine phosphorylation in *Bacillus Anthracis*

Aakriti Gangwal¹, Neha Dhasmana², Nishant Kumar², Yogendra Singh¹

1. Department of Zoology, University of Delhi, Delhi-110007
2. CSIR-Institute of Genomics and Integrative Biology, Mall Road, Delhi-110007

Presenting Author
aakriti1011@gmail.com

Protein modifications play a very important role in providing proteomic diversity in prokaryotes. The expanded proteome in turn helps the bacterium in regulation of various cellular pathways involved in cell cycle, metabolism, cell architecture, stress responses, protein degradation, pathogenesis and growth. Some of the post translational modifications (PTMs) are phosphorylation, ubiquitination, nitrosylation, methylation, glycosylation, acetylation and lipidation. Among these, protein phosphorylation is the most widely studied and investigated modification. Prokaryotes have many kinases and phosphatases that catalyze the phosphorylation and dephosphorylation of proteins on specific amino acid residues. These protein kinases and phosphatases plays a very important role in different physiological processes in response to various signals and thus helps in the survival and growth of the bacteria. Serine/threonine phosphorylation is one modification among these, which is extensively studied in eukaryotes, however in prokaryotes it is still in its infancy. Genome analysis revealed that the enzymes responsible for these modifications show high homology with their eukaryotic counterparts and thus named eukaryotic like serine/threonine kinases and phosphatases (eSTKs and eSTPs). *Bacillus anthracis*, the causative agent of anthrax is a Gram-positive, aerobic, spore-forming bacterium. The primary infectious form of *B. anthracis* is a spore that infects the host via three different routes, which are inhalational, gastrointestinal or cutaneous infection. However, the spores are generally non-toxic and cannot manifest the disease alone; rather, it is the germination process that is the cause of the pathology with the secretion of toxins and virulence factors. Our work focuses on phosphatases and kinases of *B. anthracis* involved in the regulation of sporulation and spore germination. We are also trying to find out novel phosphatases that might play a role in this phenomenon for a more effective disease prevention strategy and treatment.

**MAI29**

Antarctic psychrophilic microorganisms for diverse biotechnological application

Abhishek Chauhan*, Laxmikant Bhardwaj Anuj Ranjan and Tanu Jindal

Amity Institute of Environmental Toxicology, Safety and Management, Amity University, Sector-125, Noida, Uttar Pradesh, India

Presenting Author
akchauhan@amity.edu
Antarctica is a continent of extremes; highest, driest, coldest, windiest, emptiest land largely covered by the Antarctic ice sheet. Approximately 2% of the continent remains free from ice and snow which is available for colonization by plants, animals and microbes. It is one of the most pristine and untouched regions of the planet, geographically isolated from other continent, where low temperature, frequent freeze-thaw cycles, periods of prolonged dark in winter, different pH levels, low organic nutrient and water availability, strong winds and UV radiation are found. The Larsemann Hills area (69°20’–69°30’S, 75°55’–76°30’E) contains more than 150 lakes at different Islands and Peninsulas. Continental Antarctica possesses a characteristic flora and fauna, which varies both qualitatively and quantitatively among the different habitats. Bacteria and other microorganisms are usually present in numbers far lower than those encountered in temperature regions. In the present study, samples were analyzed for common human pathogenic microorganisms (Escherichia coli, Salmonella and S. aureus. Pseudomonas) and other useful microbes. Nine lake water and soil samples were collected by using gamma sterilized bottles and bags. The samples were transported to the lab in while maintaining the temperature 1-4°C with ice pack enveloped conditions. Samples were studied for Psychrophilic bacterial count, Pseudomonas spp., Staphylococcus aureus, Salmonella and Total MPN Coliform per 100 ml. Psychrophilic counts were found in the range of 12 cfu to 1.6×10² cfu in all the samples. MPN Coliform per 100ml was found to be absent in all the samples. No growth and characteristics colonies observed when tested for Salmonella and S. aureus. Pseudomonas sp. was found in ST-2 lake water sample as characteristics colonies (Optimum Growth) were observed on selective media at 22 and 25°C. Actinomycetes spp. were also present in soil samples. Further morphological, biochemical and molecular identification are in progress to study the diverse biotechnological application.

Keywords: Antarctic Microorganism, Antarctic Freshwater Lake, Larsemann Hills area, East Antarctica

Evaluation of ground water quality through leaching of sewage waste in Delhi, India
Ashwani Kumar, Anuj Ranjan, Khushbu Gulati, Shalini Thakur, Tanu Jindal
Amity Institute of Environmental Toxicology, Safety and Management, Amity University, Noida, Uttar Pradesh
Presenting Author
aranjan@amity.edu

Many developing countries are struggling to fulfil the requirement of safe drinking water due to increasing population. Handling groundwater resources and hazard assessment include identification of proxy indicator for bacterial contamination as crucial step. This study was planned to evaluate groundwater potability by leaching of contaminants (physico-chemical and microbial) from unlined
drains using lysimetric set ups imitating natural field conditions. Estimation of mean values of physico-chemical and microbial parameters found higher than permissible limits of World Health Organization (WHO) in control leachate, drain leachate as well as in drain samples. However, all the groundwater samples for preliminary test were found within WHO permissible limits. Physico-chemical parameters in drain leachate were significantly higher as compare to groundwater samples. Electrical conductivity (272 %), total dissolved solid (230 %), total hardness (420 %), alkalinity (166 %), biological oxygen demand (265 %), chemical oxygen demand (651 %) and dissolved oxygen (87 %) were found in higher range than control samples. Total bacterial count was recorded higher as 74 cfu/ml in ground water, 9.8 × 10³ cfu/ml in Khyberpass control leachate and 3.9 × 10⁴ cfu/ml in Khyberpass drain sample leachate. This study has demonstrated that when water is passing through the soil column of the lysimeter the microbes as well as the chemical pollutants adsorbed to the soil particles leached down to the aquifer and diluted into the ground water ecosystem. The study was carried out on unlined drains (non-concrete). Hence the unlined drains and unprocessed effluent water joining the water streams are additional risk factors for groundwater contamination.

Key words: Groundwater, Lysimeter, Leaching Pollution, Unlined drain

Diet and lifestyle – factors modulating the population dynamics of gut microbiota and human health

Anuradha Sharma¹, Arpita Bhatt¹, Zainab Afreen¹, Dr. S. Nanda², Anna Senrung¹, Dr. Anju Jain¹

1. Department of Zoology
2. Department of Biochemistry, Daulat ram College, University of Delhi

Presenting Authors
anuradhaaiims.as@gmail.com, arpitabh119@gmail.com, syedazainab.1998@gmail.com

The health of an individual is governed by his/her lifestyle and dietary practices. The human body harbours an enormous and diverse number of microbes in the GI tract. This gut microbiota is influenced by our eating habits and lifestyle. Roughly, there are ten times as many microorganisms within the gastro-intestinal (GI) tract of humans as there are somatic cells within the body. The impact of microbiome can be beneficial or detrimental depending on their relative identity and abundance of constituent microbial population. Studies have shown that some bacterial phyla like Actinobacteria, Bacteroidetes, Firmicutes, and Proteobacteria are the most populated ones to be influenced by dietary habits and lifestyle. The amount and the type of macromolecule consumption in our diet is the major factor responsible for the diversity of gut microbiota. The non-dietary lifestyle factors like smoking, stress, obesity along with geographical and environmental factors also are known to have a significant impact on the gut microbiota. The interaction of the host with the diverse array of gut microbiota determines the host’s immunity standards. The diverse population of
beneficial gut bacteria is important to keep harmful bacteria away as they compete for nutrients and sites of colonisation. Here, in this review paper, we summarise the studies performed across the world determining the regional and dietary effects on the population dynamics of microbes in the gut with relevance to human health.

**MAI32**

**Molecular and biochemical characterization of the microbial diversity obtained from the intestinal content of two exotic carps; Mirror carp (*Cyprinus carpio var. specularis*) and Silver carp (*Hypophthalmichthys molitrix*)**

*Bhawna Dhawan and R.K. Negi*
Department of Zoology, University Of Delhi

**Presenting Author**
bhawna.dhwn@gmail.com

Different investigations (culture dependent or culture independent) are used to identify bacterial isolates obtained from different environmental samples. In the present study, Culturable approach has been used to identify the microbial diversity in fish gut sample obtained from the fishes collected from Gobind Sagar Reservoir in Himachal Pradesh. For molecular characterization of bacteria, 16S rRNA gene amplification tool has been used to identify the isolates. Along with the fish gut, water samples were also used to isolate the bacterial strains which sum up to 23 different isolates. For further analysis, different biochemical and antibiotic resistance were analyzed. Among these, an isolate designated as BSCA has shown significant 16S rRNA gene sequence similarity with species *Streptomyces lavenduligriseus*. Strain of this species was found to produce secondary metabolites that are antimicrobial in action and are in interest of researchers. Here, strain BSCA also identified with the ability to produce different secondary metabolites. Hence, in order to identify them, Gas Chromatography Mass Spectroscopy (GC-MS) has been performed for the identification of biochemical components. Also, antimicrobial activity has been tested against these pathogenic isolates. Methods like Cross-streak, antibiotic-disk diffusion, have been done to check the resistance and sensitivity of these bacteria. Further, isolated gut bacteria were screened and quantitatively assayed for enzyme production. Amylolytic, cellulolytic, lipolytic and proteolytic microflora was identified and studied among the isolated gut samples in relation to the fish feeding habit.

**MAI33**

**Understanding the Role of Microbes in Cancer**

*Taru Kohli 2, Mahesh S. Dhar 2, Girish Sharma1, 2*

1Amity Center for Cancer Epidemiology and Cancer Research, 2Amity Institute of Biotechnology, Sector 125, Amity University Uttar Pradesh, NOIDA, India

**Presenting Author**
sharmagi03@gmail.com
Microbes can be a double edged sword that can act as either friend or foe, having promising as well as detrimental effects on human health. Some microorganisms are known to cause cancer, as in case of gastric cancer caused by Helicobacter pylori, whereas others such as probiotic lactic acid bacteria (Bifidobacterium, E. coli, Lactobacilli) have demonstrated anti-cancerous potential. These bacteria are also known to produce tumor-suppressing agents. Epidemiological studies revealed that about 20% of cancers have a microbial cause that includes Burkitt’s lymphoma (Epstein-Barr virus, EBV), cervical cancer (human papillomavirus, HPV), gastric cancer (Helicobacter pylori) and liver cancer (hepatitis B and C viruses). This indicates that there is tremendous potential of controlling such microbe–related progressions for cancer prevention. The process of oncogenesis is a multistep process providing abundant opportunities for microbial interventions to prevent cancer and related infections by developing vaccines against oncogenic microbes and deploying them to individuals at risk before exposure. Many bacterial interventions for treatment of cancer are in various phases of clinical trials. The presentation shall discuss the role of microbes in management of some cancers.

**Keywords**: Cancer-causing microbes, probiotic, vaccine.

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**Soil contamination reflects changes in ciliated protist community**

1Harpreet Kaur, 1Shashi, 1Surinder Kaur, 1Laxmi Narula, 1Komal Kamra*, 2Rup Lal, 3Alan Warren

1Ciliate Biology Lab, SGTB Khalsa College, University of Delhi, Delhi, India
2Department of Zoology, University of Delhi, Delhi, India
3National History Museum, London, UK

**Presenting author**

hk2171@gmail.com

River Yamuna maintains a reasonably good quality from its origin in the Himalayas to its entry into Delhi, India. 80% of the pollution in the river’s total length of 1375 km occurs in the 46 km stretch (3.3% of its total length) as it flows through Delhi, rendering the mighty river into a sewage drain. As free-living ciliated protist species differ widely in tolerance to pollutants, the present study was conducted to catalogue ciliate communities (with classical and molecular analyses) at two select locations (soil water interface) along the river – the point where the river enters Delhi (S1) and 17 Km downstream where the largest sewage drain (Najafgarh drain) empties into the river (S2). Soil and water quality at these locations was analysed. Physicochemical parameters show significant increase in the Biological Oxygen Demand, turbidity, sulphates, phosphates and nitrates indicating higher level of pollution at S2 as compared to S1. There was a significant change in the ciliate communities at these two locations, both in soil and in water along the banks. Detailed analyses, showing correlation between ecological parameters of the two collection sites and ciliate communities thereof, will be presented.
A panoramic view on CRISPR/Cas: mechanism, history and application prospects

Harshita Mishra and Rup Lal

Molecular Biology Laboratory, Department of Zoology, University of Delhi, Delhi-110007

Presenting Author

harshitamishra5585@gmail.com

CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats) are the nucleotide sequence composed of spacer-repeat segments, of which spacers are known to have originated from foreign genetic material. Adjacent to these regular spacer repeat sequences lie CRISPR associated (cas) genes which encode various proteins required for cascade of events leading to the cleavage of foreign DNA next time it invades. Cas1 and Cas2 proteins help in acquiring new spacer sequences from plasmid or phage DNA sequences which is called adaptation. Various cas proteins are required in different type of CRISPR/Cas division system for the next step of biosynthesis of small CRISPR RNA called precursor crRNA. This precursor crRNA is processed into crRNA with the help of trans activating CRISPR RNA (tracrRNA) in type II system. Cas9, single effector protein, is required in Type II system while various Cascade (CRISPR associated complex for antiviral defence) proteins are required in other system which leads to the next step of invader DNA cleavage. Cpf1 protein in Type V-A CRISPR-Cas system can process premature crRNA without the necessity of tracrRNA. Crucially required Protospacer Adjacent Motif (PAM), with the help of crRNA:tracrRNA as a guide, identifies self and non self and proceed to make a double stranded cut in foreign DNA. This property of cleaving DNA has been harnessed elegantly in genome engineering for versatile purposes. CRISPR has carved niche of its usefulness in various fields. CRISPR/Cas9 applications are worth mentioning in genome editing for inducing precise Insertion and Deletion (INDEL) mutations, correcting defunct gene, multiplex targeting without off target effects and investing tedious efforts in comparison to other available techniques. It can be utilised in strain typing, differentiating pathogenic bacteria, ex-vivo drug delivery, drug therapeutics, producing biomedical products, tracing cell lineage, cellular barcoding and usage in food microbiology industry. Various web tools are available for guide RNA designing and predicting off targets. The successful clinical applications of CRISPR/Cas system have raised the ethical issues of future designer babies and interference with natural evolution. Here, mechanism of Type II CRISPR/Cas system, chronological history and various mentioned applications are explored.
**Prediction of potential vaccine candidate proteins for bacterial vaginosis by In silico analysis using reverse vaccinology approach**

**Jaspreet Kaur**

Assistant Professor, Department of Zoology, Maitreyi College, University of Delhi, India,

Presenting author

kaurreet21@gmail.com

Bacterial vaginosis (BV) is one of the highly prevalent vaginal disorders of women of reproductive age, causing serious health implications. The pathogenesis of BV is considered a polymicrobial infection, with *Gardnerella vaginalis* as the most predominant bacterial species that is responsible for the production of antibiotic-resistant biofilm on the vaginal epithelium. Since, there is no vaccine currently available against bacterial vaginosis, thus potent vaccine candidates against *G. vaginalis* have been predicted by *in silico* analysis using core proteome of three strains of *G. vaginalis*: *G. vaginalis* 409-05 (NC_013721), *G. vaginalis* ATCC 1409 (NC_014644) & *G. vaginalis* HMP9231 (NC_017456) in this study. Extracellular proteins and proteins localized in cell wall and outer membrane with adhesion probability of $\geq 0.5$, number of trans-membrane helices $\leq 2$ as well as no similarity with human, mouse and pig proteome were selected. We also aimed to predict epitopic peptides of the selected proteins found in core proteome of *G. vaginalis* that bind with class I MHC CD8+ and class II MHC CD4+ molecules. The selected epitopes were also screened for parameters like hydrophillicity, surface accessibility, beta turn and flexibility, which are the required criteria for a potent epitope. Docking analysis of the selected epitopic peptides with their corresponding HLA receptors was also done. The efficacy of the predicted epitopes was observed through substantial data obtained in the present study, though, wet lab experiments would be required to substantiate our results but, it is definitely a step towards focusing the experimental efforts on the subset of potential immunogenic peptides that will increase the probability of success in developing subunit vaccine against bacterial vaginosis.

**Physico-chemical and biological analysis of soil samples collected from different sites in and around Delhi, India.**

**Jeeva Susan Abraham¹, S. Sripoorna¹, Renu Gupta², Ravi Toteja¹ Swati Maurya¹, Geetu Gambhir¹, D.K. Singh³and Seema Makhija¹**

¹Ciliate Biology Laboratory, Acharya Narendra Dev College, University of Delhi; ²Department of Zoology, Maitreyi College; ³Department of Zoology, University of Delhi

Presenting author

jeeva18.SA@gmail.com
India is endowed with a wide variety of climates and soils and has a rich biodiversity in both fauna and flora. Soil types are a major factor in determining what types of plants will grow in a certain area as plants use inorganic elements from the soil. In the present study, we investigated the relationships between the soil ciliate community and environmental factors at different habitats in and around Delhi. The physico-chemical analysis of soil is based on parameters such as soil texture, moisture content, pH, electrical conductivity, organic carbon content, organic matter and nitrogen content etc. In addition to physico-chemical parameters, the presence of microorganisms like fungi, bacteria and other microscopic life forms available within the soil are also vital. Ciliates are virtually present in all environments where eukaryotic life has been found. That is why they are one of the most successful groups of protists. Ciliated protozoa have been reported to be potential bio-indicator of soil health and quality due to their unique characteristics and key role in soil processes. In the present investigation, soil sample taken from various sites were analyzed for the presence of ciliates. Ciliate species belonging to a total of 10 genera were found in the soil sample. Ciliates identified were Oxytricha sp., Vermioxytricha sp., Gastrostyla sp., Sterkiella sp., Amphisiella sp., Paraurostyla sp. and Lacrymaria sp., Colpoda sp., Coleps sp., Spathidium sp. An in depth investigation will allow us to create a key on the basis of quality of soil and type of ciliate species. This study may also help in assessing soil quality on the basis of type of ciliate species present in soil samples collected from various ecotypes. Although many studies on soil ciliates have been carried out though there is still little knowledge about relationships between soil ciliate communities and physicochemical properties.

MA138

Role of environmental factors in the survival of multi drug resistant (MDR)

Jyoti Sharma1*, Anuja Mishra

1Department of Biotechnology, IAH, GLA University, Mathura-281406, U.P., India

Presenting author
js561734@gmail.com

Multi drug resistance is the resistance of microbes against a number of drug’s targets which allows them to thrive in the presence of specific drug molecules. It is one of the most alarming problems of the 21st century towards public health. A bacterium which carries several antibiotic resistance genes within its genome are referred to as multi drug resistant or superbug or a super bacteria. Antibiotic resistance genes usually resides on the extra-chromosomal genetic material present in a bacterium i.e., over its plasmids DNA. Thus facilitating their transfer to the wild varieties and transforming them into MRD strains. MDR is a uniquely contagious, potentially fatal infection that is not treatable with current therapeutic techniques. Genetic transformation processes such as conjugation, mutation, transformation and transduction have an ability to transform bacterial cells into MDR. Some common
multidrug resistant bacteria are *E. faecium, Staphylococcus aureus, K. pneumonia, Acinetobacter baumannii, Pseudomonas aeruginosa*. Among all bacteria Methicelline Resistant *Staphylococcus Aureus* (MRSA) is the most fatal causing serious infections. Some common environmental factors are also plays critical role to transform a bacterium into an MDR aiding their survival within the environment as potential pathogens. Successful transmission of pathogens also relies on various environmental factors such as temperature, pollution, dissolved chemicals and relative humidity that may influence bacterial growth and division. Pollution from sewage sludge, animal slurry, disinfectants and fabric softeners may be linked to the rise in bacteria resistant against the most powerful antibiotics. Antibiotics and other chemicals that could drive antibiotic resistance enter rivers and soils in many ways and produce different types of MDR bacteria. At last it could be concluded that by reducing environmental pollutions and by preventing the misusing of antibiotics the growth of MDR can be reduced. The strategies discussed in this study are the need to adopt alternative approaches for the discovery of next generation of antibiotics as well as replacement of conventional antibiotics to peptide antibiotics.

**Key words:** Resistance, Transduction, Conjugation, Transmission, Pathogens.

**MA139**

**Assessment of microbes and persistent organic pollutant in lakes of Larshmann hills area, Antarctica**

**Laxmikant Bhardwaj**, **Abhishek Chauhan**, **Anuj Ranjanand and Tanu Jindal**

Amity Institute of Environmental Toxicology, Safety and Management, Amity University

Sector-125, Noida, Uttar Pradesh, India

**Presenting Author**

lkbhardwaj@amity.edu

The Larsemann Hills is an ice-free area consists of two major peninsulas (Storness and Brookness), four minor peninsulas and approximately 130 islands and more than 150 lakes at different Islands and peninsulas in the area of 50 km². It is located halfway between the Vestfold Hills and the Amery Ice Shelf on the south-eastern coast of Prydz Bay, Princess Elizabeth Land, East Antarctica (69°30’S, 76°19’58”E). Continental Antarctica holds a typical flora and fauna which varies both qualitatively and quantitatively among the different surroundings. 22 lake water samples were collected from the locality of Bharati Research Station. Assessment of Persistent Organic Pollutant’s (POPs) was done by using Gas Chromatography-Mass Spectrometry. Lake water samples were extracted, concentrated and injected to GC-MS along with POPs standards. In all Lake Watersamples, the concentration of POPs was below 0.05 ppb for Polychlorinated Biphenyls (PCB) & Polycyclic Aromatic Hydrocarbon (PAH) and 0.01 ppb for Pesticides. In this view, more sophisticated instruments at pico-gram (pg) level are required; however, concentrations less than 0.05 ppb and 0.01 ppb are not harmful. These
samples were also analyzed for the detection of Coliform bacteria, Faecal Coliform and *E. coli*. In Antarctica, coliforms are generated by two sources: local vertebrate populations and human activities. Coliform bacteria are not pathogens themselves but their presence indicates the possibility of finding pathogens. Four lakes water samples were found to be contaminated with Coliform bacteria, however, Faecal coliform and *E. coli* were absent when tested with selective media. Presence of most probable number (MPN) coliform indicates that the degree of pollution and sanitary quality of lake water. Coliform contaminations are found in the lakes which are in the locality of those areas which are regularly accessible (L-3, L-1D, L-7A, Murk water). However, there are other factors which may lead to coliform contamination such as migration of microbes through birds and transport of food items from ship to research station. Moreover, the presence of coliform bacteria in the samples indicates an alarming situation and need to be investigated further.

**Keywords:** Microbes, POPs, Lake Water, Larsemann Hills, East Antarctica

**MAI40**

**A review on entomoremediation as a biorational approach to treat contaminated soil in agroecosystems**

**Manas K. Dhal, Pushpa Singh and S.K. Sagar**

Swami Shraddhanad College (University of Delhi), Alipur, Delhi-110036

**Presenting Author**

manaskdhal@gmail.com

Over the year the use of modern agricultural technologies, include increasingly specialized systems and even monocultures, mechanical cultivation and harvesting, injudicious and indiscriminate use of mineral fertilizers and pesticides leads to contamination in soil and water as a result global agroecosystems are becoming more susceptible for which there is augmented public awareness of soil ecology and the importance of maintaining soil health in agroecosystems. As we know that the invertebrates communities are sensitive indicators of soil quality but day by day their population under threat due to unhealthy soil. A good quality or a healthy soil has the properties to support life processes such as plant anchorage and nutrient supply, retain optimal water and soil properties, support soil food webs, recycle nutrients, maintain microbial diversity, remediate pollutants, and sequester heavy metals. Previous studies states that among the invertebrates, insects are the dominant group not only in diverse population but contributed a lot to maintain soil health. Therefore the concept came to exist so as to use of insects to treat the contaminated soil is called entomoremediation. This is a holistic approach which was critically projected under the umbrella of bioremediation technique that needs to be harnessed in line with global realities of involving organisms like microorganisms and earthworms in soil decontamination. It has been reported that some of the insects like collembolans, ants, beetles and termites have great role for maintaining soil
ecosystem. These species need for mass rearing so as to use them in dumping or contaminated areas. Still many more insects varieties have to be explored and exploited which are neither threatened nor endangered in order to develop a rational biological method to achieve overall healthy soil in an agroecosystem.

**Key words**: Agroecosystems, invertebrates, bioremediation, entomoremediation, biological

MAI41

**Identification of novel mutations in Zika virus circulating in Asia and America**

Ekta, Neelam Gandhi, Pooja Arora*

*Zoology Department, Hansraj College, University of Delhi

Presenting Author

apooja1483@gmail.com

Zika virus is an enveloped virus having non-segmented, single-stranded 10kilobase positive-strand RNA genome. It belongs to the family Flaviviridae and is transmitted primarily by *Aedes* mosquito. It was isolated from Zika forest in Uganda in 1947 and hence named Zika virus. Till recent years virus was associated with mild sporadic outbreaks. However, first major outbreak was reported from islands of Yap in 2007 followed by a recent outbreak from Brazil in 2015. During Brazil outbreak Zika pathogenesis was associated with microcephaly for the first time suggesting that virus has evolved to be more pathogenic. In this work, phylogenetic analysis of Zika virus isolated from North, South America, Asia and Oceania was performed. In our analysis, around hundred and fifty one full genome sequences were analyzed. All the sequences were obtained and analyzed using Virus pathogen database and analysis resource (ViPR). Interestingly, maximum likelihood based phylogenetic analysis of Zika virus revealed that there was no clustering of geographically related strains. Furthermore, phylogenetic analysis of various viral proteins was also performed which revealed the presence of highest variations in NS5 protein whereas NS2A was relatively conserved. Meta-analysis revealed ninety-four highly conserved and significant mutations in the genomic sequences (n=28 P<0.01, n=66 p<0.001). In accordance to our phylogenetic analysis, NS5 showed highest variations (n=19, p<0.01, n=17, p<0.0001) whereas there were very few highly significant mutations in NS2A region (n=6 p<0.01, n=1 p<0.001). In this study, we compared various full genome sequences and Zika virus circulating in various parts of the world. We performed phylogenetic analysis as well as identified highly significant novel mutations in the genome of ZIKV. We further wish to extend our study for identification of recombinant events in the genome of Zika virus. Since crystal structure of ZIKV NS5 is available, we will utilize modeling based approaches to identify possible effect of various mutations on NS5 structure as well as use computational approaches to create NS5 interactome.
Evaluation of estrogentic potential of genistein administration in Indian freshwater catfish, *Heteropneustes fossilis*.

**Preeti Khandelwal, Pooja Kumari, and Neeta Sehgal**

Department of Zoology, University of Delhi

**Presenting Author**

kaushikpujap@gmail.com, preekool.15@gmail.com

Aromatase is the terminal enzyme in steroid biosynthesis hence serves as a potential target of EDCs (Endocrine Disrupting Compounds). It is encoded by *cyp19* genes. EDCs readily enter the aquatic bodies from various sources and fish species are at high risk of exposure. Genistein is an isoflavone, which has potential to disrupt the endogenous endocrine-signaling pathways by binding to estrogen receptors competitively and induction of vitellogenin (vtg) synthesis in male fish. It is abundant in soya-derived foods, and in the effluent from wood pulps mills or sewage treatment plants. The present study was undertaken to study the effect of different concentrations of genistein administration in *Heteropneustes fossilis* and to evaluate its potency as estrogen mimicking compound taking estradiol-17β as a positive control. Expression of *vtg* and estrogen receptor (*er*) genes in liver and aromatase in ovary and brain was quantified. Biochemical parameters such as levels of calcium ion, SGOT, SGPT, cholesterol and respiratory burst activity in serum were estimated. The activity of transaminases (SGOT, SGPT) was not affected on administering estradiol or genistein. This suggests that both of these compounds were not hepato-toxic, but a dose dependent increase in serum cholesterol was observed on genistein administration. Genistein exposure reduced serum [Ca²⁺] levels in either sex of catfish and estradiol injection resulted in increased calcium ion concentration. Transcription of *cyp19a* was upregulated in ovary but downregulated in testis, whereas *cyp19b* expression in the brain of catfish in both the sexes is upregulated. Estrogen receptors (*era* and *erβ*) of catfish were also sensitive to genistein exposure. Estradiol (25μg/100gm body weight) administration upregulated the relative expression of *vtg* in catfish whereas a similar dose of genistein induced downregulation of *vtg* expression but not in a dose-dependent manner. In conclusion, our results show that genistein can disrupt endocrine pathways by exhibiting estrogenic/ antiestrogenic activity in catfish, but its effect varies in either sex and also with dose.

Antibacterial and antifungal activity of raw and processed honey against microbes causing skin infection

**Rajesh Kumar Shah and Dhrubojyoti Gogoi**
Honey is a traditional medicine that is used in the treatment of several human ailments. It is considered to be the natures best all round remedies. No toxicity or side effects of honey have been reported till date. Its cost effectiveness and ease of availability makes it more valuable. In the present study the antibacterial and antifungal activity of raw and processed honey collected from different sources were tested against microbes causing skin infections. Antimicrobial activity was tested by agar well diffusion method against *Staphylococcus aureus* (MTCC 87), *Escherichia coli* (MTCC 10312), *Pseudomonas aeruginosa* (MTCC-3542), *Proteus mirabilis* (MTCC-3310), *Bacillus cereus* (MTCC 1305) and *Aspergillus niger* (MTCC-9652). Results showed a significant antimicrobial activity by all the honey samples. Raw honey showed more activity than processed one. *Staphylococcus aureus* was found to be most sensitive against all honey samples and showed maximum zone of inhibition as compared to others.

**Keywords**: Honey, Pathogen, Skin infection and Antimicrobial activity.

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**MAI44**

**Molecular taxonomy of Hammerschmidtiiella indicus using small subunit (18S) of ribosomal DNA sequence from Meerut, India**

Sangeeta Pal

Department of Zoology, Deshbandhu College, Kalkaji, New Delhi-110019

**Presenting Author**

sangsaat21@gmail.com, Phone – 09456006199

Molecular markers have often been used for taxonomic identification and phylogenetic analyses in different species groups. Evolution of rDNA is relatively independent of changes in morphology, and analyses of these genetic data have been shown to provide good phylogenetic resolution. Phylogenetic relationships of *Hammerschmidtiiella indicus* was investigated using nucleotide sequences of the region of 18S rDNA. DNA extraction, amplification and sequencing is done by using Primer sequences designed is (Forward primer 5' - AAACGGCTACCACATCCAAG-3' and Reverse primer 5' - CCAAGCACATGAACCAAATG-3'). Sequences were uploaded on NCBI to search for the most similar reference sequences and positions of 18S gene were determined with the help of BLAST (available at www.ncbi.nlm.nih.gov). Subsequently, nucleotide sequences of various species were aligned using the aligning tool Clustal W (Thompson *et al.*, 1994). The sequences were entered in the MEGA for construction of the phylogenetic tree. Data were analyzed
using maximum parsimony (MP) and neighbor-joining (NJ) methods by using MEGA version 4.0 (Tamura et al., 2007). Pairwise comparisons and Electropherogram of sequencing sample is also done. The base pair sequence of large subunit of ribosomal DNA of parasite submitted to NCBI GenBank under the accession number GU968649. Different studies have demonstrated that the 18S region of nuclear rDNA provide useful genetic marker for the accurate identification of sibling species and morphospecies. Phylogenetic relationships of species of the genus were investigated using nucleotide sequences of the region of 18S rDNA. for primary sequence data by using neighbour-joining and maximum-parsimony approaches. Hammerschmidtia indica is the first species of this genus to have small ribosomal subunit rRNA gene regions sequenced for the purposes of species discrimination. However, further sequences are required from additional species of the genus Hammerschmidtia to reveal the position within the nematoda. Their validity is also strongly supported by molecular evidence inferred from rDNA sequence. The tree topologies derived from the phylogenetic analysis inferred from the 18S rDNA data-set is in agreement that it is closely related sister-taxa genetically viz., L. portentosae, T. icemi and A. tetraptera. Further studies with additional molecular markers are needed to determine the divergence between H. indica and other nematodes.

MAI45

Orf selected genome fragment libraries: Tools to unravel microbial proteomes!

Vaishali Verma¹, Amita Gupta², Vijay K. Chaudhary*²

¹Department of Biochemistry, University of Delhi South Campus, New Delhi, India.
²Centre for Innovation in Infectious Disease Research, Education and Training (CIIDRET), University of Delhi South Campus.

Presenting Author
vaishali1verma@gmail.com

Microbes, one of the oldest and most abundant habitants on earth have continuously evolved with their human hosts. The interactions of microbes with human hosts are central to health and disease necessitating their in-depth study. As a repository of microbial gene products, comprehensive metagenomic expression libraries can serve as key tools for numerous applications including functional annotation of novel microbial genes for discovery of new biomolecules like enzymes, mapping of protein-protein interaction networks, and genome-wide identification of immunodominant epitopes. However, conventional strategies used for construction of such libraries usually involve random fragmentation of genomic or cDNA, which leaves majority of clones off-frame (only 1 in 18 is in-frame). Essentially, only 5-6% of the library clones encode functional proteins, and remaining off-frame clones contribute to unwanted background noise, drastically affecting the utility of such libraries. This study describes the development and optimization of a split TEM-1 beta-lactamase-based simple, robust, and one-step system for enrichment of clones encoding Open Reading Frames (ORFs). It is based on a periplasmic E. coli enzyme TEM-1 beta-
lactamase, which confers resistance against ampicillin. The enzyme can be dissected into two protein fragments, namely Bla-Alpha (24-195 amino acids) and Bla-Omega (196-286 amino acids), which do not interact by themselves, but re-constitute the activity when brought together by a mediator, which could be an in-frame protein inserted between the two fragments. Thus, if the mediator were in-frame, it would allow translation of full-length beta-lactamase that can confer resistance against ampicillin. On the contrary, if the mediator were off-frame, this would result in translation of incomplete beta-lactamase protein, which would not confer resistance against ampicillin. Hence, selection of clones on increasing concentrations of ampicillin provides an opportunity to enrich clones encoding ORF. The utility of the system has been exemplified by construction of a large ORF-selected M. tuberculosis H37Rv whole genome fragment library. The ORF selected genome-fragment library contains greater than 95% in-frame clones, clearly demonstrating the efficiency of the selection system. This study is expected to enable generation of comprehensive and highly functional metagenomic expression libraries, which can facilitate numerous functional genomics and proteomics-based applications.
Poster Presentations
Session B
Innovative Sciences
Session
Effect of insecticide on polytene chromosomes of 
*Sarcophaga ruficornis* (fab.)

1*Nimita Kant, 2Rashmi Singh and 3Akanksha Singh*

1*,2Department of Zoology, Shivaji College, University of Delhi, New Delhi-110027, India.  
3Department of Zoology, Sri Aurobindo College, University of Delhi, New Delhi-110017, India.  

**Presenting Author**

singhakanksha.au@gmail.com, rashmirrsingh@gmail.com

The present study investigated the effect of cypermethrin on polytene chromosomes of an invertebrate animal (*Sarcophaga species*). *Sarcophaga ruficornis* is a cosmopolitan flesh fly. These flies are known to spread the myiasis disease and are also used in forensic entomology context. During the present study the seven day old pupae of *S. ruficornis* were dissected out and the polytene chromosomes from the foot pad were removed. The effect of cypermethrin directly associated with soil pollution. These insecticides are potentially harmful for animals living in soil as well as kill beneficial insects, weeds, birds, fishes and non-target plants. Polytene chromosomes form after several cycles of replication (endoreplication) and produce numerous sister chromatids that do not separate and remain fused together on a single chromocentre. This feature allows us to observe the mechanisms of the stress responses and the function of heat shock genes in response to thermotolerance and adaptation to chemical stresses. In the present study, a cytological investigation of the cypermethrin induced chromosomal puff was made to identify the genetic loci responsive to these stress factors. *Sarcophaga ruficornis* have been used for toxicity testing because they are extensively distributed, highly responsive to environmental stress and its life cycle represents all the four developmental stages of the fly. After the treatment of cypermethrin a large puff is induced at the chromosome arm IIL in the region 12A. The puff induction presumably reflects the synthesis of heat shock proteins by mRNA expression and these proteins are also called as chaperons. The same puff is induced in other sarcophagid species after the treatment by heat shock and other chemical agents. This single prominent puff in polytene chromosomes show stress response and thus cypermethrin is proved to be used as a biomarker tool for the assessment of genotoxic substances.

**IPP2**

Green energy based portable embedded system solutions for remote area applications

*Amit Sehgal and Sukhbinder Singh Rait*

Department of Electronics, Hansraj College, University of Delhi, Malka Ganj, Delhi – 110007

**Presenting Author**

amitselah112@gmail.com, Tel: +91-9873035542
In this work, authors demonstrate the design of Green energy based portable embedded system solutions for remote area applications. The work comprised of implementation of the design of our portable solar LED (Light Emitting Diode) bulb in real time. The solar LED bulb is a novel lighting solution using the combination of solar energy (the most abundant, renewable, clean (no harmful by-products of the energy conversion process) energy source) and LEDs (solid state light source) (environment friendly, efficient, with longer life times that incandescent and compact fluorescent lights) coupled with efficient secondary energy storage devices all together combined in a single portable package. The Solar LED bulb is further extended with options of cell phone charging through an output port available on the device itself. The Solar LED bulb would be provided for its utmost portability. The prototype comprised of all salient features with reduced cost achieved by tweaking its electronic design. With an emergent need to overcome shortage of electricity supply at remote areas, the work aims at advanced development of a cost effective solar energy based portable energy conversion module for quick charging of communication gadgets. While designing the module, the focus comprised of portability, accessibility, cost effectiveness and robustness. Thus, we designed portable solar stations with light weight storage batteries and open source electronics. The solar stations will be used to provide power to solid state LED lights for illuminating the event site, tents, enclosures, and provide for charging ports for charging cell phones or other communication equipment. The authors also designed a prototype to use the much flexible yet neglected Thermo-Electric devices for providing heating and cooling options for medical or daily usage using Peltier elements. The advantage of thermoelectric elements is that they provide for heating and cooling at the same time. One side can be used for cooling and the other side can be simultaneously used for heating and the cycle can be reversed by simply reversing the current direction. The Solar LED bulb designed had a run-time of 8-10 hours whereas thermoelectric cooler had a run-time of 1-1.5 hours on a single charge.

IPP3

Comparative Codon and Amino Acid Usage Bias among the sequenced Genomes of Bacterial Phylum Firmicutes


*Ramjas College, University of Delhi, Delhi-110007
#Department of Zoology, University of Delhi, Delhi-110007

Presenting Author
dev83.sharma@gmail.com
Firmicutes are low G+C Gram positive bacteria which can be found in a variety of different habitats. Due to their ubiquitous presence and varied life styles Firmicutes are important candidate to study codon usage bias. In this investigation, bias in codon usage of 362 Firmicutes genomes were analyzed by estimating different indices of codon bias such as Nc (effective number of codons), SCUO (synonymous codon usage order), RSCU (relative synonymous codon usage) as well as sequence patterns of codon contexts. The results revealed several characteristic features of codon usages in Firmicutes like 1) A and U-ending codons were preferred over G and C-ending codons, 2) The most frequent codon contexts found were AAA-GAA, GAA-GAA and AAA-GAU, 3) direct relationship of GC content with the usage of specific amino acids like alanine, proline, glycine, valine and leucine. The habitat of Firmicutes was found to influence the codon usage. Based on average Nc values it was found that pathogenic Firmicutes have more bias in codon usage as compared to non-pathogenic. Similarly mesophiles and aerobic Firmicutes showed more extent of codon usage bias as compared to Thermophiles and non-aerobes respectively.

IPP4

Assessing soil health using soil quality indicators involving physical, chemical and biological properties of Delhi ridge and garden soil

Mani Garg, Ritesh Gautam, Sonam Ydav, Rishu Jain, Govind Ram, Jyoti Singh, Lakshita Arya, Sheersha Pawar, Jaya Malhotra and Dinesh Kumar Gautam*

Department of Zoology, Hansraj College, University of Delhi

Presenting author
jayamalhotra1508@gmail.com

Soil consists of relative proportions of clay, silt and sand particles. Different combination or arrangement of each soil particle gives the soil its texture. Soil was collected from Delhi ridge and garden area of Hansraj College. Soil texture classification was performed using sieve method. The values of each particle were plotted in the soil texture triangle that describes 12 soil texture classes according to particle size. Delhi ridge soil belonged to the silt loam type of soil whereas the garden soil was sandy loam type. Silt loam has majority of silt particles that has particle size in between of clay and sand. It is a fertile, soft and smooth in texture. Sandy loam is generally gardening type of soil like the sample collected from Hansraj college garden area. It is predominantly made of sandy particles with varying amounts of silt and clay particles. This soil type has good drainage capacity. Any soil above pH 6 is considered suitable for plant growth. Garden soil (pH 6-7) was acidic as compared to Delhi ridge area (pH 7-8). A lower pH decreases the availability of macronutrients whereas higher pH affects the availability of micronutrients to the plants. Presence of sulphates in
ridge area depicts the source of waste water in the soil. Nitrate was observed in gardens soil as many leguminous plants that have \textit{nif} gene for nitrogen fixation are planted in the area. Chloride ion was positive in both soil samples as it considered important in photosynthesis and fights against plants diseases. Soil microorganisms perform more than 60\% of soil metabolic processes. To study bacterial community of the soils, it was plated on different growth medium. Bacteria displaying different morphological features were isolated and cultured. Gram staining of isolated bacterium was performed. 16SrRNA gene was amplified using colony PCR and genomic DNA of bacterial samples. Few samples from ridge area have been sequenced that belonged to genus \textit{Arthrobacter} and \textit{Staphylococcus}. Garden had few species from \textit{Bacillus} genus. The results depict that although the soil sample were collected from nearby areas but the soil quality completely varied because of different soil management practices.

IPP5

**Structural and functional inferences of a novel hipBA\textsuperscript{Xn} toxin-antitoxin module from Xenorhabdus nematophila**

Mohit Yadav\textsuperscript{a} and Jitendra Singh Rathore\textsuperscript{*a}

\textsuperscript{a}Gautam Buddha University, School of Biotechnology, Greater Noida, Yamuna Expressway, Uttar Pradesh, India

Presenting Author

jiteniitr@gmail.com, jitendra@gbu.ac.in

Bacterial multidrug tolerance is an extensive considerable issue for human health. In this condition antibiotics are not able to eradicate infections. A major cause for this is an emerging small population of dormant bacteria called persisters. Such phenotype of cells is evolved from the involvement of toxin-antitoxin (TA) modules. In which, \textit{hipBA}\textsuperscript{Xn} TA module that codes for the HipA\textsuperscript{Xn} toxin and the HipB\textsuperscript{Xn} antitoxin, is a type II TA module. In this study \textit{hipBA}\textsuperscript{Xn} TA module from \textit{Xenorhabdus nematophila} was characterized for first time. 3-D models for HipA\textsuperscript{Xn} toxin and HipB\textsuperscript{Xn} antitoxin from \textit{Xenorhabdus nematophila} were generated using replica exchange Monte Carlo simulations. Various ligands were also screened, among which adenine for toxin and DNA for antitoxin were best suited. Functional annotation was also done in form of gene ontology (GO) terms. Further, the interaction between a toxin HipA\textsuperscript{Xn} and antitoxin HipB\textsuperscript{Xn} was \textit{bona fide} through endogenous toxicity assay. This structural and functional study of \textit{hipBA}\textsuperscript{Xn} TA module will provide aid in new antibiotic drug discovery.

Abbreviations:
\textit{E. coli}, \textit{Escherichia coli}; \textit{X. nematophila}, \textit{Xenorhabdus nematophila}; ADE, Adenine; DNA, Deoxyribonucleic Acid; TA, toxin-antitoxin; I-TASSER, Iterative threading assembly refinement; LOMETS, Local meta threading server; Hip, High persistence; GO, Gene ontology.
**Key words:** *X. nematophila*; toxin-antitoxin system; HipA<sup>Xn</sup> toxin; HipB<sup>Xn</sup> antitoxin; ligand; Endogenous toxicity

### IPP6

**Generation of acid free, chlorine free and azo free hand made paper by implementing 4R’S of paper making: Reduce, Reuse, Recycle and Recreate.**

Jyoti Arora<sup>1</sup>, Avni Gupta<sup>1</sup>, Arshia Bhatt<sup>1</sup>, Bhavya Sirohi<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>

<sup>1</sup>Department of Zoology, <sup>2</sup>Department of Chemistry, <sup>3</sup>Department of Physics, Miranda House, University of Delhi, Delhi -110007, India

**Presenting author**

jyoti.arora@mirandahouse.ac.in

Twelve large trees are cut to produce 1 tonne of paper from virgin pulp. Large-scale deforestation results in habitat loss and fragmentation causing extinction of species and also accelerates global warming. Hence, there is a need to shift to more eco-friendly and sustainable processes in paper making. Hand Made Paper making using recycle fibres is the ideal solution to these problems. In India, handmade paper industry is one of the important export-oriented sectors. The popularity of handmade paper over mill made paper is due to its aesthetics and eco-friendly characteristics. Synthetic dyes are commonly employed for imparting colour in handmade paper industry because they are readily soluble, economic and exhibit good light fastness. But most of these dyes contain azo group which on reduction produces carcinogenic or harmful amines. In the present study, an attempt has been made to make handmade paper through eco-friendly processes that include recycling used paper for pulp production and using natural dyes as colourants. The natural 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. Research and innovations on different dimensions of Environment result in establishment of Miranda Tech: The Green Technology Park that work towards a common goal of creating a Zero Solid Waste Zone and a Clean, Green Campus. Paper recycling plant is an important component of Miranda Tech where paper waste collected from different departments and administrative office of the college is recycled. In this study, shredded paper and shredded white cotton rags were added to a Hollander beater to make pulp, that was treated with mordant (alum) and sodium bicarbonate and natural dyes (extracted from plants). Paper sheets were prepared from dyed pulp by Univat and Screw Press. Paper sheets were also made using plant fibres (e.g. bamboo pulp). Finally, paper sheets were dried under sun followed by calendering, trimming, and used for recreating different products. The paper generated by implementing eco-friendly processes is acid-free, chlorine-free and azo-free, and also conform to the stringent regulations imposed by regulating agencies world-wide.

**Key Words:** Handmade paper, Natural Dyes, Eco-friendly, Azo free
Coumarin triazolylated thiazolidinone derivatives: Synthesis and apoptotic inducer activity

Pooja\textsuperscript{a}, Nimisha Sinha\textsuperscript{b}, Yogesh Kumar\textsuperscript{c}, R.P.Singh\textsuperscript{a}

\textsuperscript{a}Assistant Professor, Sri Venkateswara College, Department of Chemistry, University of Delhi.
\textsuperscript{b}Assistant Professor, Sri Venkateswara College, Department of Biochemistry, University of Delhi.
\textsuperscript{c}Bio-Organic Laboratory, Department of Chemistry, University of Delhi

Presenting Author
nimisha10@gmail.com

Coumarin, triazoles and thiazolidinones are one of the most preferred biological scaffolds frequently used in medicinal chemistry. These can be obtained both from natural products as well as by synthetic methods. The pharmacological, biochemical and therapeutic applications of the above mentioned pharmacophores have fascinated the researchers. Among these biological applications, induction of apoptosis is one of the applications which have got immense importance due to devastating nature of down regulation of apoptosis which leads to cancer. In this study, novel coumarin compounds based on triazolylated-thiazolidinone were synthesized via multistep chemical synthesis followed by their purification and characterization using different techniques. Further, these compounds were tested for their cytotoxic activity on mammalian oral squamous cell carcinoma cell line SCC-4. Cytotoxicity using MTT assay revealed that the three compounds displayed variable toxicity levels at variable concentration and approximately 50% of the cells became non-viable. Furthermore, Caspase-3/CPP32 Colorimetric Protease Assay was carried out to determine the caspase-3 levels and the results of caspase-3 assay in SCC-4 cell lines indicated that treatment of cells with the coumarin derivatives induced apoptosis in the carcinoma cells as there was a significant increase in the expression of caspase-3 post-incubation.

Keywords: Coumarin; Apoptosis; Caspase-3

Ethnobotanical Study of Flora of Manipur, A Biodiversity Hotspot Region of North East India

Suresh Kumar\textsuperscript{1}, Pushp Lata Negi\textsuperscript{2}, Khaling Mikawlrawn\textsuperscript{3}, Kartik Thakur\textsuperscript{4}, Sakshi Singhal\textsuperscript{5}, Pranav Punia\textsuperscript{6}, Sunil Kumar\textsuperscript{7}, Prashasti Sharma\textsuperscript{8}, Shwetna Sharma\textsuperscript{9}, Sangeeta Kumari\textsuperscript{10}, Samridhi Sehgal\textsuperscript{11} & Ankit Dhoundiyal\textsuperscript{12}

1,3,9-12 Department of Botany, Ramjas College, University of Delhi, Delhi, India
2, 4-6 Department of Zoology, Ramjas College, University of Delhi, Delhi, India
6, 8 Department of Life sciences, University of Delhi, Delhi, India
The present study reports the ethnobotanical survey carried out in 5 villages (Khangshim Village, Minou Village, Nungourok Village, Molnoi Village and KhoibuKhullen) of Manipur (North East India), emphasising on medicinal plants used for ailments of various diseases /infections. Interviews of the traditional healers, elders and informants were conducted for collecting and documenting medicinally important antimicrobial plants. The authenticities of the usages of the acclaimed medicinal plants were repeatedly verified by contacting various local healers and elders. Plants used for ailments of various diseases were collected with due permission from the tribal leaders/ healers through the guidance of elders and informants. Herbariums of the important plant samples were also prepared for future verifications. The collected plants were identified by using the books Flora of Manipur, and Herbal Medicines of Manipur. In total 5 healers, 4 youth leaders, 6 village elders, 4 church pastor, 6 tribal leaders, 2 NGO workers and 3 informants were interviewed. Most of the traditional healers (4/5) were women, only one (1/5) was male. The healers were of the age group of 50-80 years. A total of 57 plants which were used for ailments related to various diseases were documented and collected. Out of 57 medicinal plants, 22 medicinal plants were selected for phytochemical screening. Aqueous and methanolic extracts of dried leaves collected from this region were tested for the presence of important secondary metabolites. Methanolic extracts were found to show more positive results as compared to the aqueous extracts, which could be due the difference in solubility of different secondary compounds in various types of solvents. Five plants (Sample A- Polygonum chinense Linn, Sample B- Clerodendrum colebrookianum Walp, Sample C- Chromolaena odorata (L.) King & Robinson, Sample D- Phlogacanthus thyrsiformis (Roxb.exHardw.) Mabb, Sample E- Rhus semialata Murr. were selected for antibacterial activity against E. coli and Staphylococcus aureus. It was observed that out of these five plant samples studied sample E showed maximum antibacterial activity against Escherichia coli and Staphylococcus aureus. Sample C (Chromolaena odorata (L.) King & Robinson) was also found to show antibacterial activity against E. coli, whereas sample A, B & D do not show any antibacterial activity against E. coli. The present study shows that all the five samples have antibacterial activity against Staphylococcus aureus. Same result is observed in antifungal activity. Sample A showed highest activity against Aspergillus flavus and sample E also showed antifungal activity. The plant extracts did not give a proper zone of inhibition but slowed down the growth with Aspergillus niger. Sample C (Chromolaena odorata (L.) King & Robinson) shows positive result in anticancer activity.

**Keywords:** Ethnobotany, phytochemical screening, antibacterial, antifungal, Manipur, North-East India.
Sustainable agriculture waste management technique for the cultivation of oyster mushroom

Surinder Kaur and Piyush Mathur

Department of Botany, SGTB Khalsa College, University of Delhi, Delhi 110007

Presenting Author

skwalia24@yahoo.co.in

India generates huge amounts of agricultural plant residues like rice/wheat straw, horse and chicken manure, fruit and vegetable residue, coir dust, husk, dried leaves and tea waste, which has potential to be recycled. Burning of agriculture waste such as wheat/rice straw causes severe pollution to human and animal health as well as results in loss of nutrients like carbon, nitrogen, phosphorus from soil. An eco-friendly approach to recycle rice/wheat straw can be mushroom farming. Mushroom cultivation is an emerging market because of its nutritional value and health benefits. Mushroom are low in carbohydrate, sodium and fat content. In addition, they are also a great source of fibre, protein and minerals such as potassium, copper, phosphorus, zinc, iron, calcium and selenium. Mushrooms also contain L-ergothioneine (a powerful antioxidant) and vitamins B and D. Consumption of mushroom at regular basis reduces the risk of obesity, diabetes, cancer and heart diseases as well as improves cholesterol level and anemic condition in humans. The most popular cultivated mushrooms are button mushroom (Agaricus bisporus), shiitake mushroom (Lentinula edodes), oyster mushroom (Pleurotus ostreatus), enokiate or enoki mushroom (Flammulina velutipes), and paddy straw mushroom (Volvariella volvacea). We selected particularly, oyster mushroom for cultivation because of its booming demand in India and related culinary, nutritional and health benefits. In this study, we explored the potential use of rice straw as a substrate for cultivating oyster mushroom. After sterilizing rice straw, spawn of oyster mushroom was mixed. Plastic bags were filled with this spawn-straw mixture and were left for few days for the formation of white colored mycelia. Fan-shaped fruiting bodies of oyster mushroom started appearing 3-4 weeks of post-mycelial growth. We started harvesting fruiting bodies when the edges of the cap surface were still curled. Here, we have developed a sustainable management technique of recycling rice straw waste for cultivating oyster mushroom.
Global substrate profiling for *Mycobacterium tuberculosis* protein kinase K using high-throughput transcriptomic and proteomic approaches

Vandana Malhotra* 1-3, Blessing P. Okon1, and Josephine E. Clark-Curtiss 1,2

Center for Infectious Diseases and Vaccinology, Biodesign Institute1, School of Life Sciences2, Arizona State University, Tempe, Arizona 85287 and Department of Biochemistry, Sri Venkateswara College 3, University of Delhi, New Delhi 110021, India

Presenting Author
vmal71@gmail.com

*Mycobacterium tuberculosis* Serine/Threonine Protein kinases play a pivotal role in regulating diverse cellular pathways that control its metabolism, physiology and virulence. Previously we have shown that *M. tuberculosis* Protein Kinase K is involved in translational control mechanisms that direct mycobacterial growth adaptation during a variety of in vitro and in vivo stress conditions. We show that PknK overexpression inhibits growth in a phosphorylation dependent manner. Using high throughput tools such as 2D-DIGE and Microarrays, we compared the phosphoproteomic and transcription profiles of mycobacterial strains overexpressing wild-type and phosphorylation-defective PknK. Phosphoprotein staining and Mass spectrometry analysis revealed transcription terminators, proteases, and several enzymes involved in carbon and nitrogen metabolism as putative cellular substrates for PknK.

Synthesis and characterization of mixed metal oxides nanoparticles for remediation of pesticides

Vatsala Dwivedi1, Navneet Manav 2, A.K. Bhagi 2

1Department of Zoology, Dyal Singh College, Lodi Road, Delhi, India-110003
2Department of Chemistry, Dyal Singh College, Lodi Road, Delhi, India-110003

Presenting Author
dwivedivatsala@gmail.com

Pesticides such as DDT (dichlorodiphenyltrichloroethane), HCH (hexachlorocyclohexane), malathion and atrazine are extensively used as they provide protection to crops from pests and also help in eradication of vector borne diseases thereby increasing the productivity of crops. The use of pesticides has increased with time as it helps in providing food security to the ever increasing population. Indiscriminate use coupled with unregulated production is a serious threat to environment as they tend to bioaccumulate in fatty tissues and are biomagnified. Bioaccumulation of excess unused insecticides or their harmful by-products generates the need that they be degraded to safer products using greener technologies for environmental remediation as they have various health
hazards associated with them. The short term impacts include allergies, asthma and hypersensitivity, and long term impacts such as cancer, hormone disruption, neurological defects and other problems associated to reproduction and fetal development. To achieve this nano sized mixed metal oxides were synthesized as they are proven catalysts due to their versatile properties especially their acid-base and redox catalytic properties. In the current study binary mixed metal oxides of $A^{II}B_{2}^{III}O_{4}$, $A^{II}B_{2}^{IV}O_{3}$, where $A$ is a bivalent metal ions such as $Ca^{2+}$, $Fe^{2+}$ and $B$ is $Al^{3+}$, $Co^{3+}$, $Zr^{4+}$, $Ce^{4+}$ were constructed and characterization was carried out by powder X-Ray Diffraction and Transmission Electron Microscope (TEM) studies. Further degradation studies were performed with pesticides using gas chromatography and results indicated that the synthesized nanoparticles are efficient in achieving remediation of these pesticides.

IPP12

In silico analysis of lipase WP_055441552 identified from Anoxybacillus suryakundesis strain isolated from a hot spring in Jharkhand, India

Antash Chaturvedi, Abhishek Singh Waths, Himanshi Kaushik, Preeti Arivaradarajan

1 Amity Institute of Biotechnology, Amity University, Noida, Uttar Pradesh, India

Presenting Author
vedi.antash@gmail.com, wathsabhishek@gmail.com, hkaushik921@gmail.com

The genus Anoxybacillus is a facultative anaerobic and moderately thermophillic, Gram positive bacteria. In the present study we describe the bioinformatic analysis of lipase WP_055441552 identified from Anoxybacillus suryakundesis strain isolated from a hot spring in Suryakund, Jharkhand. A multiple sequence alignment (MSA) of lipase WP_055441552 with other closely related lipases using CLUSTALW indicated a conserved GDSL motif. It has been found that lipases with GDSL motif have the potential of hydrolysis as well as synthesis of some commercially important ester compounds that has germane applications in industries such as pharmaceutical, biochemical etc. The various physical and chemical parameters of WP_055441552 were computed by ExPASy ProtParam tool. Its calculated molecular weight and theoretical pI were found to be 28 kDa and 4.87 respectively. Its instability index was 34.20 that deemed it as stable one. Also lipase WP_055441552 is characterized by the total of 35 negatively charged residues (Asp+Glu) and 23 positively charged residues (Arg+Lys). The Conserved Domain Database (CDD) of WP_055441552 showed that the three amino acid residues Ser 44, Asp 221 and His 224 form the catalytic triad. Also, the amino acids Ser 49, Gly87 and Asn117 bind and stabilize the oxyanion. Further a three dimensional model of WP_055441552 was constructed using SWISS-MODEL and the model was validated through RAMPAGE. The Ramachandran Plot Analysis of the constructed model showed that 91.3% residues fall in favoured region, 7.3% residues fall in allowed region and only 1.7% residues accounting to 3 amino acids fall in the outliers. The physical, chemical and structural
features identified hereby will be exploited to understand the basis of thermostabilization in WP_055441552.

IPP13

Preparation and characterization of paper from agricultural waste

Afrin Shaikh, Rinal bhayani, Dr. Shivani Patel

Shree M. & N. Virani Science (Autonomous) College, Rajkot, Gujarat

Presenting Author

afrinshaikh1905@gmail.com, rinalbhayani@gmail.com

Paper and Agricultural waste are one of the utmost types of solid waste that are dumped in mammoth quantities all over the globe per year. This waste become a saddle of cities and creates problems. On the other hand, waste management is not so strong in all cities. Therefore, recycling of wastes and waste paper is the alternative option to reduce this saddle. However, there are few small and medium scale recycling paper units and factories in cities. But due to high cost and lack of investment they are laid back. To overcome this situation, eco-friendly paper production would be a great solution. The objective of the study was to develop a low-cost method and produce eco-friendly paper from agricultural waste to reduce this waste saddle. In this study, eco-friendly handmade paper production method was initiated on the basis of ratio between waste paper and waste such as sugarcane, grass, leaves etc. Analysis of the handmade paper through certain parameters such as GSM, burst index and brightness index, shows that they are varied. It was also pointed that this production requires low investment than the conventional paper making process. In return this study has a lot of environmental benefits such as easy degradation.

IPP14

Cost effective protocol for isolation of plant DNA using commercial detergents

Margi Mungalpara, Charmy Popat, and Shivani Patel

Shree M & N Virani Science (Autonomous) College. Rajkot

Presenting Author

mascotent98@gmail.com, charmi.popat.cp@gmail.com
Extraction of highly purified DNA involving less number of steps is crucial in field of molecular biology to carry out downstream processes. Particularly in plant cells due to presence of huge amount of phenolic compounds, isolation becomes even more tedious. In the present study, one of the standardized plant DNA extraction protocol using SDS was carried out to analyse quality of DNA. Simultaneously, an alternative way to extract DNA from plants involving commercially available and homemade detergents was performed out of curiosity. Surprisingly the results were satisfactory yeilding sufficient DNA quality. The downstream application of the isolated DNA was PCR. Hence the protocol designed by us can be used as cost effective alternative method for the plant DNA isolation.

Screening of Plant Growth Promoting Traits from halotolerant Bacterial Isolates of Groundnut ArachishypogaeaL Rhizosphere
Jahanvi Jethwa, Heer mankad and Shweta Bhatt*


Presenting Author
heer.mankad@yahoo.com, jethwajahanvi999@gmail.com

Plant growth promoting rhizobacteria (PGPR) are naturally occurring soil bacteria that colonize plant roots and benefit to plants through providing growth promotion. Plant Growth in agricultural soils is influenced by many abiotic and biotic factors. One of the major factor is salt which is increasing day by day. This increase in salt concentration can causetoxicity in plant. It also affects the sodium-potassium ion channel pump in plants and difficulty in uptake of nutrients & water. The rate of transpiration also decreases indirectly. There is increase in level of ethylene in root. Halotolerant plant growth. Bacteria are those which promote the growth of plant at high salinity. At present we arestudying on groundnut plant as Gujarat is the largest producer of groundnut and it is important cash crops of our country. Thirty Six bacterial strains were isolated from Farenian and Junagadh, Gujarat, India and were screened for growth at 2%, 4%, 6% NaCl concentrations. All the isolates showed varied growth at different NaCl concentrations. They were further screened for plant growth promoting traits such as Nitrogen fixation, Phosphate solubilization, Ammonia production, Siderophore production, at 6% NaCl concentration. Out of total isolates 17 isolatesshowed Nitrogen fixation, 20 isolates solubilized phosphate, 27 Ammonia producers, and No Siderophore producers. The isolates were further analyzed for extracellular enzyme production including Amylase, Lipase, Protease, Cellulase, and Pectinase. From total isolates 25 gave positive result for amylase, 19 for lipase, 35 for protease and 10 for cellulase. And from this total 36 isolates of Junagadh and Fareni 17
isolates F7, F10, F14, F17 of Fareni and J1 to J13 of Junagadh gave all 3 PGP traits that were nitrogen fixation, phosphate solubilization and ammonia production at 6% NaCl. So these 17 isolates would be use in future research work.

**Key words**: Plant growth promoting rhizobacteria (PGPR), extracellular enzyme

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**Analysis of Dye Degradation Ability of Nickel Nanomaterial.**

**Het Mehta and Ragini Raghav**

Shree M. & N. Virani Science College, YogidhamGurukul, Kalawad Road, Rajkot-360005, Gujarat

**Presenting Author**

znhmehta@gmail.com

Azo dyes are a group of organic, colored compounds which are a major pollutant in wastewater from textile, paper, printing, leather and other industries. They are reported to be potential mutagenic and carcinogenic agents. These color pigments are stable and less prone to biodegradation, making the effluent treatment difficult and expensive. The conventional methods of effluent treatments- physicochemical methods such as flocculation, coagulation and filtration results in incomplete removal and degradation of these dyes, while techniques such as electrochemical treatments etc. are expensive. The partial or incomplete degradation results in formation of carcinogenic aromatic amines. They dyes are detrimental to human beings, and animals and a major cause of pollution to the environment. There have been several studies on employment of various oxide nanomaterials such as iron, copper, zinc, titanium etc. for their photocatalytic potential, which can be exploited for dye degradation. In this study we report a facile method for synthesis of stable nickel nanomaterials via sol gel method. Nickel sulphate was used as metal precursor and sodium borohydride was employed as reducing and capping agent. The brown black precipitates of nickel nanomaterials were characterized using UV-vis spectroscopy. The synthesized nickel nanomaterials were exploited for their ability to degrade azo dyes such as Congo red, Methyl orange and Janus green. The dye degradation ability of nanomaterial was investigated after incubation of dyes (25 mg/L) with nickel nanoparticles with exposure to artificial light. Nickel nanoparticles display effective degradation of all the three azo dyes and can be extended to other azo dyes. Furthermore, the inexpensive nickel nanoparticles display feasibility to be employed in industries for effluent treatment for effective and economical dye degradation.

**Keywords**: nickel nanomaterial, dye degradation, UV-vis spectroscopy, azo dyes.
Comparative Analysis of Photocatalytic Dye Degradation Ability of Iron Oxide and Zinc Oxide Nanomaterials.

Hiral Parekh, Shalini Patel, Neeta Karont and Ragini Raghav*

Shree M. & N. Virani Science College, YogidhamGurukul, Kalawad Road, Rajkot-360005, Gujarat

Presenting Author:

hparekh547@gmail.com, shalini369patel@gmail.com

Effluents from the dyes exploited in paper, plastic, textile and other industries possess a threat to the environment. There are several physico-chemical processes for effluent treatment to reduce the load of these coloured pigments in waste water. However, the conventional methods are often found to be less effective and not economical. Most extensively employed dyes in industries belongs to class of compounds called as azo dyes. These dyes are displaylow biodegradability as are resistant to aerobic digestion and are stable on exposure to light. Oxides of various nanomaterials such as iron, zinc, nickel, copper etc. have been recently employed for their photocatalytic ability for azo dye degradation. In the present study, we have analysed the azo dye degradation ability of oxide nanomaterials of iron and zinc. The oxide nanomaterials were synthesized via chemical route. Iron oxide nanoparticles were synthesized by co-precipitation method employing ferrous sulphate and ferric chloride as precursor and sodium hydroxide as reducing agent. Zinc oxide nanoparticles were synthesized by reduction of zinc chloride by potassium hydroxide. The synthesised nanomaterials were characterized using UV-visible spectroscopy. The dye degradation ability of oxide nanoparticles were analysed for commonly employed azo dyes- methyl orange and congo red. The degradation ability was investigated by UV-vis absorption spectra of the dye solutions (25 mg/L) with concentration of iron oxide and zinc oxide nanomaterials and incubation in artificial light. The oxide nanoparticles display effective degradability for congo red than methyl orange, which was evident from the decrease coloration of the dye solution. Within 24 hours of incubation of dye solution with nanomaterials, 90% congo red was degraded by iron and zinc oxide nanomaterials, while<50% in case of methyl orange. The dye degradation ability of oxide nanoparticles are promising and can be extended to other azo dyes. Furthermore, the photocatalytic ability of nanomaterials can be enhanced using UV illumination and the effect of increase in concentration of nanomaterials can be studied.

Keywords: oxide nanomaterial, iron oxide, zinc oxide, dye degradation, UV-vis spectroscopy.
Some natural extracts from plants as low-cost alternatives for synthetic PGRS in rose micropropagation

Khushali Dodiya, Urmi Chauhan, Preetam Joshi*


Presenting author
khushalidodiya142@gmail.com

Effect of various plant extracts during in vitro culture of rose (Rosa hybrida L. cv. bush rose), with the objective of replacing synthetic Plant Growth regulators (PGRs) to reduce the production cost, was studied. Test extracts included sweet lime juice, orange juice, sweet corn extract, tomato fruit extract and coconut water. Significant increase in shoot multiplication (15.41±1.12 shoots/explant), shoot length (3.66±0.08 cm), fresh weight (7.48±0.71 g) and dry weight (1.68±0.075 g) was observed when coconut water (@ 10 % v/v) was used in the standard MS medium. Addition of tomato fruit extract in the MS medium did not show any noteworthy effect on growth in rose micropropagules. Total chlorophyll and other biomolecules varied with the change in the type and concentration of plant extract. Highest accumulation of biomolecules was recorded on coconut water (@ 10 % v/v) supplemented MS medium followed by sweet corn extract and orange juice. Although tomato fruit extract (@10% v/v) enhanced the total chlorophyll biosynthesis but at the same time depressed the accumulation of other biomolecules. Treatment of plant extract was given in two different ways; a) incorporation in the medium prior to autoclaving (PrA) and, b) post-autoclaving addition of filter sterilized extract (PoA). No significant changes were noted in growth when mode of application was changed. To know the physiological pandemonium in the cells, peroxidase and IAA-oxidase activity was noted. No abnormal changes in the activity of these enzymes were recorded in the propagules grown on different plant extracts. The total cost of synthetic 6-benzylaminopurine (BA) can be reduced upto 98% by replacing it with natural plant extract.

A new method of purification and isolation of genomic DNA from obstinate medicinal plant using certain chaotropic molecules.

Pahal Komal, Bansi Ghadia and Preetam Joshi
Department of Biotechnology, Shree M and N Virani Science College, Rajkot (India) 360005

Presenting author
komalpahal16@gmail.com
In this paper we are describing a new method for isolation of good quality DNA from mature leaves of some medicinally important plant species, viz. Asparagus racemosus, Withania somnifera, Abrus precatorius, Commiphora wightii and Carissa carandas. These plants are valued for their immense medicinal properties and these medicinal properties are due to presence of some important secondary metabolites like polyphenols, terpenes, flavonoids, alkaloids, gums, resins etc. Although these secondary products are responsible for medicinal value of these plants, the same secondary product create problems at the time of DNA isolation. To overcome this difficulty, we suggest a simple method in which DNA is dexterously bounded to diatomaceous earth in a solution of different chaotropic agent (viz. NaClO₄, NaI and NaBr) and alienated from disturbing compounds. Current method confirms that secondary products, along with polysaccharides and proteins, can be noticeably reduced by using silica matrix along with chaotropic agents. The illustrated method is rapid, simple and highly reliable for the isolation of DNA from obstinate plant species.

**Key words:** DNA isolation, medicinal plants, CTAB, Chaotropic agents, Diatomaceous earth.

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**IPP20**

**Preparation of eco friendly bioinks using natural dyes**

**Krisha Ghetia and Shivani Patel**


**Presenting Author**

kemipatel98@gmail.com

Humans have been using ink for about 5,000 years. Ink is a liquid or paste that contains pigments or dyes and is used to colour a surface to produce an image, text, or design. We use ink to write and draw. In printing press and for lithographic printing the ink which is in paste form i.e. thick ink is used. Today there are more kinds of ink than ever, each made from a different combination of chemical ingredients including Nickel, ferrous sulphate, titanium dioxide, aniline dye and other synthetic dyes. With such a wide range of chemicals and uses it is difficult, if not inappropriate to broadly condemn or praise the use of all types of inks. Today people are showing interest in using the organically prepared things. Thus, people who are health conscious and are aware of chemical side effects will prefer to use the naturally prepared ink and we can reduce the environmental pollution also. In present study, the various pigments extracted from the plants is used as component to make the ink, in place of synthetic dyes. Many of these extracts shows promising result to make eco-friendly and biological based ink for day to day use.

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**IPP21**
Degradation of environment pollutant dye, methyl orange using silver nanoparticles synthesized by green approach

Poonam Dwivedi and Marut Jain

Department of Chemistry, Ramjas College, University of Delhi, Delhi-110007

Presenting Author
marutjain08@gmail.com

Green synthesis of nanomaterials is the most emerging method, as this is simple, cost effective, eco-benign, energy efficient, relatively reproducible and often results in more stable materials. Physical and chemical properties of metal nanoparticles are significantly different from those of the bulk materials. Silver nanoparticles (Ag NPs) among all metal nanoparticles, have been paid more attention due to their specific electrical, thermal, optical and electromagnetic properties. Furthermore, having a high surface to volume ratio, Ag NPs can dramatically enhance the interaction between reactants and catalysts. Greensynthesis of metal nanoparticles involves using microorganisms, enzymes, fungus, and plant sources. One pot synthesis of Ag NPs using plant source involves reduction of silver salt with plant source in aqueous medium. This method has advantage over chemical/physical methods as plant source functions both as reducing as well as capping agent. Formation of Ag NPs can be easily monitored visually from the change in colour of the reaction mixture. Very recently, Anacardium occidentale, Hyphaene thebaica, Abutilon indicum, Solanum tricobatum, Erythrina indica, beet root, mangosteen, and olive etc., have been reportedly used to synthesize Ag NPs. Silver NPs have been characterized by many physicochemical and morphological techniques. Dyes are the major effluents from various industriesthat require better and improved wastewater-treatment measures. A representative dye, Methyl Orangeis a major effluent from textile and food industry and is also a well-known carcinogen. It has already been reported that, reduction of methyl orange by NaBH₄ only is thermodynamically feasible, but kinetically not, but in presence of Ag NPs, reduction reaction becomes thermodynamically as well as kinetically feasible as Ag NPs reduces the activation energy. The degradation kinetics has been studied using UV-visible spectroscopy.

Prediction of Antigenic Promiscuous MHC Class II binders of Mycobacterium tuberculosis capable of inducing Interferon gamma

Medha, Parul, Palvi, Garvita, Swati, Monika Sharma, Sadhna Sharma*
Mycobacterium tuberculosis (MTB) is a notorious pathogen in causing Tuberculosis disease in humans. Successful penetrance of this pathogen is evident from the fact that almost one third of the human population is infected. Host cell response to tuberculosis is by large a cell mediated immune response where cytokines and Th1 cells plays the crucial role. Many studies have enlisted the important role of Interferon gamma (IFN-g) in deriving the host cell immune response to MTB infection. IFN-gamma activates the pathogen infected macrophages which in turn elicits microbicidal role. It also helps in maintaining an equilibrium within the inflammatory and immunopathology of the host cell immune responses. We have selected four hypothetical proteins namely Rv2626, Rv2627, Rv2628, and Rv2032 which are part of DosR regulon of MTB genome. These genes enable the pathogen to survive within the host cell in a dormant state which is classified as the latent phase tuberculosis infection. By using two of the validated immunological database namely IEDB and PROPRED we found the promiscuous T-cell (CD4) epitopes within these genes. These epitopes were then scanned using IFNepitope server for predicting IFN-gamma secretion inducing MHC class II binders. These peptides were then cross-verified for their antigenic properties using another antigenicity predicting database VaxiJen v2.0. We found that approximately two to three of the peptide epitopes within these genes are probable antigens; strongly binding alleles of MHC class II as well as capable of inducing IFN-gamma secretion. We strongly recommend that further insight into this bioinformatics results will help in understanding the prospective candidates for an efficient MTB vaccine which can be targeted against both active and latent MTB infection. The peptides will be further validated experimentally.

A bacteriophage based novel post-harvest protection strategy for perishable crop

Pinal Ghadiya, Nishani Sakariya, Jeenal Mehta and Anil Kumar Singh*

Presenting Author
sakariyanishani9399@gmail.com, pinal.ghadiya@gmail.com
Post-harvest decay of fruits and vegetable is one of the major concern as about 20-25% of the harvested fruits and vegetables are decayed by pathogen. Plant pathogens are often known as disastrous microorganisms around the world. These pathogen induce decay on a large number of agricultural crops during the growing season and post-harvest. However chemical pesticides, insecticides, antibiotics are used as a weapon for controlling the pathogen, but has major obstacles like contamination of perishable agricultural product with pesticide residue and many pesticide resistant superbugs are emerging. So the recent trend is shifting towards safer and more eco-friendly alternatives for the control of the post-harvest decay. *Erwinia carotovora* is a plant pathogen which causes soft rot and stem rot disease in crops like carrot and potato. To control this pathogen, we isolated a bacteriophage against it. For post harvesting use and to increase the shelf life, we use the bacteriophage against the pathogen and it requires matrix on which it can be immobilized. The coating we used is a biodegradable, neutral polymer, chitosan on fruits and vegetables. The chitosan incorporated with agents like bacteriophage, which will prevent the crop from getting infected by the pathogen.

**In vitro comparative study of antibiotics alone and its combination against Mycobacterium, Salmonella and Shigella by dilution method**

*Nishtha Desai, Durva Parekh, Ravi Ranjan*


Presenting Author

nishthadesai99@gmail.com

A limited repertoire of antimicrobial agents is currently in use for the treatment of infectious diseases. The *in vitro* activities of some antibiotics and their synergistic effect were compared against pathogenic bacteria. Inhibitory effect of nine antibiotics against three pathogenic bacteria was determined by the dilution method. Rifampicin was the most active agent tested against *Mycobacterium smegmatis*, inhibiting 96.76% of strains at a concentration of 100µg/ml. Streptomycin and tobramycin exhibited effectiveness against *Salmonella typhi* and *Shigella sonnei* by inhibiting microbial growth 93.08% and 98.93% respectively. Antibiotic synergy studied by the same dilution method by combination of three showed that effectivity of synergistic combination was more as compared to individual antibiotics. Synergism among rifampicin, penicillin and clarithromycin was tested for *Mycobacterium smegmatis* and found 98.34% inhibition of organisms. Azithromycin, co-trimoxazole and streptomycin synergism was demonstrated for the combinations against *Salmonella typhi* by inhibiting 94.34% bacteria in liquid media. *In vitro* test can be further tested by clinical trials for validation of results.
Characterization and Partial purification of antibacterial compound from endophytic actinomycetes *Micrococcus yunnanensis*

**Palak Sardhara, Asha Humble, Ravi Ranjan***

Shree M & N Virani Science (Autonomous) College, Rajkot, Gujarat

**Presenting Author**

palaksardhara2113@gmail.com

Endophytic actinomycetes are considered as one of the relatively unexplored potential source in search of antibiotic producer against antibiotic resistant pathogenic bacteria. Endophytic actinomycetes from medicinal plants were screened to evaluate their antibacterial potential. A total of 11 different isolates were obtained from different parts of plant, among which 27.27% showed antibacterial activity against one or more pathogenic bacteria. A potent strain showing antibacterial potential against antibiotic resistant *Staphylococcus aureus* was characterized. This organism was designated as *Micrococcus yunnanensis* strain rsk5 on the basis of morphological, biochemical and molecular characteristics. Antibacterial substance was extracted by solvent extraction and partially purified by chromatography. Ethyl acetate was found to be suitable solvent for extraction of antibacterial substances from the culture filtrate. Further separation of metabolites from metabolic mixtures was done by thin layer chromatography using chloroform-methanol (24:1, v/v). It was partially purified by flash chromatography followed by HPLC and analyzed by ultraviolet visible spectrophotometer to get absorption maxima at 208.4 nm. This is the first report describing the isolation of *Micrococcus yunnanensis* from plant source showing antibacterial potentials against human pathogen.

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**Purification of cold active lipase from psychrophiles**

**Preeti Reddy, Leena Ambasana***

Shree M. & N. Virani Science College, (Autonomous) Rajkot, Gujarat.

**Presenting Author**

reddypreeti08@gmail.com

Psychrophiles are microorganisms that live and grow better in temperatures that are about -10 to 20°C (14 to 68°F). The enzymes as well as other cellular proteins from psychrophiles are of great interest because of their activity at low temperature. Therefore, the isolation of psychrophilic bacteria
from natural sources and their identification are important in terms of discovering novel industrial enzymes. Keeping this view, in present study, an attempt was made to isolate psychrophiles, study its enzyme profile and purify lipase from it. Psychrophiles were isolated from frozen food stuffs and deep freeze ice and were further screened for industrially important lipase production. Identification of the isolates was done based on biochemical and morphological characterization. Optimum temperature for the growth of psychrophiles was also determined. Here the main aim was to purify lipase from psychrophiles which shows activity and stability at low temperature. Optimum conditions like pH, temperature and incubation period for production of extracellular lipase were also determined.

IPP27

Analysis of heavy metal contamination of urban soils and street dusts in Delhi-NCR region and its phytoremediation

Ram Sunil Kumar Lalji1*, M. Ramananda Singh1, Gargi J.1, Bikram B.1, Rishika R.1, Zaheer A.1, Garima K.1, Preeti G.1, Clinton T.1K. K. Halder2, Jaiswar Gautam L.3

1Department of Chemistry
2Department of Physics, Kirori Mal College, University of Delhi, Delhi, India.
3Department of Chemistry, Dr. B. R. Ambedkar University, Agra (U.P.), India

Presenting Author
sunilkumarram1980g@gmail.com

Due to rapid urbanisation of Delhi-NCR, there has been tremendous increase in the number of the vehicles and the construction activities. These activities have led to increased level of heavy metal concentrations and other pollutants in the soil along the roads, highways and the industrial regions. This gets reflected in the increased level of heavy metal in the shrubs and other plants along the roads in this region. For the purpose of the study Delhi was divided into five zones and soil samples were collected. The present study aimed at assessment of the heavy metals especially cadmium along the said zones and analysis of pH of the chosen soil samples. The cadmium concentration was as high as 7.58 mg g\(^{-1}\) at AIIMS while the pH varied from 5.5 to 8.3 at different locations. The higher values of concentration of Cd in these places is indicative of anthropogenic inputs, either due to heavy traffic, on-going construction, major dumping sites and landfill. At the same time the concentration values in various zones were found to decrease with the increase in distance from the roadside. For the phytoremediation process five plants namely panda (Ficus Benjamina Panda), enermi (Clerodendron Enermi), hibiscus (Rosa-Sinensis), kaner (Thevetia Peruviana) and mulberry (Morinda Citrifolia)
were chosen and grown considering their economic feasibility, availability, life span etc. and it was found that hibiscus and kaner have shown better uptake capacities for cadmium metal.

**Keywords:** Heavy metals, soil, Phytoremediation, cadmium metal, pH

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**IPP28**

**Assessment of pigment system and biochemical response of hydroponically grown Vigna Radiata under heavy metal stress**

Aishwarya Karelia, Janki Ramani, Praveen Gupta*


**Presenting author**

ramanijanki71@gmail.com

With the expansion of the world population, the environmental pollution and toxicity by heavy metals increasing continuously. Heavy metals including Lead, Nickel, Cadmium, Copper, Cobalt, Chromium and Mercury are hazardous heavy metal pollutants that cause toxic effects to plants as well as animals; they act as stress to plants and affect the plant physiology and cause severe health problem in animals. Pb(NO₃)₃ has been taken as a source of lead at the 300 μM, 600 μM and 900 μM concentration and *Vigna radiata* has been grown hydroponically in Hogland solution along with control plant. With increasing level of lead were reduced in germination and growth compared to control plants. Expected result from this project is that the possibilities hyperaccumulation of lead can be observed in root, stem and leaf. But in stem and leaf the amount of accumulation would be less compared to root. Study would also provide the better insight in phytoremediation and development of heavy metal tolerant plant in future.

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**IPP29**

**Study of differentially-expressed genes (DEGs) in Argyrin A, an anti-proliferative drug treated samples of intestinal adenomatous polyps using an integrated bioinformatics analysis**

Rishabh Jain and Rekha Kumari*

DS Kothari Centre for Research and Innovation in Science Education, Department of Zoology, Miranda House, University of Delhi, Delhi 110007

**Presenting Author**

rishabh173@gmail.com

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Cell cycle regulation is a result of interplay of cyclin and cyclin dependent kinases (CDKs). One of the cyclin dependent kinase inhibitor, 1B gene (CDKN1B), which encodes the protein p27 (Kip1) is shown to play an important role in controlling the cell cycle, growth and division. The p27 normally blocks cells from entering the DNA synthesis phase of cell division and induces apoptosis through the inhibition of 20S proteasome, hence a tumor suppressor gene. Argyrin A, a cyclic peptide drug derived from the myxobacterium *Archangium gephya* is useful to prevent the destruction of the p27 protein. In order to find DEGs in the treated and the control samples of the Argyrin A a microarray dataset, GSE8565, was retrieved from Gene Expression Omnibus (GEO, NCBI). The GEO2R tool was used for prediction studies using bioinformatics tools to evaluate these datasets. DEGs were found out with the help of Gene Ontology (GO) and pathway enrichment tools and annotation was done. DAVID and Cytoscape software were used to study the Protein-protein interaction (PPI) among DEGs. Also their biological function and interaction were analysed to understand pathway enrichment of selected DEGs. In this study we identified a total of 121 DEG genes. An important relationship was detected among FGF1, FGFR2, VEGFA, FLT1, ERAP1, LRP1. These genes were mainly involved in the cytokine-cytokine interaction, vasculature development, angiogenesis, RAS, Rap 1 and PL3K-Akt signalling pathways. Further probing at the protein level can help in developing increased understanding of the genes that are differentially regulated at the time of treatment of the Argyrin A drug. The detailed graphical representations of the analysis and results will be discussed.

### IPP30

**Bio prospecting of turmeric and beet root extract**

**Chudasama Smitaba P., Dr.Shivani Patel*  
Shree M. & N. Virani Science (Autonomous) College, Rajkot, Gujarat**

**Presenting Author**

chudasamasmitaba@gmail.com

Turmeric (*Curcuma longa*) and beet root (*Beta vulgaris*) extract contains pigments that are used for various purposes in ancient time. The turmeric pigments were extracted with various solvents like methanol, ethanol, and distilled water using evaporation method and pigments from beet root are extracted by soxhlet apparatus with methanol and distilled water having slightly acidic condition. Then the pigment are dissolved in respective solutions and used for studying various prospects like as pH indicator, as gel tracking dye, staining of cells and stages of cell cycle and as dyeing agent for clothes. Among the turmeric extracts pigments are more likely dissolved in ethanol and pigments of beet root are in methanol. The both pigments indicate pH. They give different colours at various pH starting from 8-13. In cloth staining ethanol extract of turmeric is more effective and beet root gives
poor results. As gel tracking both turmeric and beet root extracts are effective and they contain negative charge. And as cell staining both turmeric and beetroot extracts gives fine results.

IPP31

*Mycobacterium tuberculosis* latency associated proteins Rv2003c, Rv1736 and Rv1737c targeting host mitochondria may have role in persistence of pathogen

Pragya1*, Sonika Bhatnagar1*, Dr. Monika Sharma2, Dr. Sadhna Sharma2

1 Ambedkar Centre for Biomedical Research, University of Delhi

2 Department of Zoology, Miranda House, University of Delhi

Presenting Author

bhatnagar.sonika@yahoo.com

Tuberculosis (TB) has become a major health problem in world and ranks alongside HIV as a leading cause of death. One of the major concerns associated with TB is its latency which helps *Mycobacterium tuberculosis* (*M. tb*) to survive in host cell under stress conditions. There are evidences of many bacterial pathogenic factors which target host mitochondria and make host cell a safe niche for intracellular pathogens. Thus, we hypothesised that *M. tb* DosR proteins may target host mitochondria and this interaction may regulate the latency. Protein sequences of DosR regulon genes of *M. tb* strain H37Rv and their orthologs in avirulent strain H37Ra, clinical isolate CDC1551, *M. bovis* BCG Pasteur strain and *M. smegmatis* were analysed by various Bioinformatic tools(MitoProt II and PsortII) for mitochondrial targeting. The Mitoprot II score of above 0.6 and PsortII score of above 30% was set as criteria for selecting proteins being targeted to mitochondria. We observed that Rv2003c, Rv1736 and Rv1737c and their orthologs in *M. tb* H37Ra, *M. tb* CDC1551 and *M. bovis* showed high probability of mitochondrial targeting under the selected criterion. The orthologs of Rv2003c and Rv1736 were absent in avirulent *M. smegmatis*, whereas Rv1737c ortholog in *M. smegmatis* did not show mitochondrial targeting. DosR regulon proteins Rv2003c (conserved hypothetical protein), Rv1736 (nitrate reductase) and Rv1737c (nitrate/nitrite transporter) and their orthologs in virulent *Mycobacterium* species show mitochondrial targeting and may have key role in regulating host cell survival. The absence of orthologs of these genes in avirulent *M. smegmatis* or the inability of *M. smegmatis* orthologs to be targeted to mitochondria further emphasize the relevance of these genes in virulent *M. tb*. These proteins may help virulent *M. tb* to adapt and persist in stressful microenvironment of host cell. The role of these proteins in regulating apoptosis needs to be validated experimentally to understand the pathogenesis of latent TB.
Evaluation of eco-friendly natural plant extract as an alternative to the synthetic fungal growth medium

Stuti Yadav, Shivani Patel
Shree M. & N. Virani Science (Autonomous) College, Rajkot, Gujarat

Presenting Author
stutiyds@gmail.com

Complex nutritive mixtures have been added to various growth mediums in past decades. Nowadays media with chemically defined components are majorly used which at the extreme purity of components become expensive. Hence complex natural extracts can always be low cost substitutes of the chemically defined expensive media. It can be thus concluded that Marigold, Rose and Jasmine flower extract contains both Carbon and Protein source to support the growth of fungus. Hence Marigold extract was designed for Fungal Growth. The biochemical analysis and chromatographic study of these extracts were carried out and these extracts were found to be promising alternative to the synthetic fungal growth medium.

Protein quantitation utilizing natural plant dye reagents

Vandan Patel, Aarti Patel*, Dr.Shivani Patel*
Shree M & N Virani Science (Autonomous) College, Rajkot, Gujarat

Presenting Author
vandanpatel2797@gmail.com

Dyes are and have always been integral part of our life. Utilization of natural dyes has diminished over years due to easily available and economically cheaper synthetic dyes. However, exploring natural dyes for biological applications can meet the shortcomings of synthetic dyes; natural dyes are biodegradable, less toxic, and non-polluting to the environment. In this investigation, aqueous and organic solvents extraction process using methanol, chloroform, 80 % ethanol, Absolute ethanol, acetone, Alkanine and acidic solvents were carried out with five different plants namely: Jatropha curcas leaves, Magnifera indica fruit peels, Delinoxregia flowers, Bougainvillea glabra pink flowers and Tradescantia pallida leaves extract to prepare dye reagents. These natural dye reagents were
used to quantitate standard protein and compared to the existing assay. The natural dye reagents procured protein quantization with better sensitivity.

**IPP34**

**Low cost automated colony counter and blood cell analysis tool**

**Yogit Babariya, Dr. Ashish Kothari* and Dr. Shivani Patel***


Presenting Author

byogitkumar@gmail.com

Practicals we daily perform in microbiology and biotechnology lab requires the perfect count of the bacterial colonies. Colony counters are used to count colonies which are grown on an agar plate. The counting is accomplished manually in the laboratory, often by use of touch pressure and a digital counter. In this project, we have designed a very simple machine and software with image analysis tool which can be installed in computer or Mobile Phone and is suitable for basic bacterial enumeration on standard agar plates. If we use automatic colony counter then we can have accurate counting of the grown colonies. The proposed machine can also be used successfully as Blood cell counter.
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