

ABSTRACT BOOK

International Webinar on “Current Challenges and Future Prospects in Microbiology”

(June 15, 2021)

Jointly organized by



**DEPARTMENT OF MICROBIOLOGY
MAHARAJA GANGA SINGH UNIVERSITY BIKANER-334004**

&



MICROBIOLOGISTS SOCIETY, INDIA

PATRON

Prof. Vinod Kumar Singh
Vice-Chancellor
M.G.S. University, Bikaner

ORGANIZING COMMITTEE

Chairman

Prof. A.K. Chhangani,
Head
Department of Microbiology
M.G.S. University, Bikaner

Organizing Secretary

Dr. Gautam Kumar Meghwanshi
Assistant Professor
Department of Microbiology
M.G.S. University, Bikaner

Coordinators

Dr. Dharmesh Harwani

Assistant Professor
Department of Microbiology
M.G.S. University, Bikaner

Dr. Abhishek Vashishtha

Assistant Professor
Department of Microbiology
M.G.S. University, Bikaner

DEPARTMENT OF MICROBIOLOGY, MGS UNIVERSITY, BIKANER

&

MICROBIOLOGISTS SOCIETY, INDIA

Jointly Organizes



International Webinar on

“Current Challenges and Future Prospects in Microbiology”



Prof. Vinod Kumar Singh
Vice Chancellor
MGS University, Bikaner
Patron

INVITED SPEAKERS



Prof. Arvind Deshmukh
President,
Microbiologists Society,
India



Prof. Ashish Bhatnagar
Head,
Deptt of Microbiology,
MDS University,
Ajmer



Prof. Tanzima Yeasmin
Deptt. of Biochem. &
Mol. Biology,
University of Rajshahi,
Bangladesh



Prof. Monica Bhatnagar
Deptt. of Microbiology,
MDS University, Ajmer



Prof. Praveen Gehlot
Deptt. of Botany,
JNV University
Jodhpur



Dr. Sarvesh Soni
Research Scientist,
RMIT University,
Australia

ORGANIZING COMMITTEE



Prof. A. K. Chhangani
Head,
Department of Microbiology
MGS University, Bikaner
Chairman



Dr. Gautam Kumar Meghwanshi
Assistant Professor
Department of Microbiology
MGS University, Bikaner
Organizing Secretary



Dr. Dharmesh Harwani
Assistant Professor
Department of Microbiology
MGS University, Bikaner
Coordinator



Dr. Abhishek Vashishtha
Assistant Professor
Department of Microbiology
MGS University, Bikaner
Coordinator

Date: 15-6-2021 (Tuesday)

Time : 11.00AM

Registration Link : <https://forms.gle/KZ889XkSRvS5JPob8>

Link to join: <https://technicalteam2.webex.com/meet/drharwani>

Catch us live on YouTube : <https://youtube/SnGBuSUGpPI>

or go directly to MGSU Bikaner, Microbiology LIVE Channel

Prizes for winners of Poster Presentation

E certificates for all the Participants

Full length papers are invited for publication as Conference Proceedings

CYANOBACTERIA: A BOON TO TACKLE OXYGEN CRISIS

Deepthi. Ch, Varsha Asha Krishna, Alekhya. Ch

Department of Microbiology

St. Pious X Degree and PG College for Women, Nacharam, Hyderabad-50076, Telangana, India.

ABSTRACT

Cyanobacteria are aquatic and photosynthetic microorganisms which live in water whose size ranges from 0.5 - 60 micrometre. They are also called 'Blue-green algae'. *Spirulina, Microcystis, Anabaena, Nostoc, Oscillatoria* are a few examples of cyanobacteria. Many people only experience algae in bad situations - such a big problem in local lakes, contaminants, red tides poisoning sea foods. But Algae also known to have a key role in production of Sustainable biofuels, CO₂ consumption, source of active pharmaceutical drug compounds and also in oxygen supplementation. Phycology researchers are on their way to appreciate 'cyanobacteria- as an important source of breathable oxygen'. In recent times, India has suffered a lot from the oxygen supplement crisis during Covid-19. Oxygen from algal biomass can be utilised by Low oxygen saturation level patients. Biological oxygen bars can be set up to put a check to oxygen supplement shortage, especially in highly polluted cities like Delhi, Varanasi, Mumbai, Lucknow after the development of this concept to commercial production level. The oxygen in today's atmosphere is almost entirely the result of photosynthetic living forms, which had its start with the appearance of blue green algae (cyanobacteria) among the microorganisms. Today the production of algae (50% of all oxygen production) is another reason for saying 'our lives depend on algae'. In modern times people are turning to algae for help. Cyanobacteria produces oxygen as a by-product of its metabolism. A single celled algal organism 'prochlorococcus' roughly produces 20% of world oxygen just on its own. That oxygen can be made fit for human inhalation and by lowering the toxicity of cyanotoxins produced. No wonder, this oxygen producing cyanobacteria may also make life sustainable on Mars. Though this will be a remarkable development in the field of microbiology, oxygen from natural trees is the best source of oxygen to protect our planet Earth.

Key Words: Cyanobacteria, Biological Oxygen Production, Tackle Oxygen Crisis

**ETHNO-MEDICINAL PLANTS USED IN THE PREPARATION OF TRADITIONAL
RICE-BEER BY THE TIWA TRIBES OF NAGAON DISTRICT OF ASSAM, INDIA**

Sanjeeb Kumar Nath

Associate Professor & HOD, Department of Botany, Dhing College

Dhing, Nagaon, Assam 782123

ABSTRACT

The Rice-beer is popular among the people of Assam bearing traditional significance. The Tiwa people of Nagaon district of Assam believe that Rice-beer has a special property that can treat some ailments in human and livestock. Some common plants which are used widely for the preparation of rice-beer have been identified. The identified plants used in rice-beer preparation have been used mainly possess ethno-medicinal value. The knowledge of the process of rice-beer preparation is restricted to certain aged and experienced persons; a documentation of the process was felt necessary. The present study reveals that nine ethno-medicinal plants are used for the preparation of rice-beer. This traditional knowledge needs proper documentation or scientific study. Henceforth the present research work is based on the survey of ethno-medicinal plants used for the preparation of the Rice beer. This paper mainly focuses on the subsequent studies at the molecular level for the efficacy of the traditional knowledge of these plants.

**ANTIMICROBIAL RESISTANCE AND VIRULENCE GENE PROFILE OF
MULTIDRUG RESISTANT *ESCHERICHIA COLI* ISOLATES FROM DIARRHEIC
NEONATAL DROMEDARY CAMELS**

Shirish Dadarao Narnaware*, Rakesh Ranjan

ICAR- National Research Centre on Camel, Post Bag No. 07, Jorbeer, Bikaner, Rajasthan 334001.

* *Email*: drshirish009@gmail.com

ABSTRACT

Incidence of neonatal diarrhea was observed in total 42 (20.68%) neonatal dromedary camels of an organized camel farm during the four years period. The diarrheic neonatal camels were dull, depressed, weak, unable to suckle and had yellowish or greenish, watery to pasty diarrhea. In three cases, mucous and blood was also observed in diarrheic feces and had subsequent mortality. Bacterial culture of rectal swabs from diarrheic camels resulted in isolation of *Escherichia coli*. Antimicrobial susceptibility studies showed that all 42 isolates exhibited multidrug resistance to six antimicrobial agents *viz.* penicillin-G, amoxicillin, cloxacillin, erythromycin, lincomycin and trimethoprim. Apart from that majority of the isolates also exhibited resistance for amoxicillin/ sulbactam (n=37), chloramphenicol (n=34), streptomycin (n=31) and ceftriaxone (n=30). Whereas, most of the isolates were sensitive to amikacin (n= 38), gentamicin (n= 38) and cephoxitin (n=26). The PCR for virulence gene profiling revealed that 38 isolates possess at least one virulence factor. The detection rates of stx1, stx2, eae, F41, K99 and sta virulence genes were 9.52%, 33.33%, 35.71%, 23.80%, 16.66% and 21.42%, respectively. Based on occurrence of these virulence genes the isolates were pathotyped as shiga toxin producing *E. coli* (STEC) (23.80%), attaching and effacing shiga toxin producing *E. coli* (AE-STEC) (7.14%), enteropathogenic *E. coli* (EPEC) (14.28%), enterotoxigenic *E. coli* (ETEC) (28.57%) and mixed pathotypes (16.66%). The three neonatal camels having bloody diarrhea and mortality were found to be of STEC (n=2) and AE-STEC (n=1) pathotype. The findings of this study indicate that neonatal camels are the possible reservoir of multidrug resistant *E. coli* pathotypes including zoonotic STEC, hence adoption of good management practices and selective use of antimicrobials deemed essential to safeguard the life of neonatal camels as well as public health.

IDENTIFICATION AND DIVERSITY ANALYSIS OF *LACTOBACILLUS* IN THE HUMAN BODY

Sneha.U¹, Priyanka.U¹, Ankush Chaudhari¹, Hadagali Ashoka^{2*}

¹BMS College of Engineering, Bengaluru, India

²BMS College of Engineering, Bengaluru, India

*Corresponding author Tel: +91-9902433100, E-mail: hadagaliashoka.bt@bmsce.ac.in

ABSTRACT

Lactobacillus sp. are facultatively anaerobic, catalase-negative, Gram-positive, non-spore forming rods that often grow better under microaerophilic conditions. The genus *Lactobacillus* is taxonomically complex and is composed of 170 species and 17 sub-species. Although they are part of the normal human gastrointestinal, oral cavity and vaginal flora, they can also be occasional human pathogens.

Our objective was to provide new insight to the relationships of Lactic Acid Bacteria (LAB) species, specifically those within genera *Lactobacillus* and to examine the utility of such an analysis in the context of LAB phylogeny.

These findings highlight the need to gather and analyse data on various *Lactobacillus sp.* in different parts of the human body like saliva, surface of tongue, vagina and gut, the number of dominant species collected through literature review were found to be 5, 11, 6, 41 respectively. The greatest diversity being present in the GUT. The sequences of these various species have been retrieved and were analysed phylogenetically for similarity among the species and 5 different trees were constructed using the MEGA software. The UPGMA tree thus obtained gave a better interpretation of the evolutionary relationship between the species.

16S rRNA METAGENOMIC ANALYSIS OF ORAL CARCINOMA SAMPLES

Dhanush B¹, Harshini K¹, Shriya Prasanna¹, Hadagali Ashoka^{2*}, Vidya Niranjana³

¹B M S College of Engineering, Bengaluru, India

³RV College of Engineering, Bengaluru, India

*Corresponding author, Tel: +91-9902433100, E-mail: hadagaliashoka.bt@bmsce.ac.in

ABSTRACT

The oral microbiota is vital for human health, and imbalances between microbes and their hosts can cause oral and systemic diseases, which are typically caused by bacteria and contribute to cancer. Oral cancer is a fatal malignancy and the sixth most common cancer worldwide. Oral squamous cell carcinoma (OSCC) is the most frequently occurring oral cancer, accounting for over 90% of all oral cancers. Metagenomics using next generation sequencing technologies has produced microbial and genomic profiles to study the relationships between microbial diversity and oral diseases. This study aims to report the oral microbiota and its association with oral cancer, using 16S rRNA Amplicon sequencing and predict the possible causative microbial genera. DNA was extracted from the buccal mucosa and jaw tissue of oral cancer patients and non-cancer individuals as controls. Metagenomic analysis was performed using the tools, USEARCH, MG RAST and COSMOS ID. The Statistical analysis was carried out using CLC Genomics Workbench 21.0.4. OTU Clustering and annotation identified 93 bacterial genera in all three samples (OSCC, OPMD, and Healthy). The alpha-diversity of oral cancer patients was higher than that of the control group, and the beta-diversity differed significantly. Furthermore, the abundance ratio of bacterial species varied considerably among the three groups. Fusobacterium, Streptococcus, Prevotella, Alloprevotella, Corynebacterium, Brevundimonas, and Caulobacterium were more abundant in the cancer group compared to the control and are opportunistic pathogens with potential correlations with OSCC. Whereas Neisseria, Rothia and Haemophilus were less abundant among the others. In this study, we observed an increased bacterial diversity in oral cancer patients and found distribution changes for some bacteria. The identified microbial signatures could be a biomarker for predicting OSCC or for clinical risk assessment of oral cancer. These findings may provide insights into the development of vaccines and/or antimicrobial therapies to prevent OSCC. Keywords: 16S rRNA Amplicon sequencing, Metagenomics, Oral microbiota, Oral Squamous Cell Carcinoma (OSCC), Oral Potential Malignant Disorder (OPMD)

NANOMATERIALS -A PROMISING ALTERNATIVE FOR BIOFUELS PRODUCTION

S. Sreedevi*, Rajeetha Mondal, P.L.Sravani

Department of Microbiology

St. Pious X Degree and PG College, Hyderabad, Telangana, India

*drsreedevi163@gmail.com

ABSTRACT

The rapidly growing population and the advent of globalization and industrialization, has trumped the worlds energy production due to exhaustive utilization of fossil fuels. This in turn will lead to sustainability problems such as huge fluctuation in prices, environmental impacts and declining quantity of fossil fuels. In order to meet the intense energy demands of future generation, sustainable and cost- effective alternate energy sources should be explored. Bioenergy in the form of Biodiesel, Bioethanol and other Biofuels have gained importance because of their inherent advantages such as renewability, sustainability and lower emission of greenhouse gases. Biofuels are commercially produced from vegetable oils, animal fats, carbohydrates, lignocellulosic biomass and microbial biomass using conventional processes like fermentation and transesterification. However, these processes offer challenges in the form of higher cost of production and other technological barriers. Hence, to make these processes energy efficient and more cost effective, efforts are required for development of production and optimization strategies. Nanotechnology offers a promising alternative that contributes efficiently to biofuel production industry using nanoparticles. Nanoparticles displays unique physical, chemical and biological properties and are differentiated from their large scaled counterparts. These properties are due to larger surface area to the volume, energy absorption, chemical reactivity and stability, greater mechanical strength that has led to wide range of applications. Various nanomaterials have been explored potentially for their capabilities in biofuel production. Nanotechnology could offer meaningful solution by altering the characteristics and properties of feed materials and biocatalyst used for biofuel production. Nanomaterials plays a vital role in energy fields due to their unique structure, high energy electrical storage capacity, high specific area and comparatively good efficiency of heating and lighting. This paper will review the production of biofuels from renewable sources using nanotechnology and the phenomenal characteristics of nanoparticles.

VIABILITY STUDY OF PROBIOTIC BACTERIA IN FERMENTED MILK BOOSTING IMMUNITY AGAINST CORONA VIRUS

K M Lakshmi Shruthi, Jameema Sidhic and Prakash M Halami*

Department of Microbiology and Fermentation Technology, CSIR- Central Food Technological Research Institute, Mysuru-50020

*Email: prakashalami@cftri.res.in

ABSTRACT

Probiotics are the live microorganism on ingestion it provides health benefits. Recent experimental results have demonstrated that the effect of the SARS-CoV-2 virus isn't limited respiratory tract. The SARS-CoV-2 virus detected within the gastrointestinal tract of COVID 19 patients, and several patients are reported with diarrhea as one of the symptoms. The utilization of probiotics for the treatment of COVID-19 Patients is a lively area of clinical research. Only one paper has been published about the usage of probiotics for the treatment of COVID-19 patients. Seventy patients with acute covid 19 symptoms have been randomly chosen. Patients were provided with an eight-strain probiotic mixture for two weeks at 2.4×10^{12} bacteria per day. Significantly more patients with diarrhea on admission who took the probiotic combination had their diarrhea resolved by day 3 (93%) compared to patients who didn't take the probiotic mix. Interestingly, the chance of respiratory failure was also significantly higher for those not taking the probiotic mixture. Immunity boosting shelf-stable curd is beneficial in this manner which consists of three different strains of probiotic bacteria like *Lactobacillus fermentum*, *Lactococcus lactis*, and *Bifidobacterium longum*. *Bifidobacterium longum* is the potential probiotic that shows increased anti-inflammatory marker IL4 and IL10 in the diseased model compared to the control. Elevated production of CRP protein can also take in control by having *B. longum* in an adequate amount. Compared to other probiotics in the market, probiotic curd has a shelf stability of 30 days concerning the colony count and pH values. Bacterial viability refers to the ability of a cell to grow and subsequently generate a colony of cells under defined environmental conditions. Viability is generally considered a prerequisite for probiotics' functionality as it relates to consumers' health promoting properties; thus, it constitutes an industrial challenge. Generally accepted CFU/ml during consumption is 10^6 , and the shelf-stable probiotics curd consisting of 10^7 CFU/ml even after four weeks of refrigeration. Due to

its health benefits and shelf stability, the particular product can be given to covid patients for their easy recovery.

BIOPROSPECTING ANTIOXIDANTS IN SOME NON-HETEROCYSTOUS FILAMENTOUS CYANOBACTERIA ISOLATED FROM CHILIKA LAKE

Sabyasachy Parida* and Biswajit Rath

Department of Biotechnology, Maharaja Sriram Chandra Bhanja Deo University

Sriram Chandra Vihar, Takatpur, Baripada-757003, Odisha

*Email: sabyasachy.biotech@gmail.com

ABSTRACT

Increased population, climatic changes and shortage of nutrition constitute global challenges demanding actions and strategic planning for securing access of food, feed, biochemicals and other biotechnological potentials in near future. Therefore, alternative sources demand innovative thinking, and for which cyanobacteria offers a great potential to meet future challenges. The present investigation is mainly focused on the study of antioxidant property of cyanobacteria isolated from Chilika lake. In the present investigation, four species of cyanobacteria *Oscillatoria princeps*, *Anabaena oscillarioides*, *Lyngbya stagnina* and *Planktolyngbya limnetica* were extracted using three solvents (methanol, acetone and benzene). Antioxidant activity was assessed by DPPH and ABTS radical scavenging assay. The methanol extract of *O. princeps*, *L. stagnina* & *P. limnetica* and acetone extract of *A. oscillarioides* exhibited higher concentration of total phenolic content (TPC) followed by benzene extract. Further, *O. princeps* showed highest concentration of TPC (0.0691 mg/ml) among the four species. The Methanolic extract of all the four test species showed the highest total flavonoid content (TFC) as compared to acetone and benzene extract. Among the four species methanolic extract of *O. princeps* showed highest TFC (0.0382mg/ml). In DPPH radical scavenging activity it was observed that the methanol extract exhibited relatively higher activity than the acetone and benzene extract. The methanolic extract of *O. princeps* exhibited highest scavenging activity (81.21%) as compared to standard (ascorbic acid i.e 88%) and the IC₅₀ of the extract was 293.4µg/ml, while that of standard (ascorbic acid i.e 226.7µg/ml). Similarly, in the ABTS scavenging assay, the Methanolic extract of *O. princeps* and *A. oscillarioides* was found to be effective in scavenging radicals and the increase was concentration dependent. Among the three solvents used, the methanolic extract displayed the highest free radical scavenging assay followed by the acetone and benzene extract.

Keywords: Antioxidant, ABTS, Cyanobacteria, DPPH, Flavonoids, Phenol

A COMPARATIVE STUDY ON THE FERMENTATION POTENTIAL OF YEAST STRAINS IN PADDY STRAW ETHANOL CONVERSION

Annu Goel^{1*} and Leela Wati²

¹Central Pollution Control Board, East Arjun Nagar, Shahdara,
Delhi 110032, India

²Principal Scientist, Department of Microbiology, CCS Haryana Agricultural University,
Hisar-125 004, India

*Email: anugoel.micro@gmail.com

ABSTRACT

With the aim to develop sustainable transportation fuel, the present work was carried out to expedite the bioethanol production from paddy straw by comparing the fermentation potential of three different yeast strains individually (*Saccharomyces cerevisiae* HAU-1, *Pachysolen tannophilus* and *Candida utilis* as well as co-culture. The lignocellulosic bioethanol production involves 3 steps- delignification, saccharification and fermentation. The paddy straw was treated with alkali (2% sodium hydroxide) resulting 87.48% lignin removal. Alkali treated straw was hydrolyzed using commercial cellulase with exoglucanase activity 30 IU/ml and endoglucanase activity 33 IU/ml at 50°C for 2h resulting about 75% saccharification of delignified paddy straw. The fermentation of paddy straw hydrolysate at 30°C for 72 h resulted in maximum 26.0 ml/L ethanol production with *S. cerevisiae* strain HAU-1. On co-inoculation of *S. cerevisiae* HAU-1 and *P. tannophilus* under similar conditions about 7% expedition in ethanol production was achieved.

ANTIHYPERTENSIVE PEPTIDES DERIVED FROM FERMENTED CAMEL MILK BY PROTEOLYTIC LACTOBACILLI (*IN SILICO* & *IN VITRO* STUDY)

Subrota Hati*, D. Solanki, Amar Sakure and Prajapati JB

Dairy Microbiology Department, SMC College of Dairy Science, Anand Agricultural University, Anand-388110, Gujarat

*Email: subrota_dt@yahoo.com

ABSTRACT

Camel milk is known for many health attributes such as anti-inflammation associated with obesity, anti-carcinogenic, anti-diabetic and antihypertensive. Rising health problems, especially hypertension was reported to heal through eating habits. Angiotensin I-converting enzyme inhibitory peptides produced by fermentation of camel milk are reported to reduce hypertension without any side effects. 09 exhibited highest PepX activity (0.893) compared to control up to 12h of incubation at 37°C. Camel milk fermented with lactic culture showed significant increase in ACE-inhibitory activity with the time of incubation. 09 exhibited highest ACE-inhibitory activity (76.75%) compared to control up to 48h of incubation at 37°C. After 48h of incubation, 09 produced 2.487% lactic acid while it reduced pH of camel milk from 6.55 to 3.17 after 48h at 37°C in camel milk. It also showed 11.33 log cfu/ml of lactic counts during the incubation of 48h at 37°C. 09 exhibited maximum proteolytic activity at the rate of 2% and 12h of incubation at 37°C. So, 2% rate of inoculation and 12h of incubation was optimized for the peptide production. 09 showed higher peptide production (47.50%) compared to control under optimized growth conditions. In case of dipeptidase activity, 09 showed dipeptidase activity (0.080) in intracellular samples while in case of extracellular extract it showed 0.277 at the 2% rate of inoculation and 12h of incubation at 37°C. In case of tripeptidase activity, 09 showed tripeptidase activity (O.D. 0.077) in intracellular extract while in case of extracellular extract, it showed tripeptidase activity (O.D. 0.296) under optimized growth conditions. 3kDa permeate and 10 kDa permeate showed highest ACE-inhibitory activity compared to other 5 kDa permeate/retentate, 10 kDa retentate and 3 kDa retentate. Extensive homology search in NCBI (Uniprot/SwissProt database) and PIR revealed the peptide matched with camel milk protein, precursor and protein fragments. Peptides were found matched with many reported sources of ACE-inhibitory peptides with the similar type of sequences.

**PRODUCTION OF ORGANIC ACIDS AND B-VITAMINS FROM INDIGENOUS
YEAST AND LACTIC STRAINS ISOLATED FROM FERMENTED FOODS OF GARO
TRIBES IN MEGHALAYA**

Sujit Das¹, B.K. Mishra¹ and Subrota Hati^{2,*}

¹*Department of Rural Development and Agricultural Production, North-Eastern Hill University, Tura
Campus, Meghalaya- 794 001*

²*Dairy Microbiology Department, SMC College of Dairy Science, Anand Agricultural University, Anand,
Gujarat- 388 110*

*Email: subrota_dt@yahoo.com

ABSTRACT

Lactic acid bacteria and yeasts are profoundly considered to produce essential vitamins like riboflavin, folate, cobalamin and organic acids which have health impacts (anti-obesity, anti-diabetics, antimicrobial and other chronic diseases prevention). These compounds are essential for cellular and metabolic activity of living system. In the study, five potent lactobacillus isolates viz, KGL2 (*L. fermentum*), KGL3A (*L. plantarum*), KGL4 (*L. fermentum*), RNS4 (*L. rhamnosus*), WTS4 (*L. fermentum*) and five yeast isolates viz, WTS1A (*S. cerevisiae*), WKF2B (*S. cerevisiae*), KGL4A (*Pichia kudriavzevii*), WBS2A (*S. cerevisiae*), NGL1B (*S. cerevisiae*) were considered for vitamins (B2, B12 and B9) and organic acids production (lactate, butyrate, acetate). However, out of the all the five lactic strains, KGL3A had shown highest B2 production (0.7µg/ml) while KGL2 exhibited maximum B12 production (0.05µg/ml) after 36 h. Moreover, WTS4 attributed highest folate production (0.09µg/ml) after 24 h. In addition, RNS4 reported the maximum organic acids production (0.77gm/l acetic acid, 0.26 gm/l lactic acid and 0.008gm/l butyric acid). Similarly, with reference to the five yeast isolates employed, WTS1A had shown high B2 production (0.5µg/ml) and WKF2B showcased with maximum B12 production (0.06 µg/ml) after 36 h followed by highest folate production (0.10 µg/ml) after 12 h. Moreover, WTS1A reported with 0.0183 gm/l acetic acid and 0.002 gm/l butyric acid production respectively. Furthermore, these vitamin and organic acids producing strains of lactic acid bacteria and yeasts could be a worthwhile substitution to fortification programmes and prove beneficial for elaboration of novel vitamin-enriched fermented food products.

Keywords: *Lactic acid bacteria; yeasts; vitamins; organic acids; fermented foods.*

EVALUATION OF ANTIOXIDANT AND PHYTOCHEMICAL POTENTIAL OF LICHENS COLLECTED FROM SIMILIPAL BIOSPHERE RESERVE, INDIA

Bijayananda Sahoo and Biswajit Rath

Department of Biotechnology, Maharaja Sriram Chandra Bhanja Deo University

Baripada-757003, Odisha, India

Email: brath_2000@yahoo.com

ABSTRACT

Lichens are fungal and algal/cyanobacterial symbiosis resulting in the production of specific metabolites. In the last decade, lichen has become a research interest related to exploring secondary metabolites compounds. Lichen is a unique organism and contains specific chemical compounds rarely found in other natural sources. In this study, the antioxidant activities of *Parmotrema andium* and *Dirinaria applanata* on methanol and acetone extract were determined by measuring free radical and superoxide anion scavenging activity, Ferric reducing power assay (FRAP), determination of total phenolic compounds and flavonoid contents and compared with known antioxidants such as ascorbic acid, butylated hydroxyanisole (BHA) and α -tocopherol. The experimental results indicated that methanol extract of *Dirinaria applanata* exhibited highest DPPH radical scavenging activity than of *Parmotrema andium*. Similarly the study results revealed, higher total phenolic and flavonoid content in *Dirinaria applanata* as compared to *Parmotrema andium*. Moreover, the tested extracts had effective reducing power and superoxide anion radical scavenging. The phytochemical analysis showed the presence of higher number of phytoconstituents in methanol extract than acetone extracts. Further, it was observed that among the test species, *Dirinaria applanata* possess more phytoconstituents than *Parmotrema andium*. The present study showed that tested extracts of lichens demonstrated important antioxidant effects which suggest that these lichens can be used as new sources of the natural antioxidant compounds.

Keywords: Antioxidant, DPPH, FRAP, lichen, Phytochemicals

**APPLICATION OF BACILLUS TEQUILENSIS LIPASE IN THE BIOCATALYTIC
ACTIVITY OF WASTE & 2T HYDROCARBON OILS AND BIODIESEL
PRODUCTION.**

Ajai Ahmed & Gautam Kumar Meghwanshi*

Department of Microbiology, Maharaja Ganga Singh University, Bikaner, Rajasthan

*E-mail: drgkm_biotech@yahoo.com

ABSTRACT

Lipase (triacylglycerol acylhydrolases, EC 3.1.1.3) catalyzes the hydrolysis and synthesis of esters of glycerol and long chain fatty acids, but only microbial lipases are commercially significant. A true lipase acts on long chain fatty acid esters. The many applications of lipases include specialty organic syntheses, bioremediation, biodegradation and biodiesel. This paper describes how to interact lipase (supernatant) 2T hydrocarbon oil and waste hydrocarbon oil and biodiesel production.. Lipase have more oil dispersion and biocatalytic activity. Bacteria have more prominent property that they breakdown and removal of nutrients and organic material in waste water so this type of study is more significant and more important. This is unique study whichever will be beneficial for future that oil dispersion which is beneficial for hydrocarbon oil eating bacteria they come in contact with oil they eat it, producing the byproduct carbon dioxide and water. One of the prominent applications of lipases was biodiesel synthesis through transesterification of vegetable oils (waste oils) with methanol. During this reaction fatty acid methyl esters (FAMES) were produced which are known as biodiesel. Biodiesel may be defined as mono-methyl or ethyl ester of the common fatty acid found in the triacylglycerols such as vegetable oils and animal fats. In the present research work lipases obtained from different bacterial isolates were used for transesterification of non-edible and cooked waste oils (Cotton seed oils) with methanol. The biodiesel produced was determined qualitatively using TLC and biodiesel efficiency was determined on Diesel Engine (Legion brothers, Bangalore, TV1 kirloskar).

PRODUCTION OF WINE FROM BLACK GRAPES AND GREEN BANANAS USING *SACCHAROMYCES PARADOUXS* AS A STARTER CULTURE

M.Swetha ^{*1}, S.Muniasamy ^{*1}, P.Ponmanickam ^{*2}

^{*1}Department of Microbiology, ^{*2}Department of Zoology, Ayya Nadar Janaki Ammal College
(Autonomous), Virudhunagar

E-mail: muniarun8818@gmail.com, swetha90951@gmail.com

ABSTRACT

Wine, an alcoholic beverage are produced by the fermentation of fruit juice especially grape, banana which have a chemical balance that allows them to ferment without addition of sugar acids, enzymes or other nutrients other than grape , other fruits have been used in wine production by researchers and qualified the wine with the name of the fruit such as banana wine . These fruits have high nutritional content, low acidity level, high protein, antioxidant content rich wine of both black grapes and green bananas.

The fruits were collected from local market of Sivakasi and wash thoroughly and processed the two fruits for fermentation process for 30 days. Then primary fermentation process can be started in both the wine. In primary fermentation process *Saccharomyces paradoux* as a starter culture for fermentation process, but in all wine preparation in primary fermentation process *Saccharomyces cerevisiae* as a starter culture but we isolate *S.paradoux* as starter culture, because *S.paradoux* strain closely related to *Saccharomyces cerevisiae* species, and their isolated *S.paradoux* ANJAC3 strain also submitted in GenBank format (MW811473).

We will utilize the grapes and banana as a source for the yeast to fermented and the wine produced during the process analysed and compared in terms of physico-chemical as well as biological parameters.

After physico-chemical as well as biological parameters analysis, it produced a good aroma, taste, color, low acidity level , high protein, antioxidant content rich wine of both black grapes and green bananas produced wine after 30 days of finished secondary fermentation process. In addition to that these both black grapes and green bananas wine processed in natural method without any addition of chemical preservatives. After 30 days of fermentation process both the natural produced wine gives a good overall acceptance by more than 10 panelists.

The values were increased in protein (0.34±4.84), antioxidant (0.24±4.45),total sugar (0.42±2.34) total phenolic content (0.62± 2.45), Vitamin C(0.82± 3.24) **mg/ml** level test as well as

acidity (0.32 ± 2.22), ascorbic(0.2 ± 11.34) , tannins level (0.13 ± 1.22) **mg/ml** values were decreased in secondary fermentation process (both wine).

Keywords : *Black grapes and green bananas wine, fermentation, S.paradoux ANJAC3 strain, GenBank, good overall acceptance.*

NOVEL PREPARATION OF BIOSENSITIZED ZINC OXIDE AND IT'S USES FOR THE ANALYSIS OF DAIRY PRODUCTS

Divya K. Shekhawat and N. Bhojak

GCRC, P.G. Department of Chemistry, Govt. Dungar College ('A' Grade),

MGS University, Bikaner-334001, India

Email: shekhawat.divyakanwar@gmail.com

ABSTRACT

Zinc is a universal and one of the most important trace elements in biological system. It performs catalytic and regulatory function, works as a co-catalyst or co-activator, acts as an indicator, shows neurotransmitter activity in synaptic vesicles and belongs to cellular signaling pathways in human body. Sensing technologies based on some features like low selectivity, high cross-selectivity and statistical analysis. The largest group among potentiometric sensors is represented by ion-selective electrodes (ISEs), the oldest and most widely used among them is a pH-sensitive glass electrode. In our work, the proposed arrays is prepared of potentiometric sensors, based on polymeric membranes and the subsequent cross-response processing will be based on a multilayer artificial neural network model. Several investigations have been carried out for the preparation of nanoparticles of zinc oxide, its biosensitization using Bhojak's effect and the preparation of novel electrode. Thus prepared biosensitized zinc oxide has been utilized for the analysis of acidic and bitter taste in milk and other dairy products.

**GAMMA IRRADIATION TREATMENT OF BAMBOO SHOOT
(*DENDROCALAMUS HAMILTONII*): EFFECT ON SHELF-LIFE EXTENSION
AND INHIBITION OF MICROBIAL DECAY**

Dushyant Singh^{1,2*}, A.C. Kharkwal¹, M.L. Aggarwal²

¹Amity Institute of Microbial Technology, Amity University, Sector-125, Noida-201313, India

²Shriram Institute for Industrial Research, 19, University Road, Delhi-110007, India

*Corresponding Author: dushyantsmicro@gmail.com

ABSTRACT

Bamboo shoots are highly nutritious but possess poor shelf life after harvest due to rapid decline of nutritious properties whereas significant increment in microbial bioburden.

Present investigation was performed to evaluate the potential of gamma radiation as a postharvest technology to preserve bamboo shoots. *Dendrocalamus hamiltonii* shoots were gamma irradiated in the dose range of 0.5 to 5.0 kGy followed by stored at 30⁰C temperature dipped into 2% NaCl solution. Acceptability of the irradiated product was assessed based on microbial, physicochemical and organoleptic attributes as well as induced radioactivity (food safety parameter). Study revealed that a dose of 2.5 kGy was sufficient to complete removal of microbial load from the bamboo shoot up to 4 log reduction when compared with unirradiated sample. No significant changes were found in physicochemical parameters including protein, pH, moisture, HCN content and minerals. Organoleptic evaluation for different parameters were lies within the acceptance criteria up to 240 days, hence a 2.5 kGy dose of irradiation had the best preservation effect on the bamboo shoots of *Dendrocalamus hamiltonii*. These results demonstrated the potential of the gamma radiation as a promising postharvest technique to maintain the various quality attributes and inhibit the microbial deterioration of bamboo shoots during storage.

Keywords: *Bamboo shoot, gamma irradiation, shelf-life, microbial analysis, Dendrocalamus hamiltonii*

SCREENING AND CHARACTERIZATION OF BIOACTIVE COMPOUNDS FROM ACTINOMYCETES AND ANALYZING ITS APPLICATION

K.Nalini and J.Briskilla

Department of Microbiology, Ayya Nadar Janaki Amml college (Autonomous), Sivakasi.

ABSTRACT

Eleven Actinomycetes were isolated from five different garden and agricultural soil samples in from Starch casein agar medium. All the soil samples exposed were to physical and chemical treatment before isolating Actinomycetes. The strains were then subjected to different biochemical characterization test and were also characterized based on ability to ferment glucose, fructose and sucrose. Hydrophobicity test is performed to assess their attachment to gastrointestinal tract (Probiotic effect). Four Actinomycetes strains (JC3, JC6, JC8, JC11) showed positive results to hydrophobicity test. Acid and alkaline phosphatase activity was measured in Actinomycetes strains. Three Actinomycetes (JC3, JC6, JC11) showed more than Acid phosphatase activity and three strains (JC4, JC8, JC11) showed more alkaline activity. Antimicrobial activity of eleven Actinomycetes strains were tested using agar well diffusion method and cross Streak method against *E.coli*, *Staphylococcus epidermis*, *Streptococcus pneumoniae*, *Enterococcus spp* and *Pseudomonas aeruginosa*. No significant antimicrobial activity was obtained. Actinomycetes strains were then tested for their Probiotic effect by their resistance to bile salts and acidic pH. Three strains (JC1, JC2, and JC5) showed more resistant to bile salts. Actinomycetes strains (JC4, JC6, JC7, JC8) showed more resistant to acidic pH.

Key words: Probiotics, Actinomycetes, Hydrophobicity, bile salt

TOXICITY STUDY OF BIODECOLORIZED DYE EFFLUENT USING *ALLIUM CEPA*

Jagiasi Sunil Radhakrishin¹ and Patel Saraswati N.²

¹ Seva Sadan's R. K. Talreja College, Ulhasnagar. Dist.- Thane , Maharashtra, India.

² Smt. C. H.M. College, Ulhasnagar, Dist.- Thane , Maharashtra, India.

Email: sunilrjagiasi@gmail.com

ABSTRACT

Industries like textile units which use large quantities of water in fabric generate considerable quantities of liquid effluent pollutants. Depending on the class of the dye, the loss of untreated wastewaters can vary from 2% for basic dyes to as high as 50% for reactive dyes. Use of Azo dyes is generally preferred over other dyes because of their advantages like color fastness, allowing creation of different shades etc. The discharge of these dyes into environment is undesirable due to their toxicity towards human, plants and environment. A wide range of available physico-chemical technologies that have been developed for the treatment/removal of synthetic dyes from waters have their own limitations. Biological treatment of wastewater using microorganisms offer plausible alternative to resolve this problem. In current study, *Ex situ* bioremediation of dye effluent collected from local dye industry was carried out using developed consortia of seven decolorizing diazotroph isolates under optimized conditions. With presumption for use of bioremediated dye effluent for crop irrigation, its effect was studied using *Allium cepa* roots. The *Allium cepa* roots showed around 24.47% and 80 % cell viability on irrigation with dye effluent and biodegraded dye effluent by consortium respectively. The Mitotic Index of 20.61 % and 73.96 % with *Allium cepa* root cells was observed with parental and biodecolorized dye effluent respectively. The higher cell viability and Mitotic Index percentage in meristematic cells of *Allium cepa* roots irrigated with consortium treated dye effluent reveals the non toxic nature of biodegraded metabolites. The studies are in progress for effect of bioremediated dye effluent toxicity on soil enzymes and Plant Growth Promoting Rhizobacterias.

Key words: *Allium cepa*, Azo dyes, Biodecolorization, Mitotic Index

**GENETIC DIVERSITY AND IMMUNE RESPONSE AGAINST *PLASMODIUM VIVAX*
VACCINE CANDIDATE THROMBOSPONDIN RELATED ADHESIVE PROTEIN
(TRAP) GENE**

Jyoti Acharya Gopa and Dharmesh Harwani

Department of Microbiology, Maharaja Ganga Singh University, Bikaner, India

jyotiacharya2@gmail.com, dharmesh@mgsbikaner.ac.in

ABSTRACT

Plasmodium vivax is the most widely distributed human malaria parasite in the world and nearby 2.5 billion people living at risk. Due to the unique biology of *P. vivax*, including its ability to form latent hypnozoites that emerge months to years to cause blood stage infections, early appearances of gametocytes before clinical symptoms are apparent. Moreover, a shorter development cycle in the vector makes perception that *P. vivax* only cause mild malaria. There has been a gap in efforts to develop a vaccine for *P. vivax* compared to *P. falciparum* vaccine. Currently, there are only two *P. vivax* candidates being tested in clinical trials and few other are being assessed in studies which contrast with the numerous *P. falciparum* vaccines candidates under evaluation. The genetic diversity in *P. vivax* antigen is a major hurdle in the development of an effective malaria vaccine. Protective efficacy of the vaccine is dependent on the polymorphic alleles of the vaccine candidate antigen. TRAP (thrombospondin related adhesive protein) is considered to be responsible for the sporozoite host interactions and is one of the important vaccine candidate genes. We investigated the genetic diversity of *P. vivax* TRAP (PvTRAP) in the field isolates of *P. vivax* to identify immunogenic regions. PvTRAP gene sequences have been amplified and sequenced to reveal B cell and T cell epitopes. The polymorphism detected in PvTRAP will certainly help in the development of stable vaccine. The overall observations will be presented.

PROBIOTIC IMMUNITY BAR FOR COVID-19 PATIENTS

Lani A. John, Ishrat Jahan Peerzade, Prakash M Halami*

Microbiology and Fermentation Technology Department
CSIR-Central Food Technological Research Institute-Mysore-570020

*E.mail:prakashalami@cftri.res.in

ABSTRACT

Probiotics are defined as live microorganisms that confer a health benefit to the host when administered in adequate amounts. Incorporation of probiotics into cereal-based products is therefore desirable since it can combine the healthy formulation of a cereal mixture, the added value of prebiotic ingredients, and the beneficial effects of the probiotic bacteria. From our preliminary studies, we found the potential probiotic bacterium *Bacillus licheniformis* MCC2514 can reduce pro-inflammatory response and increases anti-inflammatory activities upon pathogen inflammation and oxidative stress to the cell. This study focused on the preparation and stability evaluation of cereal bar infused with probiotic bacteria that can provide immunity for COVID-19 patients. For safety, commercial rice crisps, oatmeal, jaggery, and peanuts were used for the preparation of the immunity bar. The probiotic *Bacillus licheniformis* MCC2514 was used as the starter culture, which is infused in the immunity bar at a feasible temperature in the preparation. The viability and stability of probiotic bacteria were assessed every 15 days of the interval by the serial dilution and plate count method. All the results obtained were in an acceptable range for therapeutics. After 45 days, the minimum viable count was 10^6 - 10^8 CFU/gm, and also, there is no change in sensory properties at least up to 45 days. This study specified that it is possible to incorporate the spore forming probiotic bacteria into a cereal bar that is collectively beneficial for immunity-enhancing in the COVID-19 patients along with fulfilling all basic probiotic properties.

CHARACTERIZATION OF METAGENOMIC DNA AND ANALYSING ITS EXPRESSION IN BL21 DE3 COMPETENT CELLS

K. Nalini and M. B. Shakthi Priyaa

Department of Microbiology
AyyaNadar Janaki Ammal College (Autonomous)

ABSTRACT

Metagenomics is the study of genetic material isolated directly from the environmental samples. Thirteen Soil samples were collected from different places in and around Sivakasi and metagenomic DNA was extracted by PEG/NaCl method. Metagenomic DNA fragments were then characterized by agarose gel electrophoresis, A 260 / 280nm ration and Neutral Polyacrylamide gel electrophoresis. DNA sample S12 and S13 contain maximum DNA bandwidth of 0.6cm Since A260/A280 ratio greater than 1.8 is suitable for analysis, three DNA samples S9, S11 and S13 selected for next stage of analysis. S11 and S13 is reported with a band width greater than 0.4cm in Neutral Polyacrylamide gel electrophoresis. Metagenomic DNA fragments were transformed to BL21 DE3 *E.coli* competent cells by heat shock method and plated on LB agar plates with and without ampicillin. pUC 19 vector is used as control DNA to check the efficiency of transformation.. Transformed metagenomic bacterial colonies were selected and inoculated in nutrient broth for analyzing the presence of any bioactive molecules. Sugar and protein levels were increased in the Metagenomic DNA transformed BL21 cells than the BL21 cells. Presence of free amino acids Cysteine, glutamine, isoleucine and Arginine were found in S11 and S9 DNA transformed BL21 cells and these amino acids were not detected in BL21 cells without metagenomic DNA No significant difference in protein bands between S9 and S11 DNA transformed cells. Extracellular amylase and protease activity was high in S9 DNA transformed BL21 *E.coli* cells compared to BL21 cells alone.

Keywords: Metagenomic DNA, PEG/ NaCl method, BL21 DE3 *E.coli* competent cells, Transformation, Neutral PAGE, .

MICROBES IN THE FIELD OF ONCOLOGY

B.Mounica, P.Dharani, D.Veena

Department of Microbiology

St. Pious X Degree and PG College for Women,

Nacharam, Hyderabad-50076, Telangana, India.

Key Words: Bacteria, Virus, Causes of Cancer, Treating Cancer

Email: mounicanaidu23@gmail.com

ABSTRACT

Cancer is a disease which shows vigorous cell proliferation. There might be many reasons for a cell to become cancerous, but microorganisms can also cause cancer in the body. They tend to enter the body as a normal infection but later turn out to be cancerous. Some examples of microbes with their Cancer causing type are: Helicobacter pylori- cause gastric cancer, Aspergillus sps.- cause myeloid leukemia, Epstein Barr virus cause nasopharyngeal cancer. Bacteria once entered into the body appear as an inflammation. They first take up host cell signalling by masking themselves from the immune cells of the host system, which leads to cellular malignancy. Viruses also do the same but the only difference is bacteria requires multiple pre-transformed host cells to turn it into an actual cancer cell. We can use the normal flora of the host and other microorganisms to treat cancer. We can achieve this by modifying the microbial genome. By altering the genome we can supply anti-cancer drugs directly to the tumor, find other tumours in the body and alert the immune system. By using this treatment there will be less to no damage to surrounding healthy tissues and cells and the rate of secondary infections will also reduce. If we achieve this method successfully, we can create vaccines for all types of cancer and reduce mortality rate caused due to cancer.

"Cancer is a journey, but you walk the road alone. There are many places to stop along the way and get nourishment- you just have to be willing to take it." ~Emily Hollenberg

Let us give the correct nourishment to make the journey a happy and beautiful destination.

MYCOREMEDIATION OF PLASTIC WASTE

(Fantastic fungi)

Tejaswi Khadke , Afreen Razia

Department of Microbiology

ST. PIOUS X DEGREE & PG COLLEGE FOR WOMEN NACHARAM, HYDERABAD

Email: tejaswikhadke@gmail.com, sk.afreenrazia@gmail.com

ABSTRACT

“Myco” means fungus and “remediation” means to restore something to its original form. Where the species of *Aspergillus* can degrade the plastic we call it as Mycoremediation is one of the type of bioremediation. Plastic is a chain of monomers with wide range of synthetic or semi-synthetic material. The studies are very important for the production and development of biodegradable plastics and for the reduction of pollution, since plastic waste can remain in the environment for decades or centuries is today one of the great challenges for the environment. Plastics that are biodegradable can be considered environment friendly, Microorganisms plays a major role to save the planet by degrading toxic plastic waste which are harming the environment. Isolation of fungal strain may able to degrade plastic waste from polluted sources, such as soil. In the present research, an attempt has been made to identify the suitable fungal species for microbial degradation of polythene, polymers (The fungus, *Aspergillus sydowii* from the genus *Aspergillus* was reported for the first time with the polythene degradation potential, however, it was reported to degrade PVC plastic⁵.) The biodegradation of plastic using the *Aspergillus* species was studied. The species *Aspergillus tubingensis*, was able to break down polyurethane (is a plastic material composed of organic units joined by carbamate links), common in industrial settings and used in refrigerators, fake leather, and many other applications. It has potential to be developed into one of the tools desperately needed to address the growing environmental problem by the usage of improperly disposed of plastic, *Aspergillus tubingensis* is generally recognized as safe by the American food and drug administration (FDA). This species can produce enzymes such as amylase, lipase, glucose oxidase, phytase, xylanase, acid phosphatase and xylosidase production.

Key Words: *Mycoremediation, Plastic waste*

NANOTECHNOLOGY APPLICATIONS IN SCIENCE AND ENGINEERING

Sunder Singh

Department of Zoology (Hydrobiology lab)

M. S. J. Govt. College, Bharatpur-321001 (Rajasthan) India

Email : sunderbtp@gmail.com

ABSTRACT

Nanotechnology is helping to considerably improve, even revolutionize, many technology and industry sectors: information technology, energy, environmental science, medicine, homeland security, food safety, and transportation, among many others. Today's nanotechnology harnesses current progress in chemistry, physics, materials science, and biotechnology to create novel materials that have unique properties because their structures are determined on the nanometer scale. This paper summarizes the various applications of nanotechnology in recent decades.

Keywords: Nanotechnology, Environmental Science, Agriculture, Food safety, Engineering.

NUTRACEUTICALS : SUPER FOODS

G. Pravalika & M. Nagavani

Department of Microbiology

St. Pious X Degree & PG College for Women Nacharam, Hyderabad-500076, Telangana, India.

Email: nagavani5mopidevi@gmail.com

ABSTRACT

A food that provides medical or health benefits, including the prevention and treatment of a disease is called “Nutraceutical”. It includes Nutrients (Vitamins, Minerals, Amino Acids, Fatty acids, etc.), Herbals (Herbs or Botanical products.), Dietary Supplements (Probiotics, Prebiotics, Antioxidants, Enzymes, etc.). It is the product derived from food sources with extra health benefits in addition to the basic nutritional value found in foods. Nutraceuticals may be used to improve health, prevent chronic diseases. In whole nutraceuticals has lead to the new era of medicine and health in which the food industry has become a research oriented sector. Current problem we are facing, on rapid spread of diseases caused by insufficient consumption of nutrients. One of the approach to solve this problem is enrichment of food with the necessary functional ingredients. The rising awareness of consumers towards the health benefit of foods and their nutritional benefits for potential disease prevention and health enhancement is the driving force of the global functional food and nutraceutical market. Nutraceuticals are present in most of the food ingredients with varying Concentration. Conc. , Time and Duration of supply of Nutraceuticals influence human health. Manipulating the foods, the conc. of active ingredients can be increased. Diet rich in nutraceuticals along with regular exercise, stress reduction and maintenance of healthy body weight will maximise health and reduce disease risk. Nutraceuticals have proven health benefits and their consumption will keep diseases at bay and allow humans to maintain an overall good health. “Let food be your medicine” - Hippocrates (known as the father of medicine).

**POTENTIAL OF INDIGENOUS STRAIN AS A CELL FACTORY FOR
BIOSURFACTANT PRODUCTION AND ITS ANTIBIOFILM ROLE AGAINST
FOODBORNE PATHOGEN**

Rajni Kumari, Shivani Keshari, Archana Gajbhiye, Radhika Chandankere*

Department of Biotechnology, Sir Padampat Singhanian University, Udaipur, India

* Corresponding author. Tel: +91 9482455395, E-mail: radhika.chandankere@spsu.ac.in

ABSTRACT

Biofilm is a major concerning issue in the food industries for its direct contribution to food spoilage, as well as transmission of food-borne diseases, which can be controlled to a great extent by using biosurfactant. In this work, a potent indigenous bacterial strain for biosurfactant (BS) production will be isolated using agro-industrial byproduct (molasses) as a carbon source and anti-biofilm efficacy against a foodborne pathogen will be evaluated. A preliminary screening will be done by assessing hemolytic activity, Cetyl Trimethyl Ammonium Bromide (CTAB) agar assay, and emulsification activity which will confirm the production of BS. The highest titer of BS will be further evaluated using critical micelle concentration (CMC). The BS produced by the isolated strain will be assessed for its stability at broad ranges of pH, temperatures and salinity. The GC-MS and NMR analyses will be studied to reveal the structure properties of produced biosurfactant. Anti-adhesion and anti-biofilm efficiency against foodborne pathogen which was further confirmed by the real-time PCR. The results will indicate that the derived BS could be explored in food and pharmaceutical industries as a potential anti-biofilm agent.

Keywords: biosurfactant, anti-biofilm, gene expression, *Enterobacter*, characterization

BIOSURFACTANT TECHNOLOGY: AN ECO-FRIENDLY SUSTAINABLE DEVELOPMENT FOR TREATING OIL-SPILLS

Shivani Keshri, Rajni Kumari, Archana Gajbhiye, Radhika Chandankere*

Department of Biotechnology, Sir Padampat Singhania University, Udaipur, India

ABSTRACT

Petroleum hydrocarbon-based fuels are prevalent pollutants in industrialized and developing countries. The source of this contamination is usually an accidental spill, uncontrolled landfills or improper storage and leaking underground storage tank. In this context, there is an immense need of isolating an indigenous and efficient biosurfactant-producing bacterial strain from petroleum reservoir. Isolate will be screened for biosurfactant production using haemolytic assay, Cetyl Trimethyl Ammonium Bromide agar plate assay (CTAB) and the qualitative oil-displacement test. The isolated strain will be identified based on partial sequenced 16S rDNA analysis. The maximum biosurfactant production will be obtained using crude oil as sole carbon source. The cell free broth containing biosurfactant will be assessed for emulsification activities and surface tension. Fourier transform infrared (FT-IR) spectrum of extracted biosurfactant will indicate the functional groups present in it. Elemental analysis of the biosurfactant by Energy dispersive X-ray spectroscopy (EDS) would reveal the biosurfactant anionic in nature. The isolated strain might represent as a potent biosurfactant-producer and could be useful in variety of biotechnological and industrial processes, particularly oil industry. And therefore, merit for further research.

Keywords: *Biosurfactant; Characterization; Growth kinetics; Biodegradation; Crude-oil*

**DETECTION, PREVALENCE AND POLYPHASIC CHARACTERIZATION OF
DIARRHEAGENIC *ESCHERICHIA COLI* (DEC) PATHOTYPES IN UNDER-FIVE
CHILDREN IN BIKANER REGION OF RAJASTHAN**

Sweta Barupal and Dharmesh Harwani

Department of Microbiology, Maharaja Ganga Singh University, Bikaner-334001, India

Email: swetabarupal8@gmail.com, dharmesh@mgsbikaner.ac.in

ABSTRACT

E. coli is an important etiological agent of childhood diarrhea and represents a major public health problem in developing countries. Diarrheagenic *E. coli* (DEC) are most frequently implicated in cases of epidemic and endemic diarrhea worldwide. DEC can be divided into five main pathotypes including Enteropathogenic *E. coli* (EPEC), Enterohemorrhagic *E. coli* (EHEC), Enterotoxigenic *E. coli* (ETEC), Enteroaggregative *E. coli* (EAEC) and Enteroinvasive *E. coli* (EIEC). The present work describes the identification of DEC pathotypes with an emphasis on their distinct epidemiological, clinical features, and specific virulence determinants. The prevalence of DEC pathotypes in the stool samples of hospitalized children in under-five children with acute diarrhea was studied using PCR assays. Selective amplification of *eae*, *bfp* genes to detect EPEC, *stx1*, *stx2* genes to detect EHEC, *lt* and *st* genes to detect ETEC, and *aggR*, *irp2*, *aaiA* genes to detect EAEC from various samples revealed the prevalence of two DEC pathotypes in the Bikaner district of Rajasthan. The observations based on the prevalence and taxonomic distribution of diarrheagenic *E. coli* pathotypes will be presented.

ENHANCED BIOREMEDIATION OF CHROMATE FROM INDUSTRIAL EFFLUENT USING BIOSURFACTANT PRODUCING BACTERIA

Tuhina Verma* and Richa Pandey

Department of Microbiology, Dr RML Avadh University, Ayodhya, 224001, India

*E-mail: tuhina.verma19@gmail.com

ABSTRACT

The enormous use of chromium compounds by various industries has led to its release in agricultural lands and water bodies through industrial wastes beyond the permissible limit due to inefficient waste treatment technology. Presence of chromium in the environment has been a subject of great concern due to their higher toxicity, non-biodegradable nature and long biological half-lives. Thus, their removal has become a matter of prime concern. Removal of chromium and other metals from contaminated site using biosurfactant offers a promising approach for effective bioremediation of chromium from soil and environment. A total of forty five bacteria tolerant to Cr(VI) concentration ranging between 100-900 $\mu\text{g/ml}$ were isolated from discharged industrial effluent. On the basis of higher MIC values, 11 bacterial strains were selected for further studies. Their MIC for Cr(VI) ranged between 950 to 1650 $\mu\text{g/ml}$. They were screened for their ability to produce biosurfactant following the standard methods. Appearance of dark blue halo zone around the bacterial culture on CTAB-methylene blue MSM agar indicated the production of anionic biosurfactant by bacteria. Blood hemolysis test is used to screen the microbes for their ability to produce biosurfactants on hydrophilic media. Results indicated that out of eleven strains, five strains TB11, TB 19, TS5, TS6 and TS12 could significantly produce biosurfactant. Further, the selected strains were evaluated for reduction of toxic Cr(VI) to less toxic Cr(III) spectrophotometrically at 540 nm by diphenyl carbazide method. Interestingly, significant Cr(VI) reduction was observed in TB11 (86.0%) and TB19 (82%), TS12 (80.0%) and TS6 (75%) strain. Based on the results of this study, indigenous chromium resistant strains having ability to produce biosurfactant could be potentially used for Cr(VI) bioremediation at polluted sites.

MOLECULAR INTERACTION STUDIES BETWEEN RIBOSOMALLY SYNTHESIZED AMPS AND FOOD SPOILAGE BACTERIA

Bandita Dutta, Dr. Rina Rani Ray*

Maulana Abul Kalam Azad University of Technology, West Bengal

*E-mail: raypcmicro@gmail.com

ABSTRACT

Ribosome mediated Anti-Microbial Peptides (AMPs) are the large group of the proteinaceous toxins which are synthesized ribosomally by the bacteria. These AMPs are also known as “Bacteriocins”, which have the potential to inhibit the growth of the other micro-organisms. There are various bacterial cells have been reported of producing the bacteriocins. Among those the Lactic acid bacteria (LAB) has the potentials to be used as the bio-preservatives in the food industry (1). Bacterial cells have the ability to produce some molecules like lantibiotics or other AMP molecules which can inhibit the growth of the other bacterial cells. Gram positive bacteria produce a lanthionine containing bactericidal peptides known as “Lantibiotics”, which has the potential to defence growth of the other bacterial species, by disrupting the integrity of the target cell by forming pore or prevent the cell wall biosynthesis. In the food or pharmaceutical industries the rise of the multidrug resistance leads to the discovery of the novel antimicrobials from the microbial cells. AMPs are the kind of novel antimicrobials which can be used for the antimicrobial drug discovery.

This paper is focused towards the in-silico approach of the inhibition of gram positive as well as gram negative food degrading bacteria by the AMPs. Different groups of Lantibiotics are identified using the Bagel 4 server (2) and they are docked to the gram positive *Staphylococcus aureus* and gram negative *Plasmodium falciparum* (3). It was observed bacteriocin was able to bind with the enterotoxin of *S. aureus*(PDB ID: 1SE4) and pepstatinA of *Plasmodium falciparum* (PDB ID: 1LS5). It was observed that the binding interaction between the bacteriocin enterolysinA and the enterotoxin showed a value of -97.4545 Kcal/mol and interaction between the bacteriocin enterolysinA and the pepstatinA showed a value of -82.2142 Kcal/mol. Further the docking result is verified by RSM (4), where The Model F-value of 3.96 and 5.08 and **P-values** less than 0.0500 indicate model terms are significant.

MICROBIAL COMMUNITY PROFILE UNDER CLIMATE SMART AGRICULTURE (CSA) PRACTICES IN RICE-WHEAT SYSTEM

Madhu Choudhary¹, HS Jat¹, Ashim Datta¹, ML Jat² and PC Sharma¹

¹ICAR-Central Soil Salinity Research Institute (CSSRI), Karnal – 132 001, India

²International Maize and Wheat Improvement Center (CIMMYT), New Delhi – 110 012, India

ABSTRACT

Low factor productivity, rice-wheat system sustainability and degrading soil, water and air quality are the major cause of concerns in western Indo-Gangetic plains (IGP) of India. Under the climate smart agriculture (CSA) practices involving tillage, crop residue, nutrient and water management practices we executed study for comprehensive understanding of microbial community composition. At ICAR-CSSRI-CIMMYT strategic research platform at Karnal (29°70'N, 76°96'E), India, six CSA-based scenarios consisting- Farmers' practice [ScI; conventional-till (CT) rice-CT wheat], partial conservation agriculture/ CA [ScII; CT rice-Zero tillage (ZT) wheat-ZT mungbean with flood irrigation], rice based partial CSA (ScIII; ZT rice-ZT wheat-ZT mungbean), maize based partial CSA (ScIV; ZT maize-ZT wheat-ZT mungbean), rice based CSA [ScV: ScIII with subsurface drip irrigation (SDI)], maize based CSA (ScVI; ScIV with SDI) were evaluated. Microorganisms directly affect the nutrient mobilization, systems' sustainability and soil resilience. Microbial DNA was extracted from soil samples and sequencing was done for V3-V4 region of 16s and ITS1 and 2 regions by Illumina Miseq sequencer. All diversity indices Shannon, Simpson, Chao1 and OTU for both bacteria and fungi were recorded higher in maize based scenarios (Sc IV and ScVI) as compared to rice based CA scenarios (ScIII and ScV). Total of forty phyla of bacteria and seven phyla of fungi were observed in six scenarios. *Proteobacteria* was the dominant in all scenarios followed by *Acidobacteria* and *Actinobacteria*. *Ascomycota* is the dominating fungal phyla followed by *Basidiomycota* and *Zygomycota*. The relative abundance of *Proteobacteria* was 29% higher in rice-based CSA scenarios and 16% higher in maize-based CSA scenarios over farmers' practice. Microbial enzymes dehydrogenase, phosphatase, and β -Glucosidase were higher in CSA scenarios over CT based scenario. Higher wheat grain yield of ~10% was recorded with CSA based scenarios over CT based scenario. Higher microbial diversity, microbial biomasses and enzyme activities in CSA scenarios compared to CT based management practices resulted in

higher yields under CSA based practices. Therefore, CSA based practices should be promoted in IGP for improving the soil health and quality for system sustainability.

Key words: *conservation agriculture; available nutrients; relative abundance; diversity indices*

Filename: Abstract book
Directory: D:\D Drive\Confernces & Seminars\Micro Dept MGSU Intern. Conf May
2021\e Posters and Abstracts
Template: C:\Users\drgkm\AppData\Roaming\Microsoft\Templates\Normal.dotm
Title:
Subject:
Author: Gautam Kumar Meghwanshi
Keywords:
Comments:
Creation Date: 8/9/2021 12:50:00 PM
Change Number: 67
Last Saved On: 8/10/2021 10:39:00 AM
Last Saved By: Gautam Kumar Meghwanshi
Total Editing Time: 1,299 Minutes
Last Printed On: 8/10/2021 10:40:00 AM
As of Last Complete Printing
Number of Pages: 37
Number of Words: 9,562 (approx.)
Number of Characters: 54,505 (approx.)