

1st

NATIONAL CONFERENCE
ON



“Biotechnology for Better Tomorrow”



NCBTBT-2023

Organized by
Microbiologists Society, India
&
Taywade College, Mahadula-Koradi, Nagpur

ABSTRACTS PROCEEDINGS

First National Conference on
“Biotechnology for Better Tomorrow”
22-24 January, 2023

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&
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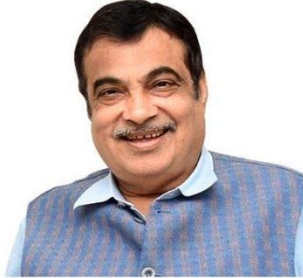
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Government of India

Do No.
Date :- 02 JAN 2023

Message

It gives me an immense pleasure to know that Microbiologist Society, India, is organizing National Conference on "Biotechnology for Better Tomorrow" at Taywade College, Mahadula-Koradi, Nagpur during 22nd January to 24th January-2023.

Biotechnology is an emerging field and offers ample opportunities for research and entrepreneurship. It is learnt that conference is being attended by eminent people from Biotechnology and allied sectors and many researchers are presenting their research during the conference.

I believe that the deliberations will deliver some concrete outcome from the conference which would benefit the people of India.

I congratulate the organizers for their initiative and wish all the best for the success of this National Conference.

With Regards !

Yours

(Nitin Gadkari)

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Rashtrasant Tukadoji Maharaj Nagpur University

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MESSAGE

I am extremely happy to know that Taywade College, Mahadula-Koradi is hosting first National Conference of Microbiologist's Society of India, "Biotechnology for Better Tomorrow" on 22-24 January 2023.

I appreciate the aim of the Conference Biotechnology for Better Tomorrow which is most suitable topic in today's global need. This Conference would provide a platform to researchers, academicians and professionals to exchange their ideas, perspectives and research in the field. Research plays key role in the development of the country and benefit of mankind. I fervently believed that the theme of this first Conference will boost the awareness of research amongst the students, teachers and academicians and bring more collaboration in future.

I extend my best wishes to Microbiologist's Society of India and Taywade College for successful organization of the Conference.



Nagpur/January 19, 2023

(S.R. Chaudhari)



NCBTBT

JANUARY 22-24, 2023

2023



श्री सच्चिदानंद शिक्षण संस्था

नोंदणी क्र. महाराष्ट्र/३०९/९० नागपूर
१३, पावनभूमी, वर्धा रोड, नागपूर-२५

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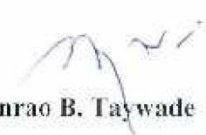
दिनांक 16/01/23



Message from President

I am extremely happy to know that the Department Microbiology is organizing 1st National Conference of Microbiologist's Society, India "Biotechnology for Better Tomorrow" on 22-24 January 2023. I take this opportunity to welcome you all to the National Conference at our campus.

I hope that this conference would certainly encourage innovative ideas among the participants paving way for few inventions and update the knowledge in the thrust area of main theme of the conference. I appreciate and congratulate organizers for taking initiative in organizing this National Conference which would definitely benefits students.


Dr. Baban B. Taywade

Nagpur/January 16, 2023

x

**MICROBIOLOGISTS SOCIETY, INDIA**

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**MESSAGE**

Welcome you all in the 1st National Conference of Microbiologist's Society, India "Biotechnology for Better Tomorrow" on 22-24 January 2023 to explore the scientific excellence growing in the field.

The goal of any conference is to bring together researchers, managers, policy makers and other group of scientific community, who are active in the related areas and to give them forum for exchanging information through the presentation and discussion of paper dealing with wide variety of topics. This conference will provide an excellent platform to eminent professional, academicians and young researchers to share and exchange ideas and aid in forging fruitful collaborations with national delegates.

I hope that, the deliberations of the participants would provide pointers for meeting the future challenges and provide a roadmap for developing inter-disciplinary research programs in the coming years. For research scholars from diverse parts of nation, this can provide valuable opportunities to getting exposed to cutting edge research themes in the microbiology.

I wish the conference a grand success.

**Osmanabad/January 15, 2023****Dr. A.M. Deshmukh**



Shri Sachhidanand Shikshan Sanstha's

TAYWADE COLLEGE

(Arts, Commerce, Science) (U.G. & P.G.)

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9822716608

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9422145290

Date :

**Message from Principal**

I am very glad that the Department Microbiology of our College is organizing 1st National Conference of Microbiologist's Society, India "Biotechnology for Better Tomorrow" on 22-24 January 2023.

As a host, it is my immense pleasure to welcome all delegates to our college. I am extremely happy to know the overwhelming response of academicians and researchers of various universities and Colleges from all over India. I hope that this conference would be very useful for participants to enhance their academic standards. On behalf of management, I thanks to Microbiologist's Society, India especially President of the Society Dr. A.M. Deshmukh for organizing their 1st National Conference of on Microbiologist's Society at our college.

TAYWADE
COLLEGE


Dr. Sharyou B. Taywade

Nagpur/January 16, 2023



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JANUARY 22-24, 2023

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Taywade College, Mahadula-Koradi, Nagpur

22-24 January, 2023

National Conference on “Biotechnology for Better Tomorrow” (NCBTBT-2023)

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Biotechnological approaches for better tomorrow

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Biological sciences are expanding their knowledge frontiers at an ever-accelerating pace. The insights into biological processes offer a broadening array of options to develop incremental and differential innovations across the medical, agricultural, and industrial biotechnology sectors.

In India, biotechnology has proved to be one of the fastest growing sectors. It has been expected to play a key role in shaping the country's rapidly developing economy. The emerging biotechnologies have been looking at combating life threatening diseases and malnutrition, reducing energy crisis, waste management and food scarcity which are among the serious challenges globally. These issues responsible for hindering the growth of the country need to be addressed through the biotech sector to advance its research and development capabilities. There is need to bring to the fore novel solutions and advanced technologies.

A myriad of developments will decide the way world will evolve. There are numerous development but not limited to the global policy approach to enable the use of new genomic technologies, new treatments regimes, dietary shifts, development of new high-tech materials, shifts in lifestyle, and progress in robotics and artificial intelligence. Success in such developments and extrapolating their long-term impact on the way will pave the way for biotechnology discoveries. For example, exploitation of the invaluable role of microbial biodiversity and the ecosystem services to create the robust scientific knowledge necessary for a bioinformed design of buildings and cities for healthy and sustainable living. The use of next-generation diagnostic tools to optimise the anaerobic digestion of municipal sewage sludge has the potential to increase renewable natural gas recovery, improve the reuse of biosolid fertilisers and help operators expand circular economies globally.

A study on scenario analysis with a 2050 time horizon appreciating the option space of agricultural biotechnology identified 45 trends and 22 uncertainties that may shape the entire agricultural socioeconomic system. This gives the range of directions the future may take and to



narrow down the way agricultural biotechnology could best future-proof food, nutrition, and health security. It is now clear that climate change has impact on agriculture. Effects on cities, gardens, lakes, and crop fields linked to shifts and volatility in weather and the resulting new environmental conditions, including new pests and diseases, are not yet fully appreciated. Therefore, the demand for climate change-related biotechnology innovation will be high.

Microbes influence the complex ecological systems. Their exploitation is expected to offer innovation options in a broad range of biotechnology fields including medicine, health care, food systems, industrial processes, resource recycling, and energy capture. Therefore, a broad fundamental biotechnology discovery research on microbiomes needs to reach its peak. A leading approach in medicine building on ongoing big data efforts, such as in the human ‘100K genomes project’ may serve as a vehicle to reach the desired state of enablement. However, an entrepreneurial ecosystem is critical for its further development.

Protein malnutrition is an emerging scenario in most of the developing countries. Diet shifts toward alternative protein sources may happen in future. Food properties such as taste, texture, palatability, color, convenience, and price decide the consumer choice. Research to make alternative protein products competitive to meat would require, among other improvements, major advances in biological insights to upgrade food sources.

The emerging problems of zoonotic infections and antimicrobial resistance (AMR) are quickly advancing threat for human health worldwide. Almost 5 million deaths are attributable to AMR phenomenon every year. Since antibiotics are failing to treat AMR-bacteria, new tools including alternatives to antibiotics are needed. Monoclonal antibodies (mAbs) can fill this role and enormous leaps forward have been made to identify and develop extremely potent human mAbs. The novel and most innovative biotechnologies mentioned herein can support this goal and add powerful tools in the arsenal of weapons for betterment of the humanity.



Understanding host-microbiome interaction through probiotic lens

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Due to perturbances in a microbial dynamic, the system some time tends to lose the key taxonomic player from the community. If the system has tendency loose such taxa, then it can be replenished by same or similar bacteria and such selected bacteria are termed as probiotics. Sometime, these probiotics also include the introduction of totally new taxa to restructure the existing biochemical network of the system. Such alteration creates new metabolic network leading to correction in overall physiology of the system.

The selection and relative stabilization of microbial community is a dynamic process that is governed by various factors in the different ecosystems. These factors include the available source of energy and different stresses which guides the microbial community structure, survival, or resilience, which in each time frame remains in a steady state. In such a state, for any ecosystem, the microbial community structure acquires a stabilized functional architecture designed by various contributing members of the community. This synergistic association of microbe forms the hierarchy of management for the utilization of carbon and energy sources. This association is defined by wide diversity and the varying levels of abundance of microbes. Most of the time the prediction of biochemical networks for these associations is based on co-occurrence network approaches which are not efficient in interpreting interspecies sharing of nutrients. Secondly, the dynamically surviving genetic complexities, attributed to diversity and abundance discover regular shifts due to the choice of energy sources that are generated over time with different intermediates. The simulation experiments or a theoretical setup provide relative answers to these scenarios, with their biased experimental designs and the selected attributes; and have a significant limitation in capturing the crucial biotransformation event by a rare community member.

To understand microbial systems at a local level, the understanding of the metacommunity from which it is drawn is required. Since for assessing the relationship between different members of community the random factors and deterministic factor decide the survival of community. In this paper, these issues and process of selection of unique bacteria with desired properties and their possible role as probiotic has been discussed with the human gut, animal gut or plant rhizosphere as a model.



Three decades of Cyanobacterial and Microalgal research and developments at Bharathidasan University, Tiruchirappalli, India.

N Thajuddin

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Microalgae including cyanobacteria (=Blue-green algae) have an ancient history of almost 3.5 billion years, exists most successful and ecologically significant organisms on earth with superior photosynthetic efficiency using sun light approximately three times more efficiently than higher plants. They can grow well in all aquatic habitats (freshwater & marine), all types of soils, agricultural fields, extreme environments (hot springs, polar regions sewage and effluents). Although majority of cyanobacteria are fully capable of independent existence in nature, some of them form symbiotic association with wide range hosts such as protists, animals and plants. Among plants, such symbioses have independently evolved in phylogenetically diverse genera belonging to the algae, fungi, bryophytes, pteridophytes, gymnosperms and angiosperms. They constitute a vast potential resource in varied areas such as mariculture, food, feed, fuel, fertilizer, medicine, industry and combating pollution. Pioneering work of the last decades has raised the status of these microbes to a level where they are being viewed with favour in biotechnologically relevant spheres.

India is bestowed with a very long coastline of over 7500 kms in addition to infinite lakes, ponds and puddles, saltpans, estuarine areas and the blessing of tropical climate has given an abundance of natural populations of blooms of diverse cyanobacteria. Thajuddin and Subramanian (1987 - 2003) have made a detailed survey of marine cyanobacterial biodiversity of a continuous stretch of the coastline of south India of over 2660 kms from Goa (West coast) to Andhra Pradesh (East coast) encompassing the coastal regions Kerala, Karnataka and Tamilnadu including Andaman, Nicobar and Lakshwadeep group of Islands had resulted in the identification of 225 species of 58 genera belonging to 14 families of cyanobacteria from in the survey of which 35 species were heterocystous and 190 species were non-heterocystous with the members of the family Oscillatoriaceae being predominant in the marine habitats. This survey also resulted in the establishment of an unique publicly accessible National Facility for Marine Cyanobacteria (NFMF) with 300 strains of marine cyanobacterial germplasm was established at Bharathidasan University by our beloved teacher Professor G. Subramanian, an eminent cyanobacterial biotechnologist with the financial support from the Department of Biotechnology, Govt. of India during the year 1991.

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Generally microalgae and cyanobacteria have several pharmacological activities such as antimicrobial, anticancer, metalloprotective, immunostimulant and antioxidant properties. In addition to their applications as biofertilizer and pollution abatement, several enzymes, amino acids, lipids, fatty acids are known from these organisms which can be made available in the market at a lesser cost since relative biomass production is much less expensive than bacteria or fungi. A novel compound monogalactosyl-diacyl-glycerol containing a palmitoyl (MGDG-palmitoyl) being reported from marine cyanobacterium *O. acuminata* NTAPC05 for the first time, as the active fraction, and its bactericidal property against ESBL producers. The carotenoids and phycobiliproteins (Phycocyanin & Phycoerythrin) an important constituent of cyanobacteria have high commercial value. Microalgae can provide several different types of renewable bio-fuels such as biodiesel, ethanol, methane, hydrogen, jet fuel, biocrude and more – via a wide range of process routes. Technologies such as blue colourant, β -lactamase enzyme and an aqua feed were developed from marine cyanobacterium *Phormidium valderianum* BDU 30501. Several marine and hypersaline cyanobacterial and microalgal isolates are proved to be very effective in bioremediation of various industrial effluents, production of antimicrobial compounds, antioxidants, siderophores, biolubricants, biosynthesis of several types of nanoparticles and other novel substances.

For long been India is celebrated for its richness in algal diversity and extraordinary contribution to the field of phycology. Although the biodiversity of the freshwater algal resources of India is critically recorded at times by renowned algologist of our country, often the actual algal populations have been greatly under-represented in the culture collections maintaining our native species. Extensive and exhaustive taxonomic and diversity surveys of freshwater microalgae and cyanobacteria had also resulted in the establishment of a publicly accessible germplasm collection of National Repository for Microalgae and Cyanobacteria – Freshwater (NRMCF) funded by the Department of Biotechnology, Govt. of India. Major tasks of the repositories are the collection, isolation, purification, identification and maintenance of microalgal and cyanobacterial cultures, supply of the cultures in a healthy live condition on demand and preparation of their informative catalogs and DNA Barcodes. So far around 20 strains of microalgae including cyanobacteria have been cultivated and exploited at the industrial scale. To make use of these organisms for our benefit, it is essential not only to understand and preserve the biodiversity of these organisms but also to gainfully exploit them in view of commercial opportunities available in economically vital areas including human health.



Role of Endophytic Bacteria for Development of Sustainable Agriculture

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Plant-microbe interactions have been the subject of several biotechnological studies, seeking sustainable development and environmental conservation. The inoculation of endophytic plant growth-promoting microbes (PGPM) in agricultural crops is considered an environmental-friendly alternative to chemical fertilization. Endophyte (Endo means inside and Phyte means plants it means inside the plant) colonize plant parts without causing any adverse effects. On many hosts, they act as plant growth-promoting, and/or biocontrol agents by direct antagonism or via the host by triggering induced resistance. Endophytes are capable of promoting plant growth both directly and indirectly. Endophytes can promote growth directly by the production and/or the regulation of plant growth hormones, the nitrogen fixation, phosphate solubilization and production of siderophores that contribute to the transportation of ferric iron into plant cells. Indirectly, bacterial endophytes promote plant growth by protecting the plant against pathogens. Endophytes confer better advantage over than rhizospheric bacteria as they reside inside the plants and used as a bio-control as well as biofertilizers for development of sustainable agriculture.

Keywords: Endophytes, Bacteria, Antagonism, Sustainable Agriculture.



New Insights Into Tissue Culture Plant Regeneration Mechanisms With Special Reference To *Adansonia digitata* L.: An Endangered Medicinal Woody Tree Species.

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ABSTRACT

An entire plant can be regenerated from an adult tissue or organ, calli or even a single cell by a process known as Plant regeneration. This involves physiological repair and replacement of tissues in plants based on the properties of Totipotency and Plasticity. Tree species carry a heavy genetic load and inbreeding may lead to reduced fertility, slower growth rates in progeny with limited environmental tolerance. In the present times, medicinal tree species raise key issues for conservation owing to their extreme life history features like life longevity, late reproductive age, accumulation of mutations etc.

Different strategies for conservation of tree species are widely acknowledged in the present times. *In vitro* conservation studies especially of a woody tree species poses a big challenge. *Adansonia digitata* L. (Baobab) is a majestic tree known for its unique medicinal properties and charismatic appearance. Looking into the vast medicinal uses of this economically important tree species, its conservation through tissue culture approaches is accomplished.

This study summarizes two regeneration pathways i.e. De novo organogenesis and Indirect regeneration with a review of environment factors influencing plant regeneration from explant source, basal medium, pulse treatment with PGRs etc. Also, a pilot scale experiment was initiated to investigate and elicit the production of bioactive compounds with antimicrobial potential using callus and suspension culture technology. Regeneration studies *in vitro* were carried out owing to poor natural regeneration due to critical seed dormancy factors. The techniques callogenesis, bud break and somatic embryogenesis were primarily used.

Compared with the conventional *In vivo* seed germination with (seeds having mature seed coat), Somatic embryogenesis and indirect regeneration using (mature seeds without seed coat), 70-75% success rate was achieved in plant regeneration making tissue culture approaches a viable tool for genetic transformation and molecular studies.

Key words: Plant regeneration, conservation, seeds, *in vitro*, somatic embryogenesis, medicinal,

Adansonia digitata



Microbial Activities Towards Soil Health And Plant Fitness -An Omics Analysis

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Microbes the unseen and relatively unsung group of living systems can effectively engage in creating a healthy ecosystem. This has led to the concept of the One Health. We have been working with relatively a few gram negative bacteria, the actinobacteria and the AM fungi to understand the interaction of the plants under biotic and abiotic stresses through the various Omic approaches. The metagenomic approach to understand the microbes during organic cultivation has helped us realize that the change between the organic and inorganic systems of cultivation is rather subtle. The actinobacteria are a distinct group of gram positive bacteria with a capacity to produce several secondary metabolites with distinct uses. We have found through transcriptomic studies that they help the plant to develop both induced systemic tolerance and induced systemic resistance apart from directly controlling the growth of several plant pathogens. The AM fungi has augmented the level of transcripts produced in plants when inoculated along with the actinobacteria. Proteomic studies have shown in sugarcane the release of several proteins that help overcome the smut fungus *Sporosorium scitamineum*.



Probiotic *Lactiplantibacillus plantarum* DHCU70 prevents obesity in mice through the regulation of gene expression of PPAR- γ and leptin

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Abstract

Probiotic strain of *Lactiplantibacillus plantarum* DHCU70 isolated from naturally fermented dahi, was obtained from Sikkim, India, had potent antimicrobial activity against *Kocuria rhizophila* ATCC 9341. Additionally, *L. plantarum* DHCU70 was well adapted to the *in vitro* environmental stresses and *in vivo* human GIT conditions. The whole genome sequence of *L. plantarum* DHCU70 has 3252 protein-encoding genes comprising 89 RNA genes (69 tRNA, 16 rRNA, 4nc RNA). Analysis revealed the presence of 20.5 kb long and 23 numbers of plantaricin encoding locus (*pln* locus) for the production of the antimicrobial compound. BAGEL analysis has shown that the *pln* locus of *L. plantarum* DHCU70 showed maximum sequence similarity with plantaricin NC8 of *L. plantarum* NC8, originally isolated from grass silage. Annotated whole genome sequence of strain DHCU70 was analyzed to ascertain probiotic marker genes. Due to the presence of genes responsible for antimicrobial activity and probiotic properties, *L. plantarum* DHCU70 was considered a suitable probiotic candidate for subsequent study. In pre-clinical trials, the anti-obesity effect of the probiotic *L. plantarum* DHCU70 was investigated on a high-fat diet (HFD) fed male C57BL/6J mice. The results of the study showed that the probiotic bacterium effectively reduces body weight (46.5g to 37.6g), organ weight, especially adipose tissue (2.97g to 2.24g), and abdominal circumference (10.5cm to 8.7cm). Probiotic treatment significantly lowered the total cholesterol (TC) by 23.79%, triglyceride (TG) by 15.2%, low-density lipoprotein (LDL) by 31.05%, aspartate aminotransferase (AST) by 42.3%, alanine aminotransferase (ALT) by 53.1% and also alleviated PPAR- γ by four-fold and leptin levels by 22 -fold. In contrast, high-density lipoprotein in serum and adiponectin levels in adipose tissue were increased by 9.55% and 0.63-fold, respectively. Treatment with probiotic DHCU70 resulted in reduced inflammation in adipose tissue. Due to the potential of *L. plantarum* DHCU70 in regulating gut microbiota and attenuating fat deposition in HFD-fed obese mice, a value-added product, probiotic carrot nectar was developed. This product in refrigerated conditions, probiotic bacteria maintained a viability of 6.4 log CFU/mL for 75 days without coliforms, yeasts and molds. Probiotic bacteria have also been found to thrive in complex gastrointestinal tract (GIT) environments, with a percent viability of 94.28% and 90.01% in SGJ and SIJ, respectively. The carrot matrix is likely to have benefited probiotic bacteria. *Lactiplantibacillus* DHCU70 contributed to the overall Vitamin A content of carrot nectar, which was 0.509 mg/100 gm,

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representing more than half of the daily need. Polyphenols, minerals, proximate properties, and sensory quality of probiotic carrot nectar were also studied. As a result, the symbiotic relationship between *Lactiplantibacillus* DHCU70 and carrot nectar provides a value-added probiotic product with having anti-obesity effect and substitute for lactose intolerance sufferers.

Keywords: Obesity, Probiotic *Lactiplantibacillus*, Lipid metabolism, Leptin, Adiponectin, Survivability, Carotenoid, Polyphenol, Sensory, Proximate, Mineral, Antimicrobial activity, Plantaricin, Bacteriocin.

All is not well: Bench to Bedside Research.

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Bench to bedside research (BBR) is a process of taking research results from the laboratory into the hospital so that it can directly benefit patients in terms of new diagnosis development, Vaccine, drugs or knowledge which helps in understanding pathogenesis and ultimately correct treatment. But even more success stories on the bench found themselves stuck on the translation path with a negligible impact on the clinic. Taking the advantage of having Research centre along with tertiary care, neurology hospital helps us to develop various Neuroinfections (8 bacterial meningitis {Baumannii meningitis, Pneumococcal meningitis, Staphylococcal meningitis, Enterobacter meningitis, Micrococcus meningitis, Haemophilus meningitis, Meningococcal meningitis, Pseudomonas meningitis}), (8 Neuroviral infections, DNA viruses: {CMV, EBV, VZV, HSV and RNA viruses: CHPV, DENV, JEV, WNV}) (Three Neuro-Zoonotic infection {Listeria meningitis, Neurobrucellosis, Bovine Brain TB}), diagnostic-prognostic kits/point of care testing and established key theories in bedside treatment. The CIIMS translation research model could be useful to a number of research institutes and universities. This model focuses on enabling and encouraging collaborative partnership between, not only, clinicians and scientists, but also, academia, health care and pharmaceutical industries and focuses on bringing scientific innovation of the patient community.



Genome Editing: Boon or Bane?

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Gene editing technologies such as site-directed-nucleases (SDNs) and oligonucleotide-directed mutagenesis (ODM) are recent additions to the wide array of genetic modification tools. Amongst these, the Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) and CRISPR-associated protein-9 nuclease (*Cas9*) together referred to as CRISPR-Cas9 tool, have emerged as one of the most popular tools for gene-editing.

In the process of domestication, crop plants have been continuously subjected to genetic changes to suit human dietary preferences and animal feed requirements. Several of the following methods cause genetic changes in plants:

1. Conventional plant breeding techniques involve the exchange of large segments of chromosomes between plants
2. Mutation breeding results in random genetic mutations and highly unpredictable changes
3. Transgenic transformation results in trans-gene insertions at random locations of plant's genome
4. Ribonuclease interference (RNAi) silences target genes and homologous genes with similar sequences, however with a fair probability of causing off-target gene silencing as well
5. Site-directed nucleases have the potential to edit precise targeted locations on the gene but have also been reported to cause unexpected off-target effects.

The following site-directed-nuclease based technologies are most commonly used for genome editing in crops and animals.

1. Clustered regularly interspaced short palindromic repeats/CRISPR associated nuclease 9 (CRISPR/Cas9)
2. Oligonucleotide directed mutagenesis (ODMs),
3. Engineered Meganucleases (EMNs),
4. Zinc finger nucleases (ZFNs), and
5. Transcription activator-like effector nucleases (TALENs).

These techniques open the possibility for targeted gene modification or alteration of nucleotides in an existing molecule of DNA or RNA, as well as insertions or deletions of large sequences in specific target locations (Agapito-Tenfen *et al.*, 2018). Among the new gene editing systems, CRISPR/Cas9 tool has emerged as the most powerful of all genome editing technologies available currently and has sparked a new revolution in biological and agricultural research. CRISPR/Cas9 technology is widely acknowledged as a powerful tool that has the potential to create genetic variability in a precise and targeted way, representing a new era in crop breeding. The system is versatile, fast and in-expensive, allowing genome editing strategies to be more accessible and

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efficient compared to other technologies such as the Zinc Finger nucleases, TALENs and other first generation genome editors. However, though the CRISPR system edits genes to create a single point mutation or even repair a mutation in the gene thereby enhancing or repressing gene expression, undesirable off target effects can also be expected to a certain extent. With the development of the high fidelity mutant Cas9 nucleases, the editing specificity has been reported to increase with negligible or no off-target effects. Undoubtedly the precision and convenience of CRISPR/Cas9 system will make it one of the most desired techniques of gene-editing in both mammalian and plant species for next few decades.

Basic Principle

The mechanics of DNA double-strand break (DSB) repair are central to the concept of gene editing. The DSB can be repaired by two mechanisms:

1. Non-homologous end joining (NHEJ) which joins two DNA strands randomly
2. Homology-Directed Repair (HDR) which uses the homologous sequence as a template for regeneration of missing DNA segment at a breakpoint.

HDR is more precise and can be used to create a vector that contains the necessary genetic material within a sequence for gene editing. The creation of a DSB at a specified location inside a genome is the key step in gene editing. To create specific DSB specially engineered nucleases are used nowadays. Clustered regularly interspaced short palindromic repeats (CRISPR) are one of these. CRISPR has been proved to be the quickest and cheapest method for gene editing.

The development of the CRISPR/Cas9 gene editing system earned the 2020 Nobel Prize in Chemistry, which has for the first time enabled scientists to make precise changes in the long stretches of DNA that make up the code of life for many organisms, including people. The prize was shared by Emmanuelle Charpentier, a microbiologist and director of the Berlin-based Max Planck Unit for the Science of Pathogens, and Jennifer A. Doudna, a professor and biochemist at the University of California, Berkeley.

Boon to Agriculture:

CRISPR-based genome editing has shown huge promise for crop improvement (Sedeek *et al.*, 2019). First, CRISPR/Cas genome editing tools can be used to significantly improve crop yield. Improving crop yield is a long-term dream for scientists and breeders. However, due to the fact that crop yield is governed by quantitative traits and is controlled by multiple genes, the science of genetic improvement for yield enhancement becomes complex. Further, how the yield-associated genes regulate each other to control crop productivity is unclear as yet. Over the past two to three decades, scientists have tried their best to increase yields through transgenic methods, unsuccessfully though. Although a single major gene that controls yield has not been found as yet, many studies do show that a few genes negatively affect crop yield. It is hypothesised that yields could be improved by either inhibiting or silencing these negative genes.

One recent study showed that CRISPR/Cas 9 genome knockout of genes *gn1a*, *depl1* and *gs3* which are negative regulators of yields in rice resulted in significantly enhancing yield parameters, including improved grain number, dense, erect panicles, and larger grain size, in rice (Li *et al.*, 2016). Another research using CRISPR/ Cas 9 genome editing in rice also showed that knockout of grain

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weight negative regulators, GW2, GW5 and TGW6, increased the grain size and weight (Xu *et al.*, 2016). CRISPR/Cas genome editing also significantly increased plant resistance to various environmental abiotic and biotic stresses, including bacteria, fungal and/or virus induced diseases. For example, CRISPR/Cas 9 edited Mildew-resistance Locus (*mlo*) gene mutants' conferred heritable broad-spectrum resistance to powdery mildew in hexaploid bread wheat (Wang *et al.*, 2014). By targeting three different Potato virus Y PVR strains, Zhan and colleagues (2019) created potato genome-edited mutants with broad-spectrum resistance to multiple Potato virus Y (PVY) strains.

The potential of gene editing in plant improvement extends to a wide range of plant varieties such as wheat and cotton which have a complex genome that makes plant breeding very complicated. CRISPR based technologies have been found to be significantly efficient in editing genes in a precise manner in several organisms including many agriculturally important crop species to enhance trait values in crop protection and crop production. Gene-editing has been used to develop herbicide tolerant plants in cotton (D'Halluin *et al.*, 2013), rapeseed, potato, rice, flax, maize, cassava, tobacco and soybean. It is unlikely that compared to transgenic HT crops, the gene edited herbicide resistant crops could pose any different concerns on weed resistance to herbicides.

CRISPR/cas9 tool have been used to induce targeted mutagenesis in cotton to fine-tune several traits including fibre quality improvement, disease control and insect pest management. For instance, CRISPR/Cas9 based genome editing could successfully control the dreaded cotton leaf curl disease (Iqbal *et al.*, 2016). Likewise, the pheromone odorant receptor OR16 gene was knocked out using CRISPR-Cas9 to disrupt mating in the bollworm *Helicoverpa armigera* (Chang *et al.*, 2017). It is possible to develop varieties that produce gossypol-free seeds using CRISPR/ Cas genome editing by knocking out an individual gene or a few genes that are associated with gossypol biosynthesis pathway. Thus, CRISPR/Cas genome editing technology opens a new era for precision cotton breeding for better cotton production.

Presently many labs are targeted to create crops that are more resilient to abiotic stresses (like drought, excessive watering, extreme temperatures, salinity, and mineral toxicity); or create crops that are more nutritious - we might be able to solve the problem of food scarcity and malnutrition throughout the world. However, how the global regulation of genetically modified food is implemented will have a significant impact on how much gene editing could help this industry.

Boon to human health:

In fact, present days we are aware of many disorders that result from the mutation of a single gene. There are also diseases caused by multiple gene mutations. All of these illnesses cost us priceless human lives. These genes may be fixed or changed with the aid of gene editing, saving many lives. Many genetic illnesses, including β -thalassemia, cystic fibrosis, diseases of glycogen storage such as haemophilia A and B, are the subject of extensive investigation today. Additionally, vector-borne and communicable diseases can be wiped out by gene editing. Researchers are using the CRISPR-CAS9 gene drive to alter the genes linked to sterility in the malaria-carrying A Gambie. The area of synthetic biology, which aims to engineer cells and organisms to perform certain functions, can use the engineered nucleases to insert or delete elements and create desired systems. Gene editing can aid families whose genetic illnesses have a history of being handed down from one generation to the next by preventing the transfer of such genes. Gene editing can provide a cure for diseases like



obesity, diabetes, mental illness, cancer, and other conditions that are spreading quickly throughout the world and may be genetically based.

The simplicity of the CRISPR-Cas9 system has enabled its widespread applications in generating germline animal models, somatic genome engineering, and functional genomics screening and in treating genetic and infectious diseases. This technology will likely be used in all fields of biomedicine, ranging from basic research to human gene therapy.

The development of the breakthrough technology known as gene editing has brought us one step closer to being able to change specific DNA areas. Despite the fact that there are other gene editing tools now in use, CRISPR has become extremely popular. Particularly when compared to conventional gene editing techniques, much may be attributed to its extraordinary precision, cost effectiveness, and time savings. Evidently, since 2011, the number of patent applications for CRISPR has increased at an unheard-of rate. Treatment of hereditary illnesses, the creation of antibiotics, and antiviral are the main goals of the patent implementation and the possibilities are endless. If it is used responsibly, gene editing can prove to be a boon to the humankind.

Biotechnology for Extenuation of Acid Mine Drainage Pollution

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Acid mine drainage (AMD) or metalliferous acidic drainage is the second largest catastrophic universal problem generated from both active and abandoned sulfidic mines and most coal mines. AMD contain a variety of toxic metals in large quantity and acidic pH, adversely affecting the surface and underground water ecosystems and even plant and human health. The activity of indigenous iron and sulphide oxidizing bacteria accelerates the oxidation process and generates an acidic metalliferous huge volume of drainage water. The generated AMD runoff damages several kilometres of the ecosystem. The treatment of such AMD requires hundreds of years. Many physicochemical methods are in use for the remediation of AMD, but they have one or other disadvantages. Application of biotechnology in general and understanding microbial technology for the neutralization of acids and selective remediation of metals, in particular, provide novel approaches for the remediation of AMD. Novel approaches may result in cost-effective, environmentally sustainable treatment. But further research is required for large-scale applications of the multidisciplinary problem of AMD.

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Overview of Epidemiology of Lumpy skin disease (LSD) a Transboundary disease in India.

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ABSTRACT

LSD is the transboundary disease of emergence and the cattle shows symptoms including fever, skin lesions, abortions, infertility mastitis and low milk production and leading to death. The LSD is spreading in India rapidly and killing thousands of cattle. The impact of this disease is creating problems in the livelihood of farmers as the milk production go down and major loss for dairy and meat industries. Studies on conventional and molecular epidemiology of LSD incidence throw light on controlling the infection and also vaccine development.

Temperature as Substantial Factor for Shaping Bacterial Diversity and Antibiotic Resistance in Distinct Thermal Gradient Microenvironments

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ABSTRACT

Distinct microbial communities occupy the various niches among various spheres throughout the Earth. Based on the adaptations to different gradients of physical or chemical parameters such as temperature, pH, pressure, NaCl etc., different microbial populations thrive significantly or extinct and vice versa. Temperature plays a crucial role in the maintaining the microbial diversity. However, very few studies have been done on the role of temperature gradient in sustaining the microbial

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diversity. A recent and similar kind of study has been done on the geothermal settings of Yellowstone and Iceland, however, the temperature range taken were warm (38°C) to boiling. The high-altitude mountain ranges of Sikkim Eastern Himalayas covered by snow and glaciers possess various geothermal settings in the vicinity. This makes a substantial environment to work on different temperature ranges simultaneously. In this study we are presenting the dependence of microbial diversity within a distinct range of temperatures from cold (10°C) to warm (37°C) and up to hot (60°C). High throughput sequencing and also culture dependent approaches were taken into consideration. Over three dozen phyla of Bacteria and over one dozen phyla of Archaea were identified, representing over 2000 distinct organisms at species level. The results have shown the predominance of phyla Proteobacteria, Firmicutes, Bacteroidetes and Chloroflexi. We found a significant concave down curve in the number of microbial taxa as the temperature increased from warm to hot. Mesophilic environment (37°C) was shown to possess large number and accumulation of microbial taxa. However, there is a significant increase in accumulation of specific taxa within a specific ideal temperature. For example, phylum Proteobacteria possess a significant linear reduction from psychrophilic to thermophilic environment. In contrast, phylum Firmicutes showed a significant linear increase from psychrophilic to thermophilic environment. The physicochemical parameters were evaluated and their correlation was checked with respect to bacterial diversity. It was shown that almost all the parameters such as pH, Na, P, Mg, Ca etc. were showing hardly any correlation with various bacterial phyla. However, temperature has shown significant correlation with predominant phyla evaluated through regression analysis with R value \square 9. We also checked the antibiotic resistance patterns through culture dependent and culture independent approaches and correlates these with temperature gradient. We found that prevalence of antibiotic resistant pattern as mesophiles > psychrophiles. And there was no antibiotic resistance in thermophilic isolates. Also, only few antibiotic classes were showing resistance such as β -lactams and Aminoglycosides. Similar results were found using metagenomic approaches. The antibiotic resistant genes obtained from metagenomic libraries belonging mainly to mesophiles. Thus, it can be hypothesized that antibiotic resistance is high at optimum mesophilic temperatures where there is huge competition for growth and survival among large communities of microbes. This may conclude that the temperature is the major factor and plays a significant contribution in shaping the bacterial community structure in any thermal gradient edifice. Also, there may be the other specific adaptations which governs the higher accumulation of specific bacterial phyla and antibiotic resistance at a specific optimum temperature. These adaptations need to be studied further.

Keywords: *Thermophiles, mesophiles, psychrophiles, antibiotic resistance, microbial diversity*

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Bridging the gap between Academia and Biotech Industry - Why & How?

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ABSTRACT

Biotechnology is a very vast field having many overlapping interdisciplinary areas and career opportunities are unlimited. When it comes to opportunities for fresh students, the supply and demand has largely remained constant over the years. Earlier fewer students pursued this field and even the opportunities were limited. Nowadays with multiple options and advanced knowledge base, opportunities are booming their way. There are options beyond core research, with the evolution of food, pharma and biotech companies, students can pursue a career in regulatory affairs, patents, production, quality control and assurance, clinical research and data management, bioinformatics, biostatistics, bioanalytical, toxicology, bio based instrumentation, bio-processes and related automation, sales and technical marketing, digital marketing of bio products, technical content writer and so much more.

The competencies of the newly graduated biotechnologist/biologists and the competency requirements of Biotech industries for fresh degree holders need to be identified based on the feedback from different types of Biotech industries. Nowadays, Academic Institutes are taking active steps to incorporate practical approaches in their syllabus and collaborate with industries for training and placements. However, there is a need to identify the specific gaps between academia and industry and try to bridge it using the concept like Learning Factories.

Most academic research does not see the light at the end of tunnel with respect to practical application or commercialization of their products or processes. The academic research work usually ends with a publication and at the most, a degree awarded to the student. There are academic institutes which carry out high-end applied research having potential industrial applications but it does not translate into a value added product or process. There is a good sign that private as well as government funding agencies like DBT are encouraging academic institutes to collaborate with private industries or startup companies to take their research forward for commercialization. The educational institutes should also urge students to find commercial/practical application of their research by giving them opportunities to undertake application based projects. There may be lots of constraints in terms of sourcing funds, getting a right partnership, IP generation and available infrastructure. But this can be possible with industrial collaborations and through various funding bodies. This will definitely help bridging the gap between academia and industry.



Computational Medicinal Chemistry and Virtual Screening Aided Approaches of Discovering Potential Molecular Targets and Natural Lead Molecules towards Multidrug Resistant *Pseudomonas aeruginosa*

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Pseudomonas aeruginosa has become a global concern due to its extreme resistance to most of the last resort antibiotics. Present study focuses on the screening of potential molecular targets involved in regulation of biofilm formation in *P. aeruginosa* and identification of potential natural lead molecules against these targets by molecular modelling, docking and simulation studies. Response regulator (GacA) and transcriptional activator (RhlR) involved in biofilm formation in *P. aeruginosa* were identified as molecular targets by metabolic pathway analysis and the three-dimensional structures of these proteins were predicted by homology modelling and validated. By thorough literature survey, 78 lead molecules were screened and their pharmacokinetic profiles were determined and best two of them selected. The binding potential of selected lead molecules against GacA and RhlR were predicted by molecular docking and their binding energy was compared with the interaction of meropenem and its usual target penicillin binding protein-3. The stabilities of best docked complex were studied by molecular dynamic (MD) simulation. This study showed that Celastrol present in *Celastrus paniculatus* and Rotiorinol present in *Chaetomium cupreum* showed better binding affinities with GacA (binding energy -7.2 kcal/mol) and RhlR (binding energy -8.0 kcal/mol) respectively in comparison with the binding of Meropenem and its target (binding energy -6.2 kcal/mol). MD simulation studies showed that GacA-Celastrol and RhlR-Rotiorinol complexes demonstrated conformational stability throughout the simulation. This study highlights the application of GacA and RhlR as prospective targets and Celastrol and Rotiorinol are the potential lead molecules towards biofilm producing drug resistant *P. aeruginosa*.

Keywords: *Pseudomonas aeruginosa*, Response regulator, GacA, transcriptional activator, RhlR, Prospective targets, Natural lead molecules



Recent Advances in Microbial Taxonomy: an Inclusive Outlook Towards the Microbial Majority

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President, Bergey's International Society for Microbial Systematics

ABSTRACT

Taxonomy of microorganisms has kept pace with the new information generated by the methods of studying these life forms over the years. The past two decades have witnessed a dramatic shift in these methods: from classical to molecular approaches, resulting into fundamental changes in how we understand microbes. Among the molecular approaches, methods have moved from being sensitive to experimental conditions to being more robust. Amongst these, sequencing of the rRNA genes has played a critical role in shaping our understanding of the microbial world. The advent in sequencing technologies, its miniaturisation and increased affordability has allowed access to sequence data spanning single whole genomes to metagenomes of communities. This has revealed an overpowering microbial majority that had remained obscure to classical approaches of cultivation in the laboratory. Due to the non-availability of cultured representatives, description of novel taxa belonging to this enormous hidden diversity cannot be validly published under the limitations of the existing rules of nomenclature. To overcome this limitation, a new code of nomenclature of microbes known from sequence data, popularly called the SeqCode was recently proposed as an alternative to the microbiological community. My session will focus on key highlights of the SeqCode and how to publish novel taxa under this code. In addition, I will also discuss the recent changes to the names of phyla that were impacted by the inclusion of the rank of phylum in the rules of the nomenclature. I will also touch upon how, you as a microbiologist can become part of these discussions and contribute to the advancement in the field of microbial taxonomy.



Mimicking nature's strategy for bioremediation of Reactive Red 120 (RR120) dye by designing bacterial consortium and optimizing its efficacy for conventional applications

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ABSTRACT

The contamination of soil and water bodies with synthetic dyes is a serious environmental threat. The indigenous microorganisms of a contaminated region naturally adapt to the toxic environment and promote dye degradation. Though this process is slow due to several interfering factors, bioremediation of dyes can be optimized by enhancing the growth and performance of indigenous strains. In the present study, screening of RR120 dye degrading bacteria from textile effluent and natural samples and optimization of their growth and physicochemical parameters for maximizing their potential was carried out. A consortium RAR was designed with 3 potential azo dye degraders, including LK-1 (*Shewanella haliotis*RDB_1), LK-2 (*Aeromonas hydrophila*RDB_3) and DL-1 (*Shewanella putrefaciens*RDB_2) in 1:1:1 ratio. A 10% inoculum (1.0 OD_{540nm}) of consortium RAR completely degraded 50ppm RR120, in 3% Yeast Extract (YE) medium, under static conditions in 2h. The optimum decolorization was observed between pH 7-8 and temperature 30°C-35°C. The consortium RAR retained significant activity in pH range of 6-10, temperature between 25°C-45°C and NaCl concentration up to 10%. It also tolerated up to 8000 ppm RR120 dye concentration and decolorized over 25 batches of 50ppm RR120 consistently. The rates of decolorization by individual strains of LK-1, LK-2 and DL-1 were less efficient as compared to the consortium RAR (124.74 mg/L/h). Besides RR120, the consortium RAR decolorized 17 structurally different dyes. The electron acceptors used in this study negatively affected the decolorization rate. The sugars and organic acids also failed to support decolorization in M₉ medium. Soymeal peptone (prepared in distilled water) supported considerable decolorization but was not as effective as 3% YE medium for dye decolorization by consortium RAR. The dye degradation was confirmed with UV-Vis spectrophotometer and HPTLC analysis. The degraded metabolites were analysed using techniques like HPLC, GC-MS and FTIR to identify stable and/ or unstable intermediate products, and a metabolic pathway was proposed for dye degradation by the consortium RAR. To confirm nontoxic nature of degraded metabolites, the samples containing degraded dye were tested for their effect on survival, growth and/or phenotypic characteristics of various biological indicators of toxicity. The treated samples supported seed germination, survival of daphnia, bioluminescence activity and antibiotic production by bacteria indicating effective degradation of textile effluents into non-toxic end products. Finally, various applications of consortium RAR were studied. Among the two matrices used for immobilization (agar and alginate), the cells immobilized in 6% Ca-alginate matrix showed better efficiency for decolorization of RR120 (~85%; 6 batches) and textile effluent (~88%; 6 batches) with a retention time of 6h. The consortium RAR also generated bio-electricity (40mV on day 4 and 695mV on day 9) with simultaneous degradation of textile effluent using the 'Two chambered H-type MFC unit'. Thus, the consortium RAR can be used as a potential bioremediation tool for treatment of textile effluents containing a range of dyes.

Keywords: bioremediation, consortium, MFC, metabolite, optimization



‘Ameliorative Strategies for Liquid Biofertilizers Production Technology’

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ABSTRACT

The diverse biota consisting of plants, animals, and microbes is present in the soil ecosystem. Soil is the shelter for different classes of microorganisms that includes Achaea, Bacteria, Fungi & Protozoa. These soil microbes play important role in maintaining the various ecological processes occurring in the soil. They are an essential component of food chains as they are in the nutrient cycling process and also other biogeochemical cycles, thus making available the nutrient to the plant-the primary producers of the nutrient. The physical structure of soil can be balanced in the case of unfavorable conditions due to presence of the microbial diversity. They are hence also known as the “soil health indicators”.

Continuous use of chemical fertilizers depletes essential soil nutrients and minerals that are naturally found in fertile soil. When one uses chemical fertilizers; they do not help replenish soil nutrients and their fertility contrary to the popular belief; but, replenish only nitrogen, potassium, and phosphorous. Though chemical fertilizers will help plants grow faster; plants will not be healthy and strong as plants grown in that manner do not have enough time to mature to develop good root growth, strong stems, or nutritious fruits and vegetables and are more susceptible to pests and diseases, as they lack a good immune system and enough resistance against these forces. Besides this, chemical fertilizers can cause root burn or fertilizer burn, as chemical fertilizers do not allow enough water intake for the plants. To overcome all these disadvantages of chemical fertilizers, biofertilizers are being used. Modern agriculture has lost its sustainability due to the excessive use of chemical fertilizers and harmful pesticides, which has resulted in higher cultivation costs, decreased food security and safety, and, finally, decreased soil fertility. Consumer concerns about food safety increased interest in residue-free agricultural productivity, and ease of registration compared to chemical competitors paved the way for researchers to focus on the production of biofertilizers and biopesticides. Biofertilizers are well known for their low cost, non-toxic, environmentally friendliness, and composition. Some microorganisms, such as plant growth-promoting bacteria, fungi, Cyanobacteria, and others, have been observed to exhibit Biofertilizer-like activities in the agricultural sector. Although plant growth-promoting bacteria are becoming more important in promoting plant health and growth because their symbiotic relationship with plants increases phosphorus and nitrogen bioavailability and water uptake, resists pests, and improves phytohormone production. As a result, there is a great need for sustainable agriculture through the use of biofertilizers and biopesticides, for which the collaboration of microbiologists, plant breeders, plant pathologists, and agronomists is required to develop innovative organic farming techniques that protect soil fertility.

The recent trends in Organic agriculture, an emerging innovative technology with the potential properties of nanomaterial and liquid biofertilizers help the development of novel, low-cost,



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eco-friendly Nano-biofertilizers. It is a holistic production management system that promotes and enhances agroecosystem health, including biodiversity, biological cycles, and soil biological activity. One of the aspects of organic farming includes the use of microorganisms in agriculture as bio-inoculants. In the present scenario solid-carrier-based bio formulations, fluid bed dried bio formulations, polymer entrapped formulations & liquid inoculants are available in the market. Among different kinds of biofertilizers that are in current use, liquid biofertilizers have shown maximum field efficiency along with a better shelf life. Another aspect of liquid biofertilizers has shown that the combined use of two or three beneficial microorganisms as inoculants performs better than single inoculations. Any organism functions better in a group as compared to an individual in an ecological niche. Keeping this principle in mind, a mixed inoculant that interacts synergistically is devised with a shelf life of two years & which gave better yield to promote an eco-friendly source for the maintenance of soil health and sustainable crop production systems.

Keywords: Liquid biofertilizers / Biopesticides, Organic farming, Chemical fertilizers, PGPR, Sustainable agriculture

IN-VITRO ANTIVIRAL ACTIVITY EVALUATION OF INDIAN MEDICINAL PLANTS AGAINST SARS CoV-2

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ABSTRACT

The highest mortality rate virus of the 21st century, initially affects the respiratory system, evades immune system fighter cells and later affects other organs if not eliminated from the body. In absence of any specific pharmacological treatment without adverse side effects, the need to find new therapeutic alternatives is clear. Ethnomedicine and ‘Ayurveda’, are holistic approaches that stimulate non-specific immunity by assisting CD4+ and CD8+ T cells to act against the pathogens to ward them off and remove root cause underlying a disease. Various phytochemicals from Indian medicinal herbs are known to act against viral receptors, their target protein sites and interfere with viral reproduction and also as potential immune cell enhancers. The current research used LCMS to identify phytochemicals in 4 Indian traditional medicinal herbs and their ayurvedic blend against SARS-CoV-2, through a pre-post treatment strategy in vitro using qRT-PCR. Herein, pre-post treatment of the extracts & their ayurvedic blend inhibited viral load significantly statistically ($p < 0.05$), with *Piper nigrum*, *Terminalia arjuna* and the 4 ayurvedic blend exhibiting maximum antiviral activity almost equivalent to standard drug Remdesivir, thereby confirming their anti-SARS-CoV-2 activity was efficient similar to synthetically derived Remdesivir. Herein, the anti-SARS-CoV-2 activity of 4 herbal extracts and their mixture was evaluated, while their brief role in stimulating the immune system in order to ward off the pathogenic organisms is discussed.

Keywords: Immunostimulatory, *Piper nigrum*, *Terminalia arjuna*, qRT-PCR, SARS-CoV-2, Remdesivir.

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SCREENING OF THERMOSTABLE ALPHA-AMYLASE FROM THERMOPHILIC BACTERIAL ISOLATES OF SIKKIM HOT SPRINGS

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ABSTRACT

The advent of green chemistry brings a high demand for sustainable catalytic process that use enzymes as a cleaner alternative to chemical catalysts. With various hydrolases available, the amylases have various biotechnological applications and contribute approximately 25% of the world enzyme market. Its major industrial applications are owed by its pivotal role in starch hydrolysis, however, most amylases used have their origin from mesophilic sources. Their applications in industries require that the ideal enzyme should be stable at high temperature and thus, this makes it desirable for continual search for thermostable/thermophilic amylases. The microbial contents in hot springs of Sikkim are a colossal treasure for diverse microbiome with novel enzymes. In this study, thermophilic bacteria from Sikkim Hot Spring have been isolated and identified by 16S rRNA gene sequencing. The isolates with highest amylolytic indices are chosen for further study. The optimum parameters (temperature and pH) for maximum enzyme production and activity have also been investigated. Furthermore, the study also aims to clone and express the alpha-amylase gene in a suitable heterologous host for its functional improvement. To the best of our knowledge, this remains the first report on characterization of thermostable amylase from Sikkim Hot Springs.

Keywords: Thermophiles, Hot springs, Thermostable amylase

"OPTIMIZATION OF CELLULASE AND XYLANASE USING CORN COB AND COCONUT HUSK FROM SOIL OF MEHSANA DISTRICT"

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Cellulases and xylanases are a group of hydrolytic enzymes and are degrading agri- cellulosic materials or waste. 16 isolates obtained from different soil sites. Among them 8 strains were selected by primary and second screening. This work focuses on different cultural conditions that were examined to assess their effect in optimizing enzyme production. Effect of temperature, pH, substrate concentration, nitrogen and carbon source, metal salts on crude cellulase and xylanase enzyme activity were studied using two substrates (corn cob, coconut husk) by solid-state fermentation. Optimum pH and substrate concentration for cellulase and xylanase production was 4.0 and 6.0 and 1.5 and 2.5% respectively.

Keywords:- cellulase, xylanase, solid-state fermentation, optimization



INVESTIGATION OF ANTIOXIDANT POTENTIAL AND PROBIOTIC PROPERTIES OF LACTIC ACID BACTERIA ISOLATED FROM DAIRY PRODUCTS

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Lactic Acid Bacteria (LAB), which are beneficial microbes well known for their ability to improve wellbeing, can be abundantly found in fermented dairy products. Dairy products are frequently utilized as carriers for these bacteria, which are mostly characterized by lactic acid bacteria, and probiotics play a significant part in this market. This study aimed to isolate and characterize LAB from dairy products with potential probiotic attributes and to evaluate the safety of these cultures. Primary screening (Gram staining, Negative staining, oxidase test, catalase test, hemolytic activity, and biochemical test such as IMViC, urease test, triple sugar ion test) of 30 isolates were carried out. Based on primary screening, 12 isolates were selected for secondary attributes like acid tolerance, bile tolerance, antibiotic susceptibility test, Cell auto aggregation, and cell surface hydrophobicity. Based on the results of secondary attributes, 5 out of 12 isolates were selected for antioxidant analysis. The antioxidant activities were examined by ferric reducing antioxidant power (FRAP) and oxygen radical absorbance capacity (ORAC). These selected isolates showed growth at pH 2 and few were able to tolerate pH 1.5 also. Auto aggregation activity and cell surface hydrophobicity of selected isolates was demonstrated by good aggregation capacity. In FRAP and ORAC assay, most of the selected LAB strains showed higher free radical scavenging activity. The genus and species of the selected LAB isolates were confirmed using molecular identification for the 16s rRNA region.

Keywords: Lactic Acid Bacteria, Probiotics, Dairy products, Antioxidant activity



SCREENING OF SIDEROPHORE PRODUCING BACTERIA FROM MARINE RESOURCES

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ABSTRACT

Iron is essential for many physiological processes in bacteria, fungi as well as in phytoplanktons. Bio-available iron in ocean is attached to organic ligands called siderophores. Siderophores are iron chelating compounds. Bacteria produce siderophore for iron sequestration to support their growth under iron limiting conditions in environment. In the current study, an attempt was made to examine siderophore producing ability of bacteria isolated from marine resources. The chrome azurol S (CAS) assay detection system is used for the screening purpose. Various samples of marine resources like marine water, sand, mud from mudflats were collected from different areas along coastal region of Maharashtra. From the collected samples, 44 bacterial isolates were isolated on Zobell marine agar. In CAS liquid assay for siderophore detection, cell free supernatant of the growing bacterial isolates were allowed to react with CAS solution. After 10 minutes of incubation at room temperature, color change from blue to orange- pink was observed with 16 isolates and the absorbance was calculated at 630nm by microtitre plate reader. Percentage of siderophore production was calculated and is more in strains GSW13 and *Bacillus subtilis* MCC2010. Thus, the study concludes that strains GSW13 and *Bacillus subtilis* MCC2010 can be promising candidates for the siderophores production.

Keywords- *Siderophore, Marine resource, Marine bacteria, Zobell marine agar, Chrome azurol S*



MICROALGAL BIOTECHNOLOGY: ASPECTS AND PROSPECTS

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ABSTRACT

Microalgae are a diverse group of unicellular photosynthetic organisms. Microalgae have recently attracted considerable interest worldwide, due to their extensive application potential in the renewable energy, pharmaceutical, and nutraceutical industries as they produce a variety of industrially important secondary metabolites. They synthesize diverse novel biologically active compounds (proteins, carbohydrates, lipids, vitamins, pigments, minerals etc) with potential applications. Several microalgal species have been identified as promising source of value-added products with unique biological qualities. Microalgae are useful in mitigation of elevated CO₂ level and treatment of waste water. The demand of microalgae as an alternative bioresource is due to a set of intrinsic advantages such as, low production cost, no requirement of arable land, minimum uptake of nutrient and the capacity to grow rapidly in both large-scale outdoor systems and indoor photobioreactors. Presently, much research attention has been focused on the value added biomolecules from marine microalgae. The marine environment is an important source of industrial products such as human nutrition, feed, agriculture, aquaculture, cosmetics, pharmaceuticals etc. Thus extensive study is under progress in our laboratory on the antioxidant, antimicrobial, anticancer, anti-inflammatory, UV protective, biofuel, phycoremediation activities of microalgae found across Odisha coast with an intention to obtain some promising novel bio-prospective microalgal species for commercial applications in future.

Keywords: *Antimicrobial, antioxidant, microalgae, pharmaceutical, secondary metabolites*



PRODUCTION OF XYLANASE BY THE WHITE-ROT FUNGUS *GANODERMA LUCIDUM* IN SUBMERGED FERMENTATION USING WILDLY GROWING NON-FOOD PLANT BIOMASS AS SUBSTRATE

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ABSTRACT

Xylanases are glycosidases (O-glycoside hydrolases, EC.3.2.1.x) which catalyze the hydrolysis of 1, 4-β-D-xylosidic linkages of the complex plant cell wall polysaccharide xylan. The relatively high cost of enzyme production has hindered the industrial application of xylanases. In this work, the main proposal was incorporated in the nutrient medium plant biomass decomposed to soluble hemicellulose-rich compounds (liquor/hydrolysate) through treatment of plant biomass in autohydrolysis process, as a strategy to increase xylanase production. In the present investigation the production extracellular xylanase by a newly isolated white-rot fungus *Ganoderma lucidum* on the low-cost aquatic and terrestrial weed plant biomass hydrolysate was studied in submerged fermentation. Six wildly growing non-food plant biomass Benghal day flower (*Commelina benghalensis*), Bermuda grass (*Cynodon dactylon*), Water hyacinth (*Eichornia crassipes*), Congress grass (*Parthenium hysterophorus*), Water lettuce (*Pistia stratiotes*), and Green foxtail millet (*Setaria viridis*) were evaluated in SmF for xylanase production. In all the experiments, temperature and pH were kept constant at 25±2°C and 5.5 respectively and the fermentation was carried under static conditions for 7 to 14 days of incubation period. The best xylanase activity was obtained when pure xylan was used as the sole carbon source. The plant biomass of *Setaria viridis* was shown to be the best inducer for xylanase production followed by *Cynodon dactylon* and *Parthenium hysterophorus*. In aquatic plant biomass of *Eichornia crassipes* and *Pistia stratiotes*, this fungus showed moderate levels of xylanase activity. *Ganoderma lucidum* produced very minimum quantities of xylanase when *Commelina benghalensis* biomass was used as carbon source.

Key words: Xylanase, white-rot fungus, plant biomass hydrolysate, inducer, submerged fermentation.

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ISOLATION AND PARTIAL CHARACTERIZATION OF MICROORGANISMS ISOLATED FROM AND AROUND THE ARID REGION OF JHILIMILI FOREST IN BANKURA DISTRICT, WEST BENGAL, INDIA

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Abstract

Different biological and environmental processes along with physicochemical nature influence the habitat for soil associated microorganisms. To study the comparatively unexplored soil microbiome of West Bengal, an arid region within Jhilimili Forest of Bankura district and a nursery nearby (22°49'0.12"N and 86°37'0.12"E) were selected. After collecting soil samples from those regions, some routine physical characteristics like soil pH, moisture content, water holding capacity, soil capillary and percolation test were performed. Soil samples were serially diluted and were plated on 2% Nutrient agar and Czapek's Dox agar media to develop, observe and isolate microbial colonies. Gram's staining and Lactophenol Cotton Blue staining were performed to determine the morphology and nature of microbial population present there. The selected isolates showed optimum growth at 37°C, but the optimal pH varied between pH 5-7. These microbes showed activity at variable glucose (2.0-5.0 mg/ml) and NH₄Cl (1.0-1.5 mg/ml) concentrations also. Further, we screened those isolates for Indole, Methyl red, Voges Proskeur and Citrate utilization (IMViC) test, followed by qualitative assay for Urease, Amylase, Phosphatase, Protease and Xylanase production. Quantitative assay for amylase showed variable activities among the isolates.

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RECOMBINANT MICROORGANISMS FOR CELLULOSIC ETHANOL PRODUCTION

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Cellulosic ethanol would reduce our petroleum dependency, as ethanol is produced from the inexpensive and plentiful feed stocks. Efficient conversion of biomass to ethanol requires development of microorganisms capable of fermenting a wide range of carbohydrates and tolerating high concentrations of ethanol. Metabolic engineering of microorganisms to utilize cellulose will be vital for improving the prospects of significant cellulosic ethanol production. Several Gram-negative bacteria such as *Escherichia coli*, *Klebsiella oxytoca*, and *Zymomonas mobilis* have been engineered for ethanol production. Enteric bacteria normally produce less ethanol, because of their poor efficiency in converting pyruvate to ethanol. A suitable ethanologenic and cellulose-producing bacteria could be developed by transferring genes that encode the ethanol-fermenting enzymes. In the present study, the cellulosic ethanol production capability of the recombinant strains were determined through simultaneous saccharification and fermentation (SSF) process using carboxymethyl cellulose and pretreated cellulosic materials as substrates.

PRODUCTION AND CHARACTERIZATION OF EXOPOLYSACCHARIDE BY BACTERIAL ISOLATES FROM SUGARCANE FIELD SOIL

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Abstract

The present study was aimed at production of exopolysaccharide by bacterial isolates from sugarcane field soil Raka village in Gondia, Nagpur region and characterization of exopolysaccharides. The EPS from all the isolates were successfully extracted and carbohydrate and protein contents were measured. Analysis of the exopolysaccharide to determine the sugar composition was done by using Liquid Chromatography-Mass Spectroscopy LCMS. The identification of isolates is very necessary in order to get their full information of physiological aspects. The morphological and biochemical characterization suggested that the isolates belong to *Bacillus* spp. and *Pseudomonas* spp. mainly. MIC values of the exopolysaccharide suggested that they are effective in inhibiting the growth of test pathogens at lower concentrations as well. The antimicrobial activities of EPSs could be used as a potential source for the development of antimicrobial drugs and may have various industrial, pharmaceutical and medical applications. However further research is necessary to elucidate the efficacy of exopolysaccharide.

Keywords: *Bacterial isolates, Exopolysaccharides; Antibacterial activity*



CHARACTERIZATION AND IDENTIFICATION OF AUTOCHTHONOUS PROBIOTIC BACTERIA IN LACTATING DAIRY COW TEATS

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Abstract

Probiotic bacteria have been isolated from various sources like food, animal gut and fermented milk samples in several investigations. Commercially available teat disinfectants are generally chemical-based (iodophor, chlorhexidine) products. The use of these products has occasionally raised concerns about the risk of chemical residues in milk. Autochthonous probiotic is part of the healthy alimentary microbiota, and have been proposed as a potential alternative therapy for the control of bovine mastitis. In the present work, an attempt was made to isolate, screen and identify possible Autochthonous probiotic bacteria from teat samples obtained from Kangayam, Cross breed (Kangayam + Sindhi), Jersey cow breed at diverse locations such as Namakkal, Tiruchirappalli, and Krishnagiri Tamil Nadu India. The results showed that at a pH of 6.5, the isolates classified as DDMT1 and DDMT4 had a percent survival rate of 0.175% and 0.141%, respectively. In 0.5% bile salt conditions, the survival rate of the same isolates was determined to be 0.672% and 0.693% for the isolates DDMT1 and DDMT4, respectively. The Minimum Inhibitory Concentration (MIC) against the indicator organisms revealed DDMT1 and DDMT4 activity against *E. coli*, *Staphylococcus* sp, *Bacillus* sp, and *Klebsiella* sp. The isolates DDMT1 and DDMT4 showed the autoaggregation abilities of 22.80% and 28.53%, respectively. Antibiotic susceptibility testing revealed that the isolates are susceptible to ampicillin and gentamicin. Besides the 16S rRNA gene sequences of the bacterial isolates DDMT1 and DDMT4, phenotypic and genotypic analysis identified and designated DDMT1 as *Clostridium sporogenes* and DDMT4 as *Pediococcus pentosaceus*. Finally, the study reports that in comparison with Cross breed (K+S) and Jersey cow breeds, the population of potential probiotic bacterial strains in the mammary gland may highly isolated from Kangayam cow breed.

Keywords: Probiotics, Cow Teats, autoaggregation, Autochthonous, *Pediococcus*

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FORMULATION AND OPTIMIZATION OF COST EFFECTIVE ALTERNATIVE BACTERIAL CULTURE MEDIA FROM BLACK GRAM AND GREEN GRAM SEEDS

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ABSTRACT

A microbial culture medium is a mixture of substances that promotes and supports the growth and differentiation of microorganisms. Culture media contain nutrients, energy sources, growth-promoting factors, minerals, metals, buffer salts, and gelling agents (for solid media). All microbes have a need for three things: carbon, energy, and electrons. The exorbitant costs of culture media have deprived the use of readymade culture media such as nutrient agar in schools and laboratories with less facility. Generally, legume seeds are found to be a good protein source for nutritional purposes. This study was carried out to find the feasibility of using legume seeds as an alternative nutrient source to grow bacteria. Green gram and black gram were used in this study. The test organisms used were *E. coli*, *Bacillus sp.*, *Klebsiella sp.*, *Staphylococcus sp.* and *Pseudomonas sp.* *Staphylococcus sp.* grows well but slowly (290 – 395 CFU/0.1ml) and generally *Klebsiella sp.* (140 - 280 CFU/0.1 ml) grows least in all the protein formulations tested. All the tested bacteria grow least in green gram. In comparison with the performance on conventional nutrient agar media, the prepared protein formulations were found to be cheap and good alternative culture media for bacteriological studies.

Keywords: Culture media, bacteria, protein formulation, nutrient agar



ISOLATION AND CHARACTERIZATION OF LACTIC ACID BACTERIA FROM GOAN TODDY VINEGAR

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Abstract

Vinegar is one of the most widely used ingredients in foods. It not only acts as a preservative but is also known to enhance the flavour and aroma of food. Acetic acid bacteria (AAB) are the dominant group of bacteria in vinegar due to its acidic pH. Few Lactic acid bacteria (LAB) are known to survive in locally produced vinegars as they are comparatively less acidic than synthetic vinegars. LAB are being extensively studied for their role in food, industrial, clinical and agricultural sectors. They are known for their health promoting abilities and as chief bio-preservative agents due to their antagonistic effects. The study aims at isolating and investigating the characteristics of LAB from Goan toddy vinegar and assessing their industrial potential. Toddy vinegar is commonly prepared all over the state by fermenting coconut sap (toddy). Samples collected, were analysed for pH and titratable acidity. LAB were isolated using cultural method. The isolates obtained were found to be gram positive, catalase negative, non-motile, non-sporing, cocci and rod-shaped organisms. They belonged to the genera *Streptococcus*, *Pediococcus* and *Enterococcus*. All the isolates produced organic acids with varying concentrations while some showed protease activity suggesting their applications in industry.



Screening and isolation of pectinolytic fungi isolated from field-grown plants

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ABSTRACT

The present study reports screening and isolation of pectinolytic fungi isolated from field-grown plants. Collected plant part fragments were plated on PDA medium plate and Percentage colonization rate was calculated. Based on macroscopic and microscopic characteristics, all endophytic fungal isolates were identified using standard taxonomical keys and monographs. All isolates were screened for presence of effective pectinolytic fungi using pectin agar plate assay. A total of 24 endophytic fungi were isolated from 75 plant fragments with colonization rate of 32.0%. Ten endophytic fungi with significant characteristics considered for pectinase screening were identified as *Aspergillus* sp.1, *Penicillium* sp., *Aspergillus* sp.2, *Pestalotiopsis* sp., *Trichoderma* sp., *Phomopsis* sp., *Fusarium* sp.1, *Colletotrichum* sp., *Fusarium* sp.2, and *Phoma* sp. Among all endophytic fungal isolates, maximum pectinase activity was exhibited by three fungi namely, *Aspergillus* sp.1, *Penicillium* sp. and *Fusarium* sp.2 whereas four fungi were found to have moderate pectinase activity. The total percentage of pectinase positive fungi was 70%. The formation of clear zone indicated pectinase activity, which was due to degradation of pectin to its monosaccharides. The screening and identifying potential sources of fungal endophytes and their active enzymes are showing great success in the field of biotechnology.

Keywords: Endophytic fungi, colonization, pectinase, pectinolysis.



ROLE OF PROBIOTICS IN OBESITY CONTROL

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Obesity is a common medical disorder marked by an excessive accumulation of fat in the adipose tissues which is known to contribute to the etiology of Type 2 diabetes, cardiovascular diseases, hyperlipidemia, atherosclerosis, and hypertension and various cancer types. Fermented foods have health benefits because of the probiotic bacteria present and the bioactive compounds produced during fermentation. Fermented foods have drawn a lot of interest in relation to obesity due to their ability to transfer living bacteria with specialised enzymatic activity as well as fermentation metabolites that may help to health promotion or illness prevention. Some bacteria increase the availability of nutrients while enhancing the flavour and texture of the original food. The benefits of eating fermented foods and potential probiotic ingestion are discussed in this review. Various species of bacteria in the gut microbiome may affect weight gain will help us to find the probiotic, prebiotic, and symbiotic for long-term weight control.

Keywords: Gut microbiome, Fermented foods, Bioactive compounds, Anti-obesity.



ENUMERATION OF MICROORGANISMS FOR STANDARD INOCULUM SIZE USING DENSITY EQUIVALENTS IN MCFARLAND UNITS, OPTICAL DENSITY AND DIRECT CELL COUNT

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ABSTRACT

Uniform cell count and number in inoculum preparation is always required, as industrial pre-inoculum to get quality products, research to get the consistent and reproducible results and testing the sensitivity and resistance of any chemical compound. The optical density (OD) measurement is generally used for determining the optimum inoculum size and might be an indirect measurement for cell count. However, this method is subjective, and the results may vary depending on various factors such as size, morphology and pigmentation etc. In the present study a correlation among the most commonly used methods i.e. spectrophotometric absorbance, direct cell count using a hemocytometer along with McFarland unit (MFU) and colony forming unit (CFU) was established. Commonly used industrial microorganisms *Pichia fermentans* and *Saccharomyces cerevisiae* was used for this study. Both the yeasts showed almost similar growth pattern, while *Pichia fermentans* grew faster under the experimental conditions. *Pichia fermentans* showed higher cell count ($1 \times 10^5/\text{ml}$) in 2 Hrs, while *Saccharomyces cerevisiae* showed a lower cell count of $7 \times 10^4/\text{ml}$ in 2 Hrs; and showed almost similar OD₆₀₀ 0.200 and 1 MFU. Thus, the results confirmed that each microorganism must be confirmed for its OD, MFU and cell count instead of using a theoretical predetermined value.

Keywords: *Saccharomyces cerevisiae*, McFarland unit, optical density



Designing and Optimization of Microbial Fuel Cell

Neha Tarun Kuity

ABSTRACT

A composite electrode was constructed and tested in a Microbial Fuel Cell setup. This configuration consisted of a composite electrode consisting of three parts: an approximately 10mm solid aluminium rod as the base, an electro-polymerized layer of ECG conducting gel, and an electro-polymerized layer of methylene blue.

The composite electrode with immobilized bacteria was tested in a bioanode setup. The cathode chamber of the cell contained sea water along with a graphite electrode. The maximum power density generated by the composite electrode in the presence of mediator was 26.2 Kw/m². This electrode configuration produced approximately 69% more power density and 53% more voltage density than control configurations of electrodes.

To identify the oxidation and reduction potentials of novel media, cyclic voltammetry test was performed and the potential at which peak occurs (E_p) and height of the peak (I_p) was found to be 0.216 V and -4.399 e-5A for segment 1 reduction and 0.130 V and 4.142 e-5A for segment 2 oxidation respectively; indicating that the novel media designed was efficiently able to transfer electrons to the surface of electrode.

Electrochemical Impedance Spectroscopy analysis determined that a significant portion of the MFCs resistance to charge transfer occurred at the surface of the anode and this resistance was significantly lowered when the distance between the reference electrode and working electrode was reduced (51% lower). EIS analysis showed that the resistance was higher and a significant portion of the ohmic resistance was contributed by the membrane.

Keywords: Microbial Fuel Cell (MFC); electrode configuration; oxidation – reduction potentials; sustainability; consortia; charge transfer; mediator; ohmic resistance



ISOLATION AND SCREENING OF AGRO-INDUSTRIALLY IMPORTANT BACTERIA FROM GOC

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ABSTRACT

Groundnut occupies an important position in the economy of developing nations. Gujarat is the leading producer of groundnut in India. Groundnut oil cake is a by-product obtained after extraction of oil from Groundnut. The GOC is rich in proteins, carbohydrates, crude fibre, crude lipid, nitrogen, phosphorus, potassium and other minerals. It is also good source of microorganisms. The waste is easily available and can be used directly for production of industrially important enzymes like amylase, protease, gelatinase and catalase. Other value-added products from GOC includes as biofertilizer and for biosurfactant producers, are studied in this work.

In present study industrially important enzymes can be produced in eco-friendly and cheaper ways, so as to convert such Waste into Wealth. Out of 30 isolates, 40% isolates are potential amylase producers, 40% isolates produced protease which are used in fabric upgrading and pharmaceutical industry. 47% isolates produced catalase which are used in food preservatives. All 100% isolates produced gelatinase which are used in pharmaceuticals and food industries. 50% isolates are nitrogen fixers, 74% isolates are Biosurfactant producers. Studies are under progress for siderophore production, phosphate solubiliser and estimation of produced biosurfactant.

Keywords: Groundnut oil cake (GOC), Enzymes, Nitrogen fixers and Biosurfactant producers.



USE OF VIOLET PIGMENT AS BIO-INK OBTAINED FROM *Chromobacterium violaceum* K2PVR22 ISOLATED FROM WATERFALL SOIL

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Abstract

The use of natural inks has declined with the discovery of synthetic ink. But the tremendous development in synthetic ink production and its prolonged usage has increased the problems of its disposal and remediation. Due to hazardous and carcinogenic properties of synthetic inks like Victoria blue, alternative eco-friendly natural ink from sources like Tsuyu kusa flower were used. As these inks are water soluble, they are not suitable to be used as permanent ink. Therefore, to combat the problems associated with the above sources for ink production a suitable option is use of bacterial pigments which are environment friendly and sustainable. The present study demonstrates optimization of violet pigment production from *Chromobacterium violaceum* K2PVR isolated from waterfall soil sample obtained from Kankavli, District Sindhudurg, Maharashtra. The highest and economical pigment production was observed in solid substrate sterile wheat. It was extracted using Dimethyl-sulfoxide and its partial analysis was carried out using UV-Vis spectrophotometry and FTIR. The pigment was found to be biodegradable, thermostable and water immiscible. The results have shown that the pigment has great potential to be used as bio-ink.



PRODUCTION OF LACCASE ENZYME AND MEDIA OPTIMIZATION USING WASTE AGRICULTURAL BIOMASS BY *Trichoderma harzianum*

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Abstract

Laccases are enzymes belonging to the group of oxidases. Laccases catalyze the oxidation of a variety of phenolic compounds, diamines and aromatic amines. Laccases are widely present in nature and are considered to be the oldest and most studied enzymatic systems. Laccase is an extracellular, multicopper enzyme that uses molecular oxygen to oxidised various aromatic and non-aromatic compounds by a radical catalysed reaction mechanism. This enzyme is found in many plant species and is widely distributed in fungi, including wood rooting fungi. In recent years researchers have discovered that laccase can be produced from fungus like ascomycetes, basidiomycetes and deuteromycetes. In the present study *Trichoderma harzianum* was obtained from MTCC Chandigarh and was tested for producing laccase enzyme on a agriculturally waste biomass of corn cob. Guaiacol was used to detect and screening laccase activity, in which a reddish brown color developed due to oxidation of guaiacol by laccases was used to measure enzyme activity spectrophotometrically at 470nm. Laccase activity was estimated by using reagent and chemical like syring aldazine, guaiacol, RBB-R and ABTS. It was observed that *Trichoderma harzianum* was able to exhibit significant laccase production and activity on corn cob as a substrate and showed optimum enzyme activity at temperature 45°C (0.14U/L), the optimum P^H at which *Trichoderma harzianum* was able to produce and exhibit enzyme activity was at PH 5.5.(0.14U/L). The optimum reaction time of the extracted laccase was at 10 minutes (0.14U/L). In a separate study it was noted that the metal ion mainly copper ion play important role in production of laccase.

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“HERBAL EXTRACT MEDIATED GREEN SYNTHESIS OF SILVER NANOPARTICLES”

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Abstract

Green synthesis of silver nanoparticles (AgNPs) has gained much interest in recent times. India is rich in medicinal flora which can be used as cost-effective non-hazardous reducing compounds in preparing AgNPs. This study aimed to investigate an efficient and sustainable route of AgNP preparation using 0.01 M aqueous silver nitrate and herbal extract of *Ocimum sanctum*. AgNPs were prepared by reacting 5 ml each of 0.01 M silver nitrate and *Ocimum sanctum* extract. The AgNPs were characterised using UV-visible spectrophotometry and tested for antibacterial activity and toxicity. Maximum AgNP production was observed in equal volume of leaf extract and AgNO₃. The zones of inhibition of leaf extract, AgNO₃ and AgNPs obtained against *Staphylococcus aureus* were 5mm, 9mm, and 15mm, respectively. Green gram seeds treated with AgNP solutions exhibited maximum sprout length (1.3-1.7cm). Owing to their antimicrobial action, the AgNPs produced using herbal extract can be used for remedial purposes. Their ability to aid plant germination and growth can be used in agriculture.

Keywords: Herbal, Green synthesis, Silver Nanoparticles.



Applications of Exopolysaccharides

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Abstract

Microbial exopolysaccharide is mainly defined as molecular compounds or substances that are secreted by a microorganism in its surrounding environment. In current scenario the industries mainly uses plant based or animal based polysaccharides which are causing harm to our environment and also it is expensive. So in order to replace it by cheap and easy sources we can use exopolysaccharides produced by micro organisms. Microbial derived exopolysaccharides are considered as either good substitute of other synthetic or natural polymers or novel biopolymers which are used in food and other industries for thickening, suspending and gelling function. Some approaches are made where it is very evident that micro organisms grows on a very cheap medium and also by extracting it and purifying it ,number of applications are found in industrial background such as gellans, dextrans ,emulsion, sialic acid, Levan, Pullulan, xanthan , starch, glycogen, cellulose, etc . These microbial exopolysaccharides are mainly used in food industry, cosmetic industries, pharmaceuticals industry, dairy industry, biomedical industry.Considering the extensive function of microbial exopolysaccharides and their importance, the function and application of microbial exopolysaccharides are discussed in this review.

Keywords- *Polysaccharides, industry, microbial exopolysaccharides*



SPIRULINA FORTIFIED CHOCOLATES: A GOOD NUTRITIONAL OPTION FOR CHOCOLATES LOVING PEOPLES

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Abstract

Arthrospira platensis is used as dietary supplements or whole food. Due to its nutritional composition, specially protein high composition, they considered as a sustainable protein source for food .The main aim of this project was to evaluate the Arthrospira platensis which is known for greater protein and amino source. Spirulina is blue green algae, which is a freshwater plant. It is one of the most researched plants in recent times. Renowed for it's intense flavor, spirulina is gaining popularity as a nutritional supplement for it's powerful nutrition profile. It is loaded with many beneficial nutrients and antioxidants that can promote overall health if included as a part of the diet, but many peoples avoid it's consumption because of it's bitter taste and fishy odour. So to solve this complexity we have created a unique formulation of spirulina chocolate by mixing spirulina to chocolate so with unique formulation we can deliver a better taste and all of it's nutritional benefits simultaneously. The chocolates were assessed for organoleptic properties. This significant study revealed the efficacy of spirulina chocolate formulation and it would definitely have wide scope in the future as a immunity booster . From our finding we get positive results for the chocolates having different amount of spirulina powder .This formulation can be considered as safe for consumption without any risk of systemic side effects.

KEY WORDS : *Spirulina protein , Chocolate , Arthrospira platensis , Amino acid*



BIOREMEDIATION OF PAHS: ISOLATION, IDENTIFICATION AND SCREENING OF MICROORGANISMS FROM OIL CONTAMINATED SOIL, DURG.C.G.

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ABSTRACT

PAHs (Polycyclic aromatic Hydrocarbons are globally major source of pollutants and have mutagenic, carcinogenic properties. Environment is polluted by oil and contaminated in various ways such as soil, water and air contamination. For bioremediation process suitable indigenous oil degrading bacterial & fungal strains can be used. My work indicates that in nature, environment has the ability to under grow, attenuation and clean-up of PHA'S in soil along with time. PAH'S degrading microorganisms present in oil contaminated soil are source for bioremediation process and have the potency to degrade PAH's and can be exploited, for oil spill clean-up in similar environments. In the present study, from oil contaminated site of Durg-Bhilai, we isolated bacteria and fungi, identified and screened for their degradation capability. Genomic DNA was isolated from selected isolates, were analyzed on 1% agarose gel electrophoresis, Based on 18SrRNA gene sequencing the isolates were identified with **Seq-Scape Program** and identified. All the selected screened strains isolated from the soil are capable of consuming oil and can be used in hydrocarbon bioremediation activity for PAH's degradation at our regime. Work done will be presented for results and discussion.



“TO STUDY THE EFFECT OF DIFFERENT PARAMETERS ON BIOGAS PRODUCTION”

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ABSTRACT

Biogas is an eco-friendly fuel produced by anaerobic digestion, that comprises of chiefly methane (55-65 %), CO₂, H₂S and traces of water vapour. Globally, biogas is used as a major source of energy for household consumption from ancient times. The work focuses on production of biogas from various organic kitchen wastes and it emphasizes on factors affecting it. Generally, it takes around 60 days for a newly made biogas plant to start the production of biogas, but in present work it was achieved in short period of 25-30 days. The effect of parameters namely substrate type, substrate concentration, substrate size, pH and temperature on biogas production was studied. It was found that the substrates such as spoiled flour, whey, crushed vegetables, cow dung gives a good yield of biogas. The biogas production was optimum at pH 6.8-7.2, at substrate concentration (1:1). The above stated findings were observed using a small prototype biogas plant.

Keywords:-*Anaerobic, Biogas, organic kitchen waste, Eco-friendly fuel, Methane, households.*



WASTEWATER EFFLUENT OF TEXTILE INDUSTRY: A SOURCE OF SYNTHETIC AZO DYE DECOLORIZATION BACTERIA

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Abstract

Global textile market size has been valued around 1000 USD in 2021 and is anticipated to grow at a compound annual growth rate of 4% from 2022 to 2030. China being the largest producer followed by India in the second position; the textile industry sector occupies the second largest in terms of employability in Indian scenario. These industries make enormous use of various dyes especially azo dyes for colouring fabrics. But release of these azo dyes in surrounding water body from textile industry without any appropriate treatment leads to major environmental contamination affecting human health. The purpose of the present study was to characterize some dye decolorizing/ degrading bacteria isolated from local textile industry effluents. Thirty-three different bacterial strains were isolated and primarily screened for their ability to decolorize the dyes as observed by halo zones on agar plates. Two of the isolates showed maximum degradation property which were chosen for detailed studies. The two potent isolates (HIR211 and Msfl2) were able to decolorize the dyes used effectively. Distortion of cellular morphology and variation of the growth pattern in presence of the dyes was observed. Ultraviolet-visible (UV-Vis) spectroscopy technique and thin layer chromatography (TLC) technique were used to characterize the probable by-products of bacterial dye degradation. The homology and phylogenetic analysis of nucleotides from 16S rDNA data shows that Msfl2 isolate belongs to the genera *Brevibacillus brevis* strain M12 LS01 and HIR211 isolate belongs to the genera *Bacillus pumilus* strain B6.

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BIOREMEDIATION OF ACID RED 2 BY *BREVIBACILLUS* SP. ISOLATED FROM DYE CONTAMINATED SOIL.**Sneha Jaiswal****Department of Microbiology, Dhote Bandhu Science College, Gondia, M.S., India***Correspondence: Sneha Jaiswal, e-mail- snehajaiswal1987@gmail.com**Abstract**

With the increased demand for textile products, the textile industry and its wastewaters have been increasing proportionally, making it one of the main sources of severe pollution problems. Bioremediation of dyes has emerged as a promising technology in the past few years for the treatment of industrial dye effluents and contaminated soil. In the present study, the decolorization potential of Acid red 2 which is an azo dye by the *Brevibacillus* sp. isolated from dye contaminated soil of the local dying houses in Nagpur-India was determined. Decolorization rate was monitored by spectrophotometrical analysis. Different parameters such as pH, time and temperature were optimized for the present study. It was found that *Brevibacillus* sp. decolorized 97.82% of methyl red (100mg/L) at pH 8 at 37⁰C within 48 hours under shaking condition. Therefore, it can be concluded that the *Bacillus* sp. can be of good potential use for the treatment of azo dye-containing wastewater based on its ability to remove colour.

Keywords: *Bioremediation, Decolorization, Acid red 2, azo dye, Spectrophotometry, Brevibacillus sp.***ECO-FRIENDLY SOLUTION FOR THE REMOVAL OF HEAVY METALS FROM WASTE WATER****Aparna Gunjal****Department of Microbiology, Dr. D. Y. Patil, Arts, Commerce and Science College, Pimpri, Pune, Maharashtra, India**E-mail: aparnadyp@gmail.com**Abstract**

The waste water contains many heavy metals such zinc, cadmium, lead, nickel, arsenic, etc. These heavy metals cause hazardous effects on the human health as well they enter the soil and water and cause water or soil pollution. The chemical methods are available for the removal of heavy metals, but they have limitations. The chemical methods are costly and cause pollution. The alternate to chemical methods is the biological approach. The use of microorganisms viz., bacteria, fungi, algae, actinobacteria, yeasts, etc. is very eco-friendly and economical, called as biosorption. The functional groups present on the cell surface can be responsible for the uptake of heavy metals by the microorganisms. Still the exact mechanism behind this is not yet clear. The biosorption technology on a large scale will be easy, fast, and economical and thus help in the treatment of waste waters.

Keywords: *Biosorption, Economical, Eco-friendly, Pollution, Waste water*



Biodecolorization of textile Reactive Red M8B dye by *Aspergillus species* isolated from soil

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ABSTRACT

The textile and dyeing industry are one of the industries, which contribute to the soil and water pollution. In the current research work the potential of the isolated Ascomycete, *Aspergillus* species for the removal of Reactive Red M8B dye was studied. The isolated Ascomycete, *Aspergillus* species was identified using microscopic analysis and cultural characteristics and found to decolorize and degrade textile dye Reactive Red M8B. This azo dye was decolorized and degraded completely by *Aspergillus* species in both shaking and static conditions in 1% glucose medium at pH 2-3 range. The biodegradation was monitored by UV- Vis spectroscopy and GCMS analysis and Octadecenoic Acid, methyl ester- (E) is the degradation product elected by GC-MS (Gas Chromatography-Mass Spectroscopy) analysis.

Keywords: Reactive Red M8B dye, *Aspergillus* species, biodegradation, azo dye, GCMS.

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SCREENING OF GUT MICROBIAL FLORA OF *PENAEUS VANNAMEI* SHRIMPS.

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ABSTRACT

The most significant aquaculture crustacean species is the Pacific white shrimp, *Litopenaeus vannamei*, also known as *Penaeus vannamei* which accounts for 70 - 80% of global shrimp production. Rapid growth, large stocking densities, a low requirement for protein in the diet, and tolerance for a wide variety of salinities are all characteristics of *Penaeus vannamei*. The majority of the functions of the animal gut, including those related to immunity, growth, health regulation, and food absorption, are carried out by bacterial metabolism in the gut. The performance and output of *Penaeus vannamei* in aquaculture can be improved by better understanding the function of the gut microbiota of this fish.

The predominant bacterial group in the intestine of *Penaeus vannamei* is proteobacteria, however other bacterial phyla can potentially be advantageous to shrimp health and development. Depending on the shrimp's growth stage, nutrition, environment, and other circumstances, the amount of opportunistic pathogenic bacteria in the intestine can alter.

The current study is concentrating on microbial-based treatments to enhance shrimp health. 15 samples of marine water, 10 samples from an aquaculture water tank and 20 shrimp samples were collected. A total of 58 microorganisms were isolated from the samples and were enriched and subjected to isolation on selective media. Initially, it was established that 22 isolates were Gram positive and 36 were Gram negative based on Gram staining. To assess possible sensitivity and pathogenicity patterns for shrimp health, all isolates underwent antibiotic sensitivity testing (AST) and hemolytic activity screening. The pathogenicity of the bacteria isolated from marine and aquaculture water samples were 5%, 27%, and 68%, while bacteria isolated from shrimp guts were 23%, 8%, and 69% of α , β and γ respectively. We tested the pH, salt, and bile tolerance of 58 marine and shrimp gut strains. Only 16 strains demonstrated any discernible resistance to the high pH, salt, and bile concentrations.

Key word: Shrimp, Aquaculture, Bio-friendly agents, AST, pH, Salt and Bile tolerance.

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AEROMYCOLOGICAL SURVEY OF FUNGAL BIODIVERSITY AND INVESTIGATION OF BIODEGRADABILITY AND ENZYMATIC ACTIVITY OF FUNGI FROM KORADI, NAGPUR REGION.

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Fungi are ubiquitous and along with bacteria they are important decomposers and disease-causing organisms of both plants and animals. Present work focuses on study of biodiversity of fungi from Nagpur region which was carried out at indoor stadium, outdoor stadium & Gym of Koradi area Dist. Nagpur. Hi-Media air sampler was used for aeromycological survey.

Pure culture of fungi were isolated and identification of fungi was done with the help of taxonomic literatures. Ascomycota was predominant group found followed by Zygomycota but Basidiomycota didn't appear. *Aspergillus flavus* and *Aspergillus niger* were found to be of high incidence. Biodegrading ability of fungi was also studied by weight loss method. Enzymatic activity of fungi were studied especially Amylolytic activity, Cellulolytic activity & Proteolytic activity. Two type of enzyme assays were conducted to determine cellulase activity i.e., endoglucanase & exoglucanase activity. Meteorological parameters like temperature, relative humidity & rainfall were also recorded on each sampling date as these parameters have intense effect on air borne fungal species both qualitatively and quantitatively.

Keywords: Aeromycology, Fungal diversity, biodegradability & Enzymatic Activity.

USE OF *Photobacterium leiognathi* PR2KSJ1 ISOLATED FROM *Harpadon nehereus* TO DETECT HEAVY METAL POLLUTION IN WATER BODIES.

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Abstract

Symbiotic bioluminescent bacteria native to marine environment can be used as bioindicators for detection and comparative quantification of toxic compounds present in water bodies. In the present work the symbiotic bioluminescent bacterium *Photobacterium leiognathi* PR2KSJ1 was isolated from *Harpadon nehereus* (Bombay duck). The organism showed maximum bioluminescence in modified Minimal Salt Medium (MSM) containing 2% Peptone, 0.5% Yeast extract, 3% NaCl and 0.3% Glycerol. The organism was also subjected to low cost media i.e. fish waste extract, whey and fruit waste extract. These low cost media were optimized to suitable parameters which included salt concentration and pH. The optimized medium (modified MSM) was used for carrying out heavy metal detection. The extent of bioluminescence exhibited by the isolates was measured in presence of heavy metals salts using LDR sensor module and this knowledge was applied to detect presence of toxic heavy metal ions in polluted water samples from Mithi river and Dahisar river.

Keywords- Bioluminescence, *Photobacterium leiognathi*, Bombay duck, LDR Sensor module, Mithi river.



AN EFFICIENT STRATEGY FOR THE TREATMENT OF TEXTILE DYES AND REAL TEXTILE EFFLUENT BY USING MIXED CONSORTIUM AND SUBSEQUENT TOXICOLOGICAL ASSESSMENT

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Abstract

A variety of dyes can be found in a textile industry effluent, many of which are recalcitrant and resistant to biodegradation. A novel consortium plant (*Fimbristylis dichotoma*) and Baker's yeast (*Saccharomyces cerevisiae*) is used to decolourize a textile azo dye Rubine GFL and real textile effluent. It shows boost in decolourisation as compared to the individual plant and to yeast with fabulous rate of efficiency of decolourisation of 92% for Rubine GFL and 68% for real textile effluent. Amended decolorization of Rubine GFL and real textile effluent was seen due to the snowballing/collective effect of various oxidative as well as reductive enzymes of FD-SC consortium. Boosted biodegradation of Rubine GFL by the FD-SC consortium was observed in the spectroscopic analysis than of plant and yeast individually could perform. Step by step observation of biodegradation of dye was confirmed with the help of HPLC, FTIR and GC-MS techniques. Toxicity assessment of the metabolites formed after degradation of dye was performed with the help of effect of metabolites on the germination of seeds in compare with actual dye solution and % germination was calculated followed by fish toxicity assessment. Gradual decolourization of the dye was observed in the sections of root cortex of *Fimbristylis dichotoma*. Along with significant reduction in BOD, COD, ADMI, TSS, TDS and pH values and positive growing effect on plantlets was observed with normal structure restoration in fish gills.

Keywords: Biodegradation, FD-SC consortium, Fish toxicity, Metabolite's profiling.

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DISTRIBUTION OF LEECH FAUNAL DIVERSITY IN FRESHWATER WETLANDS AND TERRESTRIAL ECOSYSTEM OF SEMADOH REGION

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Abstract

Leeches (Hirudinea) constitute a relatively small monophyletic group of highly specialized annelids and play important roles as invertebrate predators in freshwater, while others are infamous for their ectoparasitic bloodsucking. They are globally distributed on all continents with one-half of all continental species, known for their local endemism. Leeches are hermaphroditic annelids with totally reduced chetae and parapodia which are dominant in other classes of Phylum. Leeches has unpaired male and female genital pores in the region of clitellum which is glandular region in the body of leech. Leech has anterior and posterior sucker from which the anterior sucker is used for attachment and useful in blood sucking while the posterior sucker is only for the attachment to host body. The body of leech is annulated in appearance, each annulus or somite is superficially divided into usually three to five sub annuli or segments sometimes these annuli may reach to ten in number. Most of the leeches are sanguivorous on vertebrates or invertebrates others are predatory mainly and very few are scavengers in their mode of feeding. Following species collected from Semadoh region of Melghat. *Herpobdelloidea lateroculata*, *Hirudo*(*Asiaticobdella*) *Birmanica*, *Poecilobdella manillensis*, *Poecilobdella granulosa*, *Poecilobdella viridis*, *Placobdella emydae*. It has been seen that due to vegetation and temperature, number of wetland leech species and population density of them varies.

Keyword: *Leeches, Diversity, Species, Distribution*



LOW COST AND EFFICIENT DESIGNING OF WATER PURIFICATION FILTER FROM LOCALLY PRODUCED AGRICULTURAL WASTE.

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Abstract

Cotton (*Gossypium hirsutum*) and Tuwar(*Cajanas cajan*) are cultivated as main economical crops in Wardha district. Nearly 150,000 hector area land is under cultivation of these crops which is 65 percent of all the crops. But one of the major drawback after harvesting of these crops is wastegeneration. Disposal of cotton and tuwar waste is major problem for farmers as it can't be use as fodder and not generate any significant revenue. Similarly, good quality drinking water is another issue in Wardha region. The present study focuses to solve both problems with effective solution. Using simple techniques, waste can be converted into valuable by products i.e. charcoal. Charcoalbased filters can use for water purification, to improve microbial quality of water and have ability to remove excess chlorine and some metals from water. The microbiological quality of water was analyzed by MPN method. This method of filtration is recognized by the Water Quality Association as an acceptable method to maintain certain drinking water contaminants within the limits as per the Environmental Protection Agency, National Drinking Water Standards. The filter can be scale up to industrial level.

Key words: *Economical crop, Agriculture waste, Charcoal, Drinking Water*



SCREENING OF POTENTIAL PROBIOTIC LACTIC ACID BACTERIA AND ITS APPLICATION ON SKIN HEALTH

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ABSTRACT

Probiotic microorganisms have the potential to influence the many aspects of human physiology acted by indigenous microbes, including the alimentary canal, skin and vagina. Probiotic bacteriotherapy can have great potential in preventing and treating the skin diseases including eczema, atopic dermatitis, acne, and allergic inflammation as a cosmetic product. In addition, supplementation with probiotics has shown promising results against various enteric pathogens due to their unique ability to compete with pathogenic microbiota for adhesion sites, nutrient competition and antioxidant activity, to stimulate, modulate and regulate the host's immune response. Probiotics as a single strain or as consortium claimed to have range of beneficial effects on human organism and have been widely marketed and consumed, mostly as dietary supplements or functional foods. Novel internal and topical interventions, ranging from probiotics/prebiotics, dietary factors to topical application products which influence microbiota, are now worthy of vigorous research. The aim of the present study is to screen the potential probiotic lactic acid bacteria and check its effect on skin health.

Keywords: *Probiotics, Lactic Acid Bacteria, Skin health, P. acne.*

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IDENTIFICATION OF MAJOR MYCOFLORA OF SCALP: A KEY FOR FUTURE CONTROL

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Abstract

Fungal species (Mycoflora) are found in normal human skin flora and sometimes associated with different dermatological pathologies. In a study, the scalp scales of 103 infected and healthy persons in Latur (Maharashtra) region were observed to contain predominantly species of fungi like *Malassezia*, *Aspergillus*, *Trichophyton*, and *Microsporum*. The percentage of these identified species in the scalp was - *Malassezia* sps. (56.31%), *Aspergillus* sps. (20.38%), *Trichophyton* sps. (3.88%), *Microsporum* sps. (2.91%) and rest was other forms of fragmented fungi. Among the scalp fungal flora, the species of *Malassezia* and *Aspergillus* are considered to be emergent opportunistic pathogens having great importance. Several classical and modern techniques have been employed by workers to identify different species from clinical samples and to evolve control mechanism. The objective of the present study was to isolate these different scalp infecting organisms and to study the morphological and physiological features, supplemented with biochemical and molecular characterization. The study has established novel ways to make simultaneous identification of different fungal species in culture. Seven different fungal genera and eighteen different species were distinctly identified in the samples. However, two species of two genera could not be ascertained. No growth was observed in 13 samples (12.62%). Interesting observations were also recorded like; *Malassezia* was not the major constituent of the heavily infected scalp (Dandruff), although *Malassezia furfur* was found in 22 samples. *Microsporum canis* and *Candida albicans*, two such species which normally found on body skin infections were found in the cultural identification of current scalp samples. As a part of confirming taxonomic identity of *Malassezia* species because of its precarious nature, a sample of identified *Malassezia furfur* (as per the above laboratory studies) was further confirmed based on its molecular rRNA gene polymorphism (5.8S). These coordinated identification methods envisaged in this piece of research certainly opened the new possibilities to study genuine mycoflora and make control over scalp infection.

Keywords: Mycoflora, dandruff, dermatology, scalp infecting fung

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ANTIBACTERIAL, PROLIFERATIVE AND CYTOTOXIC STUDIES OF CONSORTIUM OF PLANT EXTRACTS AGAINST BURN WOUND SEPSIS CAUSING ORGANISMS

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ABSTRACT

Burns disrupt the protective barrier of skin and opens the portal for entry of microbes which leads to sepsis in the wound. Microbial invasion and drug resistance necessitates the adoption of traditional medicinal plants as they have enormous potential to treat bacterial infections. The present study focuses on consortial extraction of different plants Ashwagandha (roots) Apamarga (Shoot) Acalypha (leaves), Ashwagandha (roots) Tulsi (leaves) Pot Marigold (flowers) and Apamarga (Shoot) Beetle (Leaves) Lavang Pipal (bark) using Water and alcohol as solvent. Three different consortia were prepared and evaluated for its antibacterial potential, cytotoxicity profile and proliferation activity on 3T3 Cell line. Antibacterial activity was assessed at the concentration range of 1% to 5% by the Agar ditch method against standard strains, resistant and sensitive isolates obtained from septic burn wounds. Results of antibacterial assay showed that prepared combinations have significant antibacterial activity. Further, Plate dilution method was carried out to determine Minimum Inhibitory Concentration, experimental data from MIC results showed that the Polyherbal recipes were effective at a range of 1-2 % i.e., 10-20 mg/ml. Variable concentrations of Polyherbal extracts were also evaluated for *in vitro* cytotoxicity and Proliferative effects by MTT assay using Murine 3T3 fibroblast cell lines. The results of Cytotoxicity and cell proliferation assays indicated non-toxic and proliferative nature of these extracts at higher concentration. Fibroblast proliferation was significantly promoted under the influence of aqueous extracts at the concentration of 0.0625 µg/ml. In conclusion, both Aqueous and alcoholic polyherbal extracts exhibited promising antibacterial and proliferative activity and are non-toxic to cells which signifies the potential of the consortia for development of topical formulation using suitable base for its use in control of burn wound infections

Keywords: *Burn wound infections, Antimicrobial resistance, Polyherbal extracts, Antibacterial activity, minimum Inhibitory Concentration, cytotoxicity studies, Non-toxic*



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ANTIBACTERIAL POTENTIAL OF ENDOLICHENIC ACTINOBACTERIA
FROM *ROCCELLA MONTAGNEI*, TAMIL NADU, INDIAVishnu Raja Vijayakumar*¹ and Dhanasekaran Dharumadurai²¹Research Scholar, Department of Microbiology, Bharathidasan University, Tiruchirappalli – 620 024 and²Associate Professor, Department of Microbiology, Bharathidasan University,
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Abstract

Lichens are a complex living form that is the result of a symbiotic relationship between two different organisms, a fungus and an alga symbiotic relationship, which provide specific habitats for diverse bacterial communities, including actinobacteria. However, there are very few reports on lichen associated actinobacteria and their antimicrobial compounds. In the present study, lichens samples were collected from various locations of Tamil Nadu, India. *Roccella montagnei* were surface sterilized, serially diluted and inoculated in the starch casein agar (SCA) enriched with lichen extract (10%) plates, sub cultured and purified. A total of 123 actinobacterial colonies were obtained from 4 lichen samples, which were grown in different substrate including tree bark and rock. Among 123 actinobacterial colonies, 17 culturally distinct isolates were purified and screened for antimicrobial activity. Two isolates showed broad spectrum antimicrobial activity, hence 2 isolates were chosen for culturally, morphologically, physiologically, biochemically and phylogenetically properties and identified as *Streptomyces* sp., MC26 and *Nocardiopsis flavescens* Y32. The antibacterial activity of compound extracted from *Streptomyces* sp., MC26 and *Nocardiopsis flavescens* Y32 showed inhibitory activity against the *Escherichia coli* and *Pseudomonas aeruginosa* pathogens. The antibacterial compound was characterized by FT-IR, GCMS and NMR. From the FT-IR analysis, we were concluded that the functional groups such as aromatics, alkane, aryl disulphides, ether and ethylene were identified from *Streptomyces* sp -MC26 and *Nocardiopsis flavescens* – Y32. Antimicrobial compound identified by GC-MS analysis were Phenol, 2,4-bis(1,1-dimethylethyl) from *Streptomyces* sp -MC26 and Lupeol from *Nocardiopsis flavescens* – Y32. Phenol, 2,4-bis(1,1-dimethylethyl) were a natural compound has some various activities such as antioxidant, anticancer, antifungal, antibacterial, allelopathic effect and prevent browning of apple (Jianguo et.al., 2018). Lupeol were has an anti-inflammatory activity and anticancer activity (Mohammed et.al., 2009). The lichen associated actinobacteria are important in symbiosis and also source for several antimicrobial compounds.

Keywords: Lichens, Starch Casein Agar (SCA), FTIR, GCMS

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CARBAPENEM-RESISTANT *ACINETOBACTER BAUMANNII* CARRYING MULTIDRUG RESISTANT PLASMID CAUSING NOSOCOMIAL INFECTION

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Abstract

Emergence and spread of *Acinetobacter* species, resistant to most of the available antimicrobial agents, is an area of great concern. It is now being frequently associated with nosocomial infections. The *Acinetobacter baumannii* isolated from the clinical samples of patients from Nagpur city and the resistant pattern of multiple antibiotics was studied. *A. baumannii* was confirmed by 16s rRNA sequencing and found to contain plasmid. The MDR plasmid carries resistance as well as virulent genes and hence is responsible for pathogenicity. An opportunistic organism *A. baumannii* found to be infecting the majority of the hospitalized patients which are immune compromised causing nosocomial infection in the hospital units. Identified Carbapenem-resistant *A. baumannii* found to be highly resistant to 3rd and 4th generation drugs like Rifampicin, Ciprofloxacin, Ceftazidime, Sulphafurazole, Cefotaxime, Cefoperazone, Doxycycline-HCl, Nalidixic acid, Amikacin, Tetracycline, Piperacillin, Ticarcillin and Nitrofurantoin. The study also reveals that the current therapeutic option like combination therapies of multiple drugs is necessary to treat infections due to resistant *Acinetobacter* species in adults as well as children. It is very important to enforce infection control measures to prevent the outbreak of these resistant *Acinetobacter* species.

Keywords: Antimicrobial agents, Nosocomial infection, *Acinetobacter baumannii*, Antibiotics, 16S rRNA, Plasmid, Pathogenicity, Carbapenem-resistant.



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ANTIMYCOTIC ACTIVITY OF *PSEUDOMONAS STUTZERI* AGAINST A HUMAN PATHOGENIC *ASPERGILLUS* SP.

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Abstract

Human pathogenic fungi cause serious skin infections that persist longer. Human pathogenic fungi, namely, *Aspergillus* spp., was isolated from 35 years old patient suffering from fungal skin infections. Isolated fungi was identified by 18S rRNA sequencing with 1200 bp fragment. Few bacteria and actinomycetes were isolated from soil sample collected from Hadapsar region of Pune that showed zone of inhibition against the isolated pathogenic *Aspergillus* sp. by dual culture method. One of the isolated bacteria that showed colony morphology similar to actinomycetes colonies was identified as *Pseudomonas stutzeri* by 16S rDNA sequencing. This study may lead to isolation of antifungal compounds which can be utilized for treating human fungal infections.

Keywords: *Aspergillus* spp., *Pseudomonas stutzeri*, fungal skin infections.

ANTI-ADIPOGENIC ACTIVITY OF *CORDYCEPS MILITARIS* IN ADIPOCYTES CELL LINE

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ABSTRACT

Inhibition of adipocytes differentiation is suggested to be an important strategy for prevention and/or treatment of obesity. In our present study, *Cordyceps militaris* showed significant inhibitory activity on preadipocytes into mature adipocytes assessed by measuring of at accumulation using Oil Red O staining concentration of 100µg/ml sample water extracted. Activity-guided fractionation led to the isolation of cordycepin (1), Adenosine (2) and tryptophan (3) total protein, vitamins, carbohydrates were determined as active compounds. All the three compounds were more effective in the prevention of early stage of adipogenesis than in lipolysis.



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Role of Probiotic Microorganisms in Combating Type 2 Diabetes-A Review

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Abstract

Diabetes is among the set of metabolic diseases in which there are high blood sugar levels over a long period of time. Probiotics supplementation is a novel therapy in combating type 2 Diabetes. A probiotic is considered typically as a viable microbial dietary supplement that positively affects the host through its impacts in the intestinal tract. The commensal bacteria that are present in our body since infancy are known to play a role in metabolism, in health as well as disease. There are several findings that dysbiosis, is linked to metabolic diseases such as diabetes, obesity, hypertension, and dyslipidaemia. Multistrain probiotics that contain seven million to 100 billion colony forming units of *Lactobacillus acidophilus*, *Streptococcus thermophilus*, *Lactobacillus bulgaricus*, and/or *Bifidobacterium lactis* administered for 6 to 12 weeks have been efficacious for improving glycaemic control in adults with Type 2 Diabetes Mellitus. The anti-diabetic mechanisms for probiotics reported encompass intraluminal and direct effects on the intestinal mucosa and microbiota, anti-inflammatory and immunomodulatory effects, antioxidative effects, effects on endoplasmic reticulum (ER) stress and expression of genes involved in glucose homeostasis and insulin resistance, with some studies pointing to more than one mechanism. This review suggests probiotics as a potential adjuvant treatment in type 2 diabetes.

Key words: Diabetes, Probiotics, Dysbiosis, Immunomodulatory effects, Adjuvant.



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PRESENCE OF *LISTERIA* AND *SALMONELLA* IN FOODS OF ANIMAL ORIGIN

Pragati Dhopte, Pragati Nayak, Shilpshri Shinde, Sandeep Chaudhari* and Nitin Kurkure

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ABSTRACT

Food borne diseases and the pathogens stands to be significant from public health point of view. One in 10 people fall ill after eating the contaminated food worldwide. Every year, unsafe food causes 600 million cases of food borne disease and 420000 deaths worldwide. Most of the food borne diseases are caused due to presence of bacteria (*Salmonella*, *Listeria*, *E.coli*) or viruses (Novovirus, Hepatitis A). In this study a total of 683 meat and milk samples from Maharashtra, Goa and Chhattisgarh regions were processed for the isolation of *Salmonella* and *Listeria* pathogens. A total of 39 isolates of *Salmonella* and 16 isolates of *Listeria* were obtained. Overall 18.70% and 12% of *Salmonella* were recorded from Maharashtra and Chhattisgarh regions, respectively. About 5% of sample from Maharashtra region turned *Listeria* positive. However samples from Goa region were recorded as negative.



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EVALUATION OF ZOONOTIC INFECTION AMONG LIVESTOCK POPULATION IN VIDARBHA REGION OF MAHARASHTRA

Pragati Bhiwapurkar, Pragati Dhopte, Shilpshri Shinde, Sandeep Chaudhari and Nitin Kurkure

Nagpur Veterinary College, Maharashtra Animal and Fishery Science University, Nagpur

Abstract

Zoonotic co-infections stands to be occupational hazards to people who work in close contact with livestock. Brucellosis and Q fever are widely spread and potentially fatal zoonotic diseases which are mainly responsible for abortions in animals also the major public health concern hence to understand the linkage of both disease the study was conducted to evaluate the prevalence of these zoonotic infections in domestic ruminants., On the basis of history of abortions ; a total 180 blood and sera sampled from (6 cattle ,33 Buffalo ,29 goats ,12 sheep) and (14 cattle 86 goats) were collected from different regions of Nagpur and Amravati districts respectively. Serological and molecular screening of all the 180 samples was done. For Brucellosis, 20% from Nagpur and 2% animals from Amravati were found to be positive in sero-diagnosis. Highest (42%) seroprevalence as well as molecular prevalence was recorded in Buffaloes (14 out of 33) of Nagpur district while 33% in cattle 0% in sheep and goat; 2% seroprevalence was found in goats and cattle of the Amravati District. For Q- Fever, 0% prevalence was recorded in all the species of both the districts. This study confirms the circulation of these zoonotic pathogens in animals and highlights the need for implementing a syndromic surveillance of ruminant abortions.



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Phytochemical analysis and antimicrobial activity of *Muntingia calabura* fruit extract: An *in vitro* study**Megha G**

Department of Biotechnology, Nrupathunga University, Bengaluru -56009

*Presenting author: gmegha752@gmail.com**ABSTRACT**

In the present study effort was aimed to evaluate phytochemical components and antimicrobial activity of *Muntingia calabura* fruit part with different organic solvent extracts by Soxhlet extraction method with analytical grade solvents viz., Ethanol and petroleum ether. This study revealed the presence of phytochemical compounds which were observed qualitatively. The *in vitro* antimicrobial activity analysis was performed by agar well diffusion method against the clinically important bacterial strains viz., *Staphylococcus aureus*, *Bacillus subtilis* and *Klebsiella pneumoniae* with the concentration of different extracts ranged from 50 to 150µL. The results of the *In-vitro studies* exhibited the concentration dependent antimicrobial activity against specific bacteria. This study reveals the presence of phytochemical components like alkaloids, flavonoids, saponins, terpenoids. The results of research greatly anticipated use of phytochemical extracts in effective antimicrobial activity against *Staphylococcus aureus* and *Klebsiella pneumoniae* strains with maximum zone of inhibition compared with standard drug tetracycline.

KEY WORDS: *Muntingia calabura*, fruit extract, phytochemical analysis Antimicrobial activity.

**ANTIBACTERIAL STUDY OF MEDICINAL PLANTS AGAINST DENTAL PLAQUE FORMING
STREPTOCOCCUS MUTANS & ITS PREVALENCE IN NAGPUR REGION****Shruti Bhakare, Komal Bawanthade & Yogesh There**

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Email: bhakare_shruti@rediffmail.com**Abstract**

Dental caries is most common chronic disease of childhood in developed & developing countries. In India, prevalence of dental caries is reported to be about 50-60%. Dental caries affects people of all ages with highest priority risk group being children's. Current study helps to determine the prevalence & to evaluate the antimicrobial activity of medicinal plants extracts against bacteria. Dental caries sample were obtained arbitrary from 50 children's of Government Dental Hospital & College, Nagpur in the age group of 4 to 14 years & examined for prevalence of *Streptococcus mutans* by using selective media. Among 50 Samples, 26 isolates were found to be positive for *Streptococcus mutans* on the basis of Morphological, Cultural & Biochemical basis. From present study prevalence found to be 52%. Antimicrobial activity of some selected medicinal plants extracts were checked against *Streptococcus mutans* by agar well diffusion method.

Keywords – Prevalence , *Streptococcus mutans* , antimicrobial



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SCREENING OF PHARMACOLOGICALLY ACTIVE COMPOUNDS TARGETED AGAINST BETA-1,3-GLUCAN SYNTHASE OF *CANDIDA* *ALBICANS* USING COMPUTER-AIDED DRUG DESIGN

Vishal Bhoir and Bela Nabar

Smt. C.H.M. College, Ulhasnagar, Thane, India

Abstract

Computer-aided drug design (CADD) comprises a broad range of theoretical and computational approaches that are part of modern drug discovery. The typical role of CADD in drug discovery is to screen out large compound libraries into smaller groups of predicted active compounds. CADD methods have made key contributions to the development of drugs that are in clinical use or in clinical trials. *Candida albicans* is an emerging threat because of its increasing resistance to traditional antifungal drugs thus becoming difficult to control and manage particularly in hospitalized patients and those with compromised immune systems. One of the important enzymes called Beta-1,3-glucan synthase, involved in cell wall synthesis of *Candida albicans* is showing resistance to many traditional antifungal drugs and thus could be used as a target to screen potential bioactive compounds against it using CADD. In this study, performing Data collection & Preprocessing and Exploratory Data Analysis steps involved in CADD resulted in screening of 150 compounds showing bioactivity against the target enzyme Beta-1,3-glucan synthase. Further analysis of pIC₅₀ values and Lipinski's descriptors of the screened bioactive compounds from the ChEMBL Databases suggested that among the 150 bioactive compounds, 135 bioactive compounds have been showing activity against Beta-1,3-glucan synthase and thus could be the potential candidates for treatment of *Candida albicans*.

Keywords: *Candida albicans*, Computer-aided drug design, antifungal drug resistance, Beta-1,3-glucan synthase, ChEMBL



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CATALYTIC AND ANTICANCER ACTIVITY OF MGO NANOPARTICLE (MGO-NPS) VIA SOL-GEL TECHNIQUE

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Abstract

Increasing concern on water pollution is one of the most crucial challenges facing in different countries. Textile industrial effluents normally contain high concentration of dyes. Since dyes are recalcitrant, stable, colorant, as well as potentially toxic and carcinogenic, their discharge into the environment poses severe threat to aesthetical, health and environmental conditions. Thus, in order to avoid these potential threats from being released into the environment, effective treatment of industrial dye-laden effluents is necessary. Extensively used physical and chemical treatment processes include adsorption, filtration, oxidation, flocculation, electrocoagulation, ozonation and reverse osmosis. Lately, these techniques are considered as cost-ineffective and insufficient. Application of biological process in effluent treatment is time consuming, ineffective towards some non-biodegradable materials and toxic compounds in effluent causes adverse effects on the microbes utilized in the treatment process. Nanoparticles have captured considerable attention, due to their unique properties at nanoscale that maximize its capability to be incorporated into various researches. Many reports have been published based on the application of several nanoparticles supporting the treatment and remediation of environmental pollutants. Metal oxide nanoparticles, specifically magnesium oxide (MgO) nanoparticles are highly promising materials designed to meet the needs of applications as adsorbents due to their destructive sorbent properties and it is exploited in heavy metal as well as waste water treatment. MgO-NPs are eco-friendly, inexpensive and exhibits several biotechnological and biomedical applications. In this report, Magnesium oxide nanoparticle is synthesized via sol-gel technique. MgO-NPs were characterized by spectroscopic and microscopic analysis. UV-visible spectrum of the MgO-NPs showed a sharp absorption peak at 215 nm. FTIR analysis exhibited absorption peak between 660 and 540 cm⁻¹ indicated Mg-O bond stretching in magnesium hydroxide. SEM images showed clover shaped structure and agglomeration of MgO-NPs. Presence of magnesium and oxygen were further confirmed by EDX profile. Catalytic activity of MgO-NPs was witnessed by the complete reduction of rhodamine-B (RhB), methyl orange (MO), methyl violet (MV) and coomassie brilliant blue (CBB) at 100 ppm concentration. The concentration (1000 ppm) showed complete reduction in CBB and MV. MgO-NP was found to be less efficient towards congo red, MO, RhB at 1000 ppm concentration. Additionally, antiproliferative effect of MgO-NPs on MCF-7 and A549 cells was assessed by MTT assay. MgO-NP was more effective against both cancer cell lines of MCF-7 and A549, with a cell viability of 48.4% and 51.2%, respectively.

Key words: MgO Nanoparticle, Anticancer and Catalytic activity



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**IN VITRO EVALUATION OF ANTI-OXIDANT AND ANTI-
INFLAMMATORY POTENTIAL OF POLYHERBAL EXTRACTS****Neha Ailani & Bela Nabar**

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ABSTRACT

The exploitation of traditional medicinal plants for treatment of skin ailments has been considered as an effective approach since ancient times. Traditional system of Indian medicine contemplates use of combined Plant extracts rather than individual ones as active phytochemical constituents in them may be insufficient to exhibit desirable therapeutic effects. In present study, Hot Aqueous extracts of Ashwagandha (roots) Apamarga (shoot) Acalypha (leaves) and Jambula (Fruit) Lavang (Fruit) Neem (Bark) Pipal (Bark) and Hot Alcoholic extract of Apamarga (Shoot) Ashwagandha (roots) Tulsi (Leaves) were prepared using Water and Alcohol as solvent by mixing equal quantities (1:1 ratio) of each herb. The main focus of current research work was to evaluate the antioxidant and anti-inflammatory properties of Polyherbal extracts in order to elucidate their therapeutic potential for use in topical Formulation for skin ailments. The antioxidant activity (free radical scavenging) was evaluated using DPPH (2, 2-diphenyl-1-picrylhydrazyl) reagent to determine the total antioxidant capacity of prepared Polyherbal extracts and the absorbance values were compared with Standard Antioxidant i.e., Ascorbic acid. According to the results, aqueous Polyherbal extracts exhibited stronger radical scavenging activity against DPPH radical showing 50% scavenging while Alcoholic Polyherbal cocktail demonstrated 30% radical scavenging. *In-vitro* anti-inflammatory activity was analyzed by protein denaturation and Human RBC (HRBC) stabilization method. The inhibition of hypotonicity induced HRBC membrane lysis was taken as a measure of the anti-inflammatory activity. The percentage of membrane stabilization for Alcoholic and Aqueous extracts were done at different concentrations using the reference drug Aspirin. Results of both antioxidant and anti-inflammatory assay suggest that selected Polyherbal extracts possess potent anti-inflammatory activity and are also a good source of natural antioxidants. However, further study is needed to identify the chemical compounds responsible for their anti-inflammatory activity.

Keywords: Polyherbals, Phytocontituents, Anti-oxidant potential, DPPH radical scavenging activity, Anti-inflammatory activity, Protein denaturation, Human RBC (HRBC) stabilization



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ANTIBIOFILM ACTIVITY OF CHEMICAL SURFACTANTS, WEAK ACIDS AND
ANTI-SCALANTS AGAINST PREFORMED BIOFILM OF *ESCHERICHIA COLI*
DRINKING WATER ISOLATES.

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The Maharaja Sayajirao University of Baroda, Vadodara, Gujarat 390002

ABSTRACT

Several water-borne disease outbreaks are linked to biofilm growth of bacteria. Almost 80% of bacteria show a biofilm lifestyle of growth in the natural environment. Biofilm formation is of major concern as it contributes to non-specific and broad-spectrum resistance towards antimicrobials. *Escherichia coli* is the principal indicator of water contamination, as its presence signifies the probability that fecal waterborne pathogens have entered the drinking water system. Drinking water coolers if improperly handled tend to develop bacterial biofilms that may include *E.coli*, which may be shed in the stored water adding to the contamination and inappropriate indication of water quality. In quest of antibiofilm agents, chemical surfactants, weak acids and anti-scalants gain importance due to their chemical nature and activity. The Minimum bactericidal concentration of these agents was determined and further their respective concentrations were checked against preformed biofilms of *Escherichia coli* by microtiter biofilm assay. The results suggest that the chemical agents that have been studied have a biofilm disrupting potential.



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Halophiles & their antimicrobial activity

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Halophiles are the microorganisms that live in extreme salty environments. Exploitation of halophiles is having special importance in the development of new molecules with potential applications in biomedicine. Current review focus on antimicrobial compounds produced by halophilic archaeal members. In current scenario antibiotic resistance is a global threat to public health due to the emergence of multi-drug resistant bacteria (MDR). There is an urgent need to identity new effective antimicrobial therapies and exploitation of all possible natural and sustainable resources from extreme environments as a promising resource for new antibiotic discovery. Many antimicrobial substances are being produced by microbial genera and recent findings about natural product research can be expanded to include a variety of halophilic microorganisms as abundant sources of bioactive compounds with pharmacological potential. Antimicrobial compounds were discovered in microbial sources from distinct salt marshes and showed their potential as new medications for treating clinically drug-resistant microbes.

Keywords: Antibiotic resistance, Bioactive compound, Halophilic archae, Antimicrobial therapy



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MICROBIOTA-TARGETED CANCER THERAPEUTICS

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Abstract

Microbiota is a complex ecosystem consisting bacteria, fungi, viruses, and protozoa that reside in various areas of the host body such as the skin, lungs, GI tract, urinary tract, and vagina and play a prominent role in regulating various functions that are associated with many pathological conditions. The gut microbiota constitutes approximately 3×10^3 bacterial cells in a commensal relationship with the host and has the ability to regulate normal inflammatory, immune, and metabolic functions. Recent research has revealed the difference in microbiota interactions with the host in healthy and diseased condition which leads to microbiota dysbiosis, causing a variety of clinical conditions such as cancer, inflammatory and metabolic disorders. Thus, imbalance in the normal microbiota can result in pathological responses that are closely related to the development and progression of cancer in various forms and sites. Modulating the imbalanced gut microbiota represents a novel option to relieve cancer symptoms and also regulate cancer progression. The current review focuses on influence of gut microbiota in cancer pathogenesis and the impact of gut microbiota-targeted treatment therapies on many aspects of cancer pathologies.

Keywords: Gut microbiota, Microbiota dysbiosis, Microbiome-targeted therapy.



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Antibacterial Activities and Phytochemical Screening of Crude Extracts from *Cadaba fruticosa* Species Towards MDR

S. V. Kombe^{*1}, S. Sinkar^{*2}, A. R. Saroj¹, S.R. Somkuwar³ A. R. Rai¹¹. Post Graduate department of Microbiology, Seth Kesarimal Porwal College of Arts and Science and Commerce, Kamptee, Nagpur- 441001 (M.S.) India². Arvindbabu Deshmukh Mahavidyalaya Bharsingi, Tah. Narkhed, Dist. Nagpur- 441305 (M.S.) India³Dr. Ambedkar College Deekshabhoomi, Nagpur, Department of Botany, Nagpurcorresponding author E-mail: suraj.kombe@gmail.com, surendrasinkar24@gmail.com

Abstract

Antibiotic resistance is becoming a pivotal concern for public health that has accelerated the search for new antimicrobial molecules from nature. Ethnomedicinal plant of the Capparaceae family, *Cadaba fruticosa* used to treat Anticancer, Antidiabetic, Antioxidant and Anti inflammatory Activity therefore, some phytoconstituents of the plant may be rich in an antimicrobial agent. In the present study, the antibacterial activity of crude extracts of *Cadaba fruticosa* leaves and stem prepared with solvents of different polarity was evaluated by the agar well diffusion method against some selected Multidrug-resistant (MDR) bacteria. Four bacteria from the global priority pathogen list, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Escherichia coli* were used in this study. Methanol, chloroform and ethanol crude extracts of *Cadaba fruticosa* showed promising broad-spectrum activity against selected MDR bacteria. Hence further detailed biochemical analysis and identification of bioactive constituents need to be carried out in the future.

Keywords: Antibiotic resistance, Ethnomedicinal, phytoconstituents, bioactive constituents



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**GREEN SYNTHESIS OF SILVER OXIDE NANOPARTICLES USING
PAPAYA SEEDS AND THEIR APPLICATION TO CONTROL URINARY
TRACT PATHOGENS****Trikal Sukare¹, Suhas Khandare², Govinda Lakhotiya³**1,2 -PG Dept. of Microbiology, Bajaj College of Science, Wardha, 3-Dept. of Physics, Bajaj College of Science, Wardha, 442001,
M.S., India

Present study involves the cost effective, eco-friendly and rapid method for the synthesis of silver oxide nanoparticles using *papaya* seeds. As synthesized nanoparticles are characterized by X-ray diffraction (XRD), UV-vis. Spectroscopy and Fourier transform infrared spectroscopy (FTIR). XRD pattern confirms the formation of AgO nanoparticles which is also confirmed from FTIR analysis. The crystallite size of the nanoparticles are found to be 35.8 nm. UV vis spectroscopy reveals the absorption of synthesized nanoparticles around 430 nm. The synthesized nanoparticles are used to study the antibacterial activity against urinary tract pathogens. The antibacterial studies are performed for different types of a bacterium: gram-positive, gram-negative, and the significant impact of nanoparticles on bacteria inhibition is observed.

Keywords: *Silver oxide nanoparticles, Papaya seeds, green synthesis, antibacterial activity, urinary tract infection.*

**NANO BHASMA- TRADITIONAL DRUG CANDIDATES FOR
CONTROLLING BACTERIAL SPECIES****Mrunali. J. Mhaskey & Vaishali. U. Thool.**

Sardar Patel Mahavidyalaya, Chandrapur, Maharashtra.

mrunali.mhaskey1996@gmail.com**Abstract**

Medicinal Bhasmas are important to treat various ailments. As originated from minerals, metals or herbs its wide spectrum utility needs to be investigated. In the study growth controlling ability of 12 Bhasmas (Lauh bhasma, Abhrak bhasma, Kasis bhasma, Tamra bhasma, Shankh bhasma, Vang bhasma, Rajat bhasma, Mandoor bhasma, Sphatika bhasma, Godanti bhasma, Tankan and Kapardak bhasma) against isolates of multidrug resistant species of *E. faecalis*, *K. pneumoniae*, and *P. aeruginosa* was carried out in minimum inhibitory assay (2.5, 5.0 and 10 mg). The solubility assay of bhasma was accomplished in order to suspend the bhasma in particular solvent for growth inhibition study. Results, indicated that Tamra bhasma (10 mg) and Rajat bhasma (10 mg) found to be growth inhibitory for all the isolates-followed by Abhrak bhasma (10 mg) bhasma. Some bhasma failed to showcase antibacterial activity against some of the isolates. And hence the bhasma showcasing growth inhibition can be promoted as antibacterial drug for further study having the basic composition of nanoparticles make.



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STUDY OF BACTERICIDAL ACTIVITY OF NANOEMULSION FORMULATIONS DERIVED FROM SOME PLANT ESSENTIAL OILS AGAINST CLINICAL ISOLATES OF *S. AUREUS*

Vaishali Pimple¹, Archana Kulkarni², Suvarna Patil³ and Seema Nimbarte⁴^{1,2} Dharampeth M.P. Deo Memorial Science College, Nagpur, Maharashtra, India.³ Taywade College, Koradi, Dist: Nagpur, Maharashtra, India.⁴ Sevadal Mahila Mahavidyalaya, Nagpur

Abstract

From past few years bacterial resistance to antibiotics is posing the severe issue to healthcare sector. Therefore there is urge to find out natural antimicrobial agents. Essential oils are one of the promising option to deal with antibiotic resistance. But poor solubility, stability and odor makes its use restricted. These limitations can be avoided by using nanoemulsions formulations of these essential oils. In present study, nanoemulsion formulations of Tea tree oil, Thyme oil, Clove oil and Cinnamon oil were synthesized using probe ultrasonicator. Physicochemical characterization and stability studies were carried out and tested for droplet size and polydispersibility index (pdi). Formulated nanoemulsions were tested against clinical isolates of *S. aureus*. The nanoemulsion formulations of Cinnamon oil demonstrated promising results.

Key Words: Antibiotic resistance, Essential oils, Nanoemulsions



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BIOLOGICAL SYNTHESIS OF COPPER NANOPARTICLES USING *AGELE MARMELLOS* PLANT EXTRACT AND ITS ANTIBACTERIAL PROPERTY.Shruti Tanwar*, Yogesh There¹, S. J. Dhoble²²Department of Physics, R.T.M. Nagpur University, Nagpur, 440033, India*Corresponding author: sumitanwar146@gmail.com¹Department of Microbiology, Taywade College, Mahadula-Koradi, Nagpur, 441111, India.**Abstract**

Aqueous extracts of *Agele marmelos* (beal) was subjected for the synthesis of copper nanoparticles (CuNPs) via green synthesis route is the new approach having more eco-friendly importance in nanotechnology. In recent times, plant bioactive compounds were used as reducing and stabilizing agents for metal ions for the synthesis of nanoparticles. In present work, fresh leaves aqueous extract act as reduce Cu^{2+} ions in CuSO_4 to Cu^0 for the synthesis of CuNPs. Synthesis of CuNPs confirmed by using Photoluminescence (PL) excitation and emission spectrum using Shimadzu RF-5301 PC Spectrofluorophotometer and absorbance spectra of UV-visible [spectrophotometer](#) at different stages during the synthesis process. In addition, other properties of synthesized CuNPs were also investigated using X-Ray Diffraction (XRD), Fourier Transform Infrared (FT-IR), Scanning Electron Microscope (SEM). Antibacterial test was carried out by using well diffusion method against *Escherichia coli*, *Proteus*, *Staphylococcus aureus* and *Salmonella*. As a result, biological synthesised nanoparticles showed antibacterial activity against all the tested organisms. Obtained results suggest that synthesised copper nanoparticles act as potential antibacterial agent.

Keywords: Green synthesis; copper [nanoparticles](#) (CuNPs); Photoluminescence (PL); UV-visible [spectrophotometer](#); well diffusion method.

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AN EMPIRICAL STUDY ON EFFECT OF COVID- 19 ON PATHOLOGY TEST

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ABSTRACT

The COVID-19 pandemic has led to a dramatic loss of human life worldwide and presents an unprecedented challenge to public health, food systems and the world of work. The economic and social disruption caused by the pandemic is devastating. COVID-19 pandemic has affected all the sectors globally. The effect of pandemic is also observed in pathology testing. The present research study aimed to study the effect of COVID-19 pandemic on different pathology tests. Total five Pathology laboratories located at Washim and Ansing in Maharashtra were selected for the present research study. The survey was done by directly visiting the Pathology laboratories. The data was obtained from Daily Analysis record of the pathology test viz.

Biomarker, Biochemical, Serological, Blood, Hormones and other test, LFT and KFT - Urine test performed in respective pathology laboratories. The data was collected for the year 2019 and during COVID-19 pandemic (2020-21). The collected data was classified in two different categories viz. monthly and annual. Further the categorized data was analyzed and comparison was made for the pathology tests performed in pre- COVID and during COVID-19 period. The percentage Increase/ Decrease was calculated. It is found that biomarker test viz. CBC, CRP, LDH, D – Dimer, Serum Ferritin and IL-6 showed maximum percent increase during COVID-19 followed by biochemical, blood and serological test. The frequency of performing hormones and other test were found to be slightly increased during pandemic period. Hence, COVID-19 pandemic has also led its consequences on diagnostic sector.

Key Words: COVID-19, pathology tests, biomarker test, diagnostic sector



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EFFECTIVE NATURAL THERAPY USING SOME COMMON WILD HERBS AGAINST STAPHYLOCCAL MASTITIS IN CATTLE'S.

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ABSTRACT

Occurrence of high antibiotic resistance among mastitis causing bacteria, needs searching for new cost effective treatment line. The present study evaluates the antibacterial efficacy of some commonly occurring wild herbs in a locality against multidrug resistant *Staphylococcus aureus* from mastitic cattle's. Aqueous, ethanolic, methanolic and ethyl acetate extracts of Four wild herbs were screened for their antibacterial activity against multidrug resistant strains of *S. aureus* isolated from mastitic cattle's by using agar well diffusion method and MIC of extract determined by the agar dilution method. Ethyl acetate extract of *Tridax procumbens* (L) showed great antibacterial activity against the tested bacterial strains. The minimum inhibitory concentration (MIC) of the ethyl acetate extracts of *Tridax procumbens* leaf was in the range from 0.10 – 0.22 mg/ml was recorded against multi drug resistance *Staphylococcus aureus* (S₄) strain. Phytochemical screening of the plant revealed the presence of tannins, alkaloids, flavonoids and saponins. The results of this study support the traditional use of *Tridax procumbens* L. whole plant as an antibacterial agent. The leaf extract of *Tridax procumbens* L. have great potential as antibacterial agents in the treatment of mastitis caused by multidrug resistant *S. aureus*.

Key words: Mastitis, *S.aureus*, wild herbs, *Tridax procumbens*.



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Occurrence and Molecular Characterization of Multidrug-Resistant *Klebsiella pneumoniae* and antibacterial activity of *Cassia tora* L. against isolated MDR strain.**Durgesh D. Wasnik¹ & P.M. Tumane²**¹Umme Salma Girls Arts and Science College, Nagpur²Post Graduate Teaching Department of Microbiology, RTM Nagpur University, Nagpur**ABSTRACT**

The present study emphasized that an occurrence and Molecular characterization of Multidrug-Resistant *Klebsiella pneumoniae* isolated from different clinical samples and antibacterial activity of *Cassia tora* L. against isolated MDR strain. During this study, 1465 different clinical samples were tested in which 1255 (85.66%) samples showed growth of bacteria. Out of 1255 samples, 1157 (92.19%) different strains of bacteria were isolated. Out of 158 *K. pneumoniae* 128 (81.01%) isolates were ESBL producer. For testing with genotyping of isolates by Multiplex PCR detection using TEM, SHV, CTX-M genes among the isolates harbouring single gene (61.53%), *bla*SHV, *bla*TEM and *bla*CTX-M were present in 42.30%, 19.23% and 11.53% strain of *Klebsiella pneumoniae*. Two or more genes for ESBL were present in 14 (26.92%) of 52 ESBL typeable isolates, *bla*TEM + *bla*SHV being the most common combination (9.61%) followed by *bla*TEM + *bla*CTX-M and *bla*SHV + *bla*CTX-M (5.76%). One strain of *Klebsiella pneumoniae* harbors all 3 genes for ESBL. Antibacterial activity of five different solvent extracts (Methanol, acetone, ethanol, petroleum ether and n-Hexane) were prepared by using Soxhlet extractor. *In-vitro* antibacterial activity was performed by agar well diffusion method. The methanolic extract was found to be more effective against all tested bacteria than other solvents. The highest antibacterial activity of methanolic leaves extract of *Cassia tora* L. was found against *K. pneumoniae* (26 mm), ethanolic extract (20 mm). Petroleum ether acetone and n-Hexane extract (18 mm) also effective against MDR pathogens. The results of the present work provide information for the potential use of the studied edible plants in the fight against MDR phenotypes.



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Broad spectrum activity of *Ehretia laevis* leaves extracts against various pathogenic microorganisms**Kshama Murarkar**

Assistant Professor Dr.R.G. Bhojar Arts Commerce and Science College Seloo, District Wardha

ABSTRACT

From ancient times the folklore herbs have been acclaimed as wealth for remedial health benefits of human beings in India. The prehistoric literary text, i.e., Ayurveda and Unani, also delineate the global practice of phytomedicine for treatment, and its formulation's concoction for hindrance of various ailments. *Ehretia laevis* is a traditional curative herb from ancient period, often designated as Khandu Chakka by local people in Maharashtra. *E. laevis* leaves are used in the treatment of, fungal infections, mouth blisters, eczema, cuts, wounds, diabetes, asthma, fever and joint pain etc. The leaf of this plant contains abundant therapeutically beneficial secondary metabolites besides primary metabolites.

This paper describes antimicrobial action of *E. laevis* dried leaf acetone and isopropanol Soxhlet extracts against isolated clinical pathogens i.e., *E. coli*, *Staphylococcus aureus*, *Pseudomonas aeruginosa*, and dry leaf Soxhlet acetone and ethyl alcohol (95%) extract against isolated oral pathogens i.e., *Streptococcus spp*, *Staphylococcus aureus* and *Candida spp*. The results revealed positive effect against all the pathogens except *Pseudomonas aeruginosa*. The extracts were positive for flavonoids and tannins tests. The results shown broad-spectrum activity against gram-negative, gram-positive bacteria as well as against yeast. The species like *S. aureus* and *Candida spp.*, are becoming resistant against most of the therapeutic drugs. In this situation further study on pharmacological drug formulations using folklore herb are required. It can be used in many herbal products i.e., oilments, toothpastes, and mouthwash etc.



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**ANTIBACTERIAL STUDY OF MEDICINAL PLANTS AGAINST DENTAL PLAQUE
FORMING *STREPTOCOCCUS MUTANS* & ITS PREVALENCE IN NAGPUR REGION****Shruti Bhakare, Komal Bawanthade & Yogesh There**

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Abstract

Dental caries is most common chronic disease of childhood in developed & developing countries. In India, prevalence of dental caries is reported to be about 50-60%. Dental caries affects people of all ages with highest priority risk group being children's. Current study helps to determine the prevalence & to evaluate the antimicrobial activity of medicinal plants extracts against bacteria. Dental caries sample were obtained arbitrary from 50 children's of Government Dental Hospital & College, Nagpur in the age group of 4 to 14 years & examined for prevalence of *Streptococcus mutans* by using selective media. Among 50 Samples, 26 isolates were found to be positive for *Streptococcus mutans* on the basis of Morphological, Cultural & Biochemical basis. From present study prevalence found to be 52%. Antimicrobial activity of some selected medicinal plants extracts were checked against *Streptococcus mutans* by agar well diffusion method.

Keywords – Prevalence , *Streptococcus mutans* , antimicrobial

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MULTIDRUG RESISTANCE PROFILES OF CLINICAL ISOLATES OF *PSEUDOMONAS AERUGINOSA*.

Tejasvini Hiwanj, Vijay N. Charde, Sweta M. Bhiwankar & Yogesh W. There

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Abstract

Multidrug resistant *Pseudomonas aeruginosa* is known as a serious threat to human health worldwide. *Pseudomonas aeruginosa* is an important causative agent of various infection. As pathogen *Pseudomonas aeruginosa* is of increasing clinical importance due to its ability to develop high level multidrug resistance (MDR). The biological cost of multidrug resistance in *Pseudomonas aeruginosa* as seen. This study aimed to isolate of *Pseudomonas aeruginosa* from urine sample and studied different types of strains of *Pseudomonas aeruginosa*. The pigment produce by the *Pseudomonas* different species. In present study 30 sample were studied out 10 sample are positive for *Pseudomonas aeruginosa* and 20 sample are negative of *Pseudomonas aeruginosa* species. On the bases of morphology biochemical characteristics *Pseudomonas aeruginosa* was found to be in the sample. Sensitivity of 10 *Pseudomonas aeruginosa* culture multiple resistance to cefepime, Tobramycin, Ciprofloxacin, Ofloxacin, Chloramphenicol. The source of *Pseudomonas aeruginosa* isolation had a significant influence on its relation to the effect of antibiotics. The number of the resistant culture was isolated from the urine. Use of antibiotics has resulted in the development of multidrug- resistant *Pseudomonas aeruginosa* infection, which is a serious threat to health of patients. To prevent further dissemination of these isolate, appropriate infection control practices must be implemented.

KEY WORDS- Antibiotics, Resistant, Sensitivity

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Advancement in Bio-Diagnostic Tools & Techniques in Biotechnology with an update on Covid-19 pandemic

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Abstract

Biotechnology plays an important role in Human healthcare and management. Getting the right diagnosis is a key aspect of healthcare. Improving Diagnosis in Health care, contribute towards the growing momentum for change in this crucial area of health care quality & safety. Biotechnology has brought down the expenses of diagnostics much of the time. In the current days, Point of care (POC) diagnostic devices are now became a next prototype of diagnosis which are used to measure & diagnose the clinical status of patients. This review describes the status of POC diagnostic tools and technologies along with their working mechanism. And the most important component in POC diagnostic devices are biosensors which emerge as a new paradigm for medical science. This review also illustrates the concept, design and device properties of monitoring and diagnostics. These diagnostic tools with their ongoing development phase have a tremendous potential for the diagnosis of ongoing Covid-19 pandemic. At the end, the mini review provides the scope and perspective of pandemic related bio-diagnostics along with the list of Covid-19 diagnostic kits approved by various countries.

Keywords : Biodiagnostics, biosensor, POC diagnostic devices, Covid-19 pandemic, diagnosis



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ANTIBACTERIAL ACTIVITY ANALYSIS OF NATURAL INGREDIENTS

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²Guide, HOD, Assistant Director, Coordinator- Biotechnology, SK Somaiya College, Somaiya Vidyavihar University, Mumbai-400077.

ABSTRACT

The ongoing conditions of the Covid-19 pandemic led to the indecisive use of chemical-based hygiene products and antibiotics. Chemical-based hygiene products negatively affect humans and the environment. The antimicrobial chemicals are causing severe side effects such as inflammation, irritations, and burning of human skin. Additionally, preservatives used to improve the shelf-life are known carcinogens and allergens. According to recent reports, microorganisms are gaining resistance to the antibiotics that are used to treat human diseases. Furthermore, increased use and releasing them into waterbodies harm aquatic habitats and lead to food chain contamination. India, the world's seventh-largest and most diversified country, has a rich biodiversity of medicinal plants. The plants contain natural phytochemicals which can function as antimicrobial agents. The present study was undertaken in order to assess the antimicrobial activity of natural plants such as Thyme, clove, cinnamon, turmeric, fenugreek, ashwagandha, and hibiscus. The plant samples were extracted using different solvents such as water, ethanol, and n-hexane. The antibacterial activity of plant extract was determined by well-diffusion assay and a comparative account would be discussed in detail.

Keywords: Chemical antimicrobials, Antibiotic resistance, plant extracts, antimicrobial activity



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**GENERATION OF NANOPARTICAL BASED BIOPESTICIDE AS GREEN
ALTERNATIVE FOR VEGETABLE CROP PEST *SPODOPTERA LITURA*****Anamika Sharma and Pragya Kulkarni**

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ABSTRACT

Spodoptera litura, Tobacco cutworm, an insect pest linked with many agricultural crops in the Asian tropics. It can also be found all throughout temperate and tropical Australasia and the Pacific Islands, as a highly polyphagous species that consumes hosts from at least 40 distinct plant families, including the economically important crop-producing groups Brassicaceae, Cucurbitaceae, Fabaceae, Malvaceae, Poaceae, and Solanaceae. Zinc nanoparticles were created by novel green chemistry method, employing the indigenous entomo-fungal strain (IBA5) as a reducing agent. The entomopathogenic fungi infect many orders of insects in a distinctive way. The preliminary insecticidal efficacy of green produced Zinc oxide nanoparticles ZnO (NPs), IBA5 spores, and combination of ZnO NPs+ IBA5 spores against *Spodoptera litura* was investigated. The prepared ZnO nanoparticles were characterized through X-ray diffraction (XRD), the surface morphology and form of ZnO NPs were validated by SEM and TEM analyses. The FTIR spectrum analysis showed that the ZnO NPs, zinc sulphate, and IBA5 Secondary metabolite, all contain a variety of functional groups. In order to examine the optical peak of ZnO NPs, UV spectroscopy was performed. The 2nd instar larvae of *S. litura* experienced 100% mortality upon application of ZnO NPs, IBA5 spores, and combinations of ZnO NPs+ IBA5 spores at various concentrations. The findings showed that ZnO NP concentrations boosted the death of the insects, and by combining ZnO NPs with fungal spores, 100% mortality was also reached in less concentration. Probit Analysis was used to calculate the lethal concentration (LC50) and lethal time (LT50) for each active formulation. The results showed that green produced ZnO NPs were excellent at controlling insects and other pests. When contrasting to synthetic pesticide, nanoparticle based one appears an Eco-friendlier insecticide alternative.

Keywords - Nanoparticles, Eco-friendly, Biocontrol agent, Insecticide, Entomopathogenic fungi.



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CHARACTERIZATION OF PLANT GROWTH PROMOTION POTENTIAL OF *MIMOSA*
PUDICA RHIZOSPHERE ISOLATERaju U. Gadpayle^{#1}, J.V. Gadpayle²¹. Y.C. Arts, Commerce & Science College, Lakhandur, Dist. Bhandara-441803². S. N. More College of Arts, Comm. & Smt. G.D. Saraf Science College, Tumsar-441912

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ABSTRACT

Mimosa pudica ('touch me not') has been used in traditional and ayurvedic medicines ranging from anti-venom, alopecia, wound healing, diarrhoea, insomnia, urogenital infections, etc. while recent studies show anti-microbial, anti-asthmatic, anti-inflammatory and antidepressant properties. *M. pudica* is well adapted to a variety of soils, soil conditions and show nitrogen fixation (root nodule). The rhizosphere microenvironment is a biogeochemically highly active zone near plant root and harbour microorganisms that influence the root system, overall plant growth as well as soil fertility. Identification and characterization of such microorganisms may have wide applications from agriculture to pharmaceutical industry. The aim of the present study was to isolate and characterize *M. pudica* rhizobial symbionts for their plant growth-promoting activity. *Mimosa pudica* whole plants were collected, brought to lab, roots were cut into pieces, washed thoroughly with sterile saline and the root cuttings (2-4 cm) were aseptically inoculated in nutrient agar. The colonies appeared were purified, Gram staining and biochemical test were carried out for primary identification. Three *M. pudica* rhizosphere strains viz. LBP1, AM1 and R8 have shown significant growth-promoting activity in seedling growth promotion experiments based on parameters - root length, shoot length, seedling height, root/shoot ratio, chlorophyll content, fresh and dry weight using moong bean (green gram), urad (black gram), methi (fenugreek), sarso (mustard) and wheat compared to uninoculated control.

Key Words: *Mimosa pudica*, rhizosphere, rhizobial symbionts, PGPR activity

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PRODUCTION OF PHENAZINE-1-CARBOXYLIC ACID (PCA) FROM *PSEUDOMONAS RSML35* AND ITS BIOCONTROL ACTIVITY AGAINST POMEGRANATES PATHOGENS

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Abstract

The Pomegranate (*Punica granatum L.*) is known as the 'fruit of paradise'. In India, it is grown in an area of about 1.25 lakh hectares with 60.64 lakh tones of production per year. Many pathogens such as *Ceratocystis fimbriata*, *Cercospora sp.*, *Colletotrichum sp.*, *Alternaria sp.*, *Aspergillus spp* *Fusarium oxysporum* and *Xanthomonas axonopodis* attack pomegranates. Phenazine compounds are studied due to their strong and broad-spectrum antifungal activity. Phenazines constitute a large group of nitrogenous heterocyclic secondary metabolites of diverse range of bacteria. Phenazine compounds produced by rhizospheric fluorescent pseudomonads are extensively studied as a PGPR trait.

The present investigation aims Phenazine-1-Carboxylic acid (PCA) Production was reported as optimum for PCA production ($941.27 \pm 1.11 \mu\text{g/ml}$). Then purified PCA was subjected to antifungal and antibacterial activity and it was found that the purified PCA antibiotic compound produced by *Pseudomonas RSML35* exhibited biocontrol activity against phytopathogens *Alternaria alternata*, *Aspergillus niger*, *Cercospora sp.*, *Fusarium oxysporum* and *Xanthomonas axonopodis pv. punicae*. PCA was subjected to determine MIC against *Cercospora punicae* and as a result MIC of PCA for *Cercospora punicae* was reported as $35 \mu\text{g/ml}$.

The present investigation aims Phenazine-1-Carboxylic acid (PCA) production. The PCA production in an optimized medium is $941.27 \pm 1.11 \mu\text{g/ml}$. The PCA was purified and subjected to antifungal and antibacterial activity. It was found that the purified PCA antibiotic compound produced by *Pseudomonas RSML35* exhibited biocontrol activity against phytopathogens *Alternaria alternata*, *Aspergillus niger*, *Cercospora sp.*, *Fusarium oxysporum* and *Xanthomonas axonopodis pv. punicae*. PCA was also subjected to determine MIC against *Cercospora punicae* and was reported as $35 \mu\text{g/ml}$.

Key words: *Pseudomonas RSML35*, PCA, *Punica granatum L.*, Biocontrol.



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MICROBIAL RESOURCE MANAGEMENT FOR SUSTAINABLE BANANA PRODUCTION IN *TAPI* BASIN: *KHANDESHI* FARMER'S LIVELIHOOD**N. V. Phirke**

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Email: nitinphirke@sgbau.ac.in**ABSTRACT**

Khandeshi farmers cultivating bananas in *Tapi*-river basin have no alternative than adopting sustainable production practices, including management of natural resources due to ongoing deterioration of soils, high annual nutrient turnover in banana eco-systems, over-exploited water reservoirs and overall cost - prohibitive stagnation of banana production to 52 metric tons per hectare. Among the probable ways to meet the ever-growing demand of qualitative and quantitative increase in banana production are i) fostering the farmers' co-operative movement in the region, ii) utilizing the tissue-culture derived and/or naturally selected high yielding varieties, iii) applying soil conditioners (organic manure and fly ash adequately), iv) managing the irrigation appropriately, v) increasing the vitality through application of amino-acid based plant growth regulators, and vi) preserving the soil health through implementation of eco-friendly technologies. The latter may include the individual or combined application of a) soil conditioner after its production from voluminous banana orchard waste; b) consortium of efficient biofertilizers specially dedicated to banana mycorrhizosphere; c) coal-combustion ash as a source of micronutrients and d) judiciously applied doses and frequencies of chemical fertilizers and irrigation water. Adoption of these sustainable production practices would help *Khandeshi* farmers to conserve and recycle the available natural resources, protect their environment, develop profitable farming systems and enhance quality of their livelihood. Overall possibilities for improving sustainability in banana production in the region are discussed.

Keywords: Sustainable banana production, soil conditioners, biofertilizers, fly ash, plant growth regulators



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ACTIVITY OF ENZYME IN *ANABAENA*, *NOSTOC* AND *LEPTOLYNGBYA* *SPECIES*.

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Abstract

Arsenic, being a toxic metal, pollutes soil, water and air including plants resulting in a severe threat for the animal kingdom including humans. Medium BG-11 was loaded with 250µg/L arsenic was percolated through the continuous flow fixed-bed bioreactor system. It is an efficient system for growth of Cyanobacteria. The system was allowed to stabilize at room temperature with a light: dark ratio of 14:10 hours. The cells of *Cyanobacteria species* were removed from midlog phase and centrifuged. Arsenic accumulation within the cells results in the induction of enzyme arsenate reductase. The activity of enzyme arsenate reductase confirms the entry and arsenic accumulation within the cells. It provides the proof of evidence that the considerably high value of Km in *Anabaena* and *Leptolyngbya* and moderately high value of *Nostoc* suggest considerable arsenic accumulation within the cell.

Keywords – *Cyanobacteria*, *arsenic*, *arsenate reductase*, *continuous flow fixed-bed bioreactor*.



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MOLECULAR BASIS OF SELECTION OF EFFICIENT ACTINOBACTERIAL ISOLATE FOR SHEATH BLIGHT RESISTANCE IN RICE

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Abstract

Agricultural eco-systems are dominated by excessive chemical inputs (nitrogen and phosphate fertilizers) resulting to be fragile under current situation. The chemical inputs benefit farmers but at the cost of soil health. Soil health is the balance in ratio of the microbial diversity and its efficacy in nutrient turnover. Among the microbial populations, actinobacteria is one of the largest phyla which represent the major portion of soil microbiota. They are Gram positive in nature, high G+C content and produce extensive metabolites under stress. Actinobacterial isolates play a dual role as plant growth promoting (PGP) and antagonistic against several plant pathogens. The attempt to classify them based on their dual role helps to benefit farming community to tackle the requirements of agricultural crops in either growth promotion or disease management which will be economical and eco-friendly approach. The current study was focused on isolation, selection and characterization of efficient actinobacterial isolate promoting plant growth and inherent antagonistic property. The actinobacterial isolate identified as *Streptomyces hyderabadensis* DBT 64 showed efficient plant growth promotion in rice. The presence of biosynthetic gene cluster PKS1 and PKS2 and secondary metabolites with antimicrobial properties confirming the antagonistic nature of DBT64 might contribute to induce systemic resistance in plants. The results depicted the innate property of soil microbiota can be enhanced in sustainable way with beneficial microorganisms in soil.

Key-words: Soil health, Actinobacteria, Antagonistic, Microbiota



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ACTINOBACTERIA INDUCED SYSTEMIC TOLERANCE IN TOMATO UNDER MOISTURE DEFICIT STRESS

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Actinobacteria are of great economic importance in agriculture for growth promotion and stress alleviation in plants. The actinobacteria *Streptomyces nigra* strain AUDT545 increased root length, shoot length, root dry weight and shoot dry weight of tomato plants under water deficit stress. Tomato plants inoculated with AUDT545 performed better with increased relative water content and survival percent under water deficit stress. Biochemical assays of actinobacteria inoculated tomato plants showed increased chlorophyll content and reduced proline, total soluble sugar, catalase and peroxidase activity.

The differentially expressed genes in AUDT545 inoculated tomato leaf transcriptomics during induced systemic tolerance (IST) were studied through RNA sequencing. A total of 241 genes in tomato were differentially expressed. The upregulated genes were mainly involved in hormone signaling pathways, photosynthesis, aquaporins, carbohydrate metabolism, fatty acid metabolism, membrane trafficking, signaling and cell wall related. Genes related to cutin, suberin and wax biosynthesis were upregulated. The downregulated genes were mainly transcription factors like ethylene-responsive transcription factor ABR1-like, mitogen-activated protein kinase, ethylene-responsive transcription factor and *aminocyclopropane carboxylate oxidase*. These differentially expressed genes were responsible for imparting water stress tolerance in AUDT545 inoculated peanut and tomato. These genes can be targeted for improving water deficit stress tolerance in plants.



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**STUDY OF PHYLOGENETIC RELATIONSHIP AND ANTIBACTERIAL ACTIVITY OF
ACTINOMYCETES FROM DIFFERENT SOIL OF AGROCLIMATES REGIONS****Dr. Shashi P. Jambhulkar & Dr. Arun B. Ingle****Assistant Professor, Department of Microbiology, Sakya Science, Commerce & Art's College,
Sakya Nagari, Nara, Nagpur****Associate Professor, Department of Microbiology, Seth Kesarimal Porwal College, Kamptee,
Dist. Nagpur-441001(M.S), India****Abstract**

The main aim and objective of this project was to isolate and characterize *Actinomycetes* from different soil of agroclimates regions having antimicrobial activity. First of all the samples were serially diluted and Inoculate on their respective selective agar plates or media. The Isolations were morphologically and biochemically characterized to their respective protocol. After distinguishing we perform antibacterial activity and Minimum Inhibitory Concentration. After several alternative, faster methods for the detection of *Actinomycetes* have been developed, the use of the polymerase chain Reaction (PCR) being one of the most promising approaches. As we know that soil microorganisms provide best resource for the Identification and Isolation of therapeutically product. Actinobacteria have a great economic importance to humans because agriculture and forests depend on their contribution to soil system by discovery new antibacterial agents against various resistant pathogenic bacteria, so we work and Isolates and study more and more *Actinomycetes* that produce effective antibiotics, those are active against Drug-resistant pathogens.

Keyword :- *Actinomycetes, Antimicrobial activity polymerase chain reaction, Minimum Inhibitory Concentration (MIC)*



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STUDIES ON EFFECT OF PLANT REDUCED SILVER NANOPARTICLES
ON GROWTH PATTERN OF *LETTUCE* UNDER HYDROPONICS
ENVIRONMENTDamini Kakde^{a*}, Minal Deolekar^b, Kapil Kamble^c^{a*}Department of microbiology, Kamla Nehru Mahavidyalaya Nagpur;^bDepartment of microbiology, Kamla Nehru Mahavidyalaya Nagpur;^cDepartment of Microbiology, Sant Gadge Baba Amravati University, MH, India;Email: damini.kakde97@gmail.com

Abstract

Presently, researchers interest are mostly focused towards synthesis of biologically obtained nanoparticles over chemically obtained nanoparticles. Naturally, Nanoparticle have been obtained from bacteria, fungi, algae, plants but work related to application of these isolated nanoparticles are reported less. Based on above background present study focus on effect of plant reduced silver nanoparticles on growth pattern of lettuce under hydroponic condition. Dose dependent response of nanoparticles on lettuce plant showed affirmative response on plant growth, photosynthetic pigments, yield, quantity. The most effective treatment of 1mg L⁻¹ of silver nanoparticles showed improvement in growth, its efficiency and yield. Also, silver nanoparticles inhibit growth of bacteria which indicates antibacterial property of isolated nanoparticles.

COW URINE: A GROWTH ENHANCER AND AN ANTIFUNGAL AGENT

A.S.Chirwatkar^{*1} S.A.Mankar² and A.M.Chandak² N.Deshmukh¹ P.Bhelawe³¹PGTD of Microbiology, RTMNU, LIT Campus, Nagpur²D.R.B. Sindhu Mahavidyalaya, Nagpur³Kamla Nehru Mahavidyalaya*Corresponding author : aartischirwatkar@gmail.com

Abstract

Agriculture is the primary source of income for most of the population in India. Use of high amount of pesticides for better crop yield is routine practices in India. These chemical fertilizer found more hazardous to human health. In order to avoid this, a suitable source is required which will increase crop yield. It can be increased by stimulating crop growth and by inhibiting microbial activities against plants. *Fusarium oxysporum* is one such fungus causes fusarium wilt and infect crops. Present research showed efficacy of cow urine as plant growth enhancer and antifungal agent. Effect of different concentration of cow urine was studied on growth of *Triticum aestivum* (wheat) and *Trigonella foenum graceum* (Methi). It was found that growth of plant increases with increase in concentration of cow urine. Maximum plant height of *Trigonella foenum graceum* was 13.43 cm with 20% cow urine while that of *Triticum aestivum* was 14.12 cm with 5% cow urine for the same time period of 25 days. Activity of *F. Oxysporum* was also inhibited by cow urine.

Key words: Cow urine, antifungal agent, fertilizer

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**TOXICOLOGICAL TOLERANCE OF CHLORPYRIFOS ON *LEPTOLYNGBYA* SPECIES
ISOLATED FROM PADDY FIELD OF BHANDARA DISTRICT, MAHARASHTRA, INDIA**Nishant V. Burade¹, Alok R. Rai²^{1,2}Post Graduate Department of Microbiology, Seth Kesarimal Porwal College of Arts, Science and
Commerce, Kamptee – 441001, Maharashtra, India¹nishantburade@gmail.com, ²alok.rrai@gmail.com**Abstract**

Exaggerated application of pesticides in agricultural practices needs immediate action for their removal from land and water. The recent scenario focuses mainly on sustainable and eco-friendly techniques for the remediation of pollutants from the environment. The present study aimed to identify tolerant *Leptolyngbya* species against the pesticide chlorpyrifos in paddy fields. The tolerance capability of *leptolyngbya* was found up to 60 ppm of Chlorpyrifos concentration and showed considerably good growth estimated by higher dry weight of biomass, total carbohydrate, total protein, and chlorophyll content as compared to control. While increasing the concentration up to 100 ppm significant inhibition was observed in above mentioned parameters. Based on the results of this work, we propose *Leptolyngbya* species as a suitable biological option for developing low-cost bioremediation strategies and for the detoxification of pesticides (Chlorpyrifos) in agricultural fields.

Keywords: Pesticide, Chlorpyrifos, Cyanobacteria, *Leptolyngbya* species**Screening of Nitrogen fixing and phosphate solubilizing plant growth promoting
rhizobacteria (PGPR) from rhizospheric soil.**

Papendrakumar soma Patle and Yogesh There

Department of Microbiology, Taywade College Mahadula-Koradi, Nagpur

ABSTRACT

Plant growth promoting rhizobacteria (PGPR) play vital role in sustainable agriculture practices. PGPR provide nutrients to the plants in various forms such as Nitrogen, Phosphate, potassium etc. nitrogen fixing and phosphate solubilizing PGPR were isolated from rhizospheric soil. 10 nitrogen fixing PGPR was isolated and further screening was done through morphological characteristics and detection of ammonia production. 5 phosphate solubilizing rhizobacteria was isolated by using NBRIP medium and phosphate solubilizing potential was checked by measure diameter of clear zone around the colonies on NBRIP medium. The study explores high phosphate solubilizing and nitrogen fixing potential of PGPR to enhance plant growth and soil fertility.

Keywords: PGPR, NBRIP, Nitrogen, Phosphate.

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ISOLATION AND CHARACTERIZATION OF PLANT GROWTH PROMOTING RHIZOBACTERIA FROM SELECTED ORGANIC FIELD SOIL OF CHANDRAPUR DISTRICT

Monali J. Jungari¹ & Vaishali Thool²^{1,2}Sardar Patel Mahavidyalaya, Ganj ward, Chandrapur, Maharashtra 442401

Abstract

Contemporary agriculture practices rely on extensive use of chemical fertilizers and pesticides to increase yield which results in the damage of soil fertility and environmental pollution. Plant growth promoting rhizobacteria are eco-friendly bacteria that live in rhizospheric region of plant root and provide many essential components for growth. The objective of the study was to characterize PGPR activity such as phosphate solubilization, nitrogen-fixing, production of IAA, siderophores production and Ammonia production of PGPR strains isolated from the rhizosphere of soybean and evaluate their effectiveness in stimulating soybean seedlings growth. Total 50 bacteria isolate from organic farm field of Chandrapur district and screened for PGPR activity. Among them 12 isolates were shown efficacious as potential PGPR. Pot study assay results showed that the highest yield was obtained in soybean inoculated with OrgS23 isolate. Further study need to be check the potential of PGPR isolates in open field land.

Key Words: *Rhizobacteria, rhizosphere soil, PGPR activity.*



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Preparation of liquid organic manure from the raw manure

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ABSTRACT

Now a days chemical fertilizers not only harm the cultivate land but also decrease its fertility increasing the chemicals in land and plants. Organic manures are significant organic source of plant nutrients. Farmer's awareness is increasing towards organic farming due to high cost of synthetic fertilizers and nutrient composition in plant all over the world. In presence study we have prepared three organic manure such as Jeevamruth , Beejamruth , Sanjeevani with the help of cow dung , *Rhizobium* soil , cow urine, jaggery, pulse flour, distilled water. Prepared manure was tested for the number of colony of *Azotobacter* and *Rhizobium*. The results indicate that, CFU value of *Rhizobium* in manure Jeevamruth, Beejamruth , Sanjeevani was found to be 1.29, 1.59 and 1.38 respectively. The CFU value of *Azotobacter* in manure Jeevamruth, Beejamruth , Sanjeevani was 7.5, 1.15 and 1.54 respectively. The efficiency and efficacy of some cow pathy like Jeevamrit and composed will enhance the biological efficiency of crop plant and improve soil health in organic farming. It will enhance the productivity of different crops and suppressing the growth of various plant pathogens by producing antibacterial and antifungal compounds.

KEYWORDS : organic manure, *Rhizobium*, *Azotobacter*, Biofertilizer



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UTILIZATION OF INDIGENOUSLY DEVELOPED BOMBYX MORI CELL LINE DZNU-BM-16 FOR THE CONSTRUCTION OF BAC-TO BAC BACMID FOR THE PRODUCTION OF PAM (PEPTIDYL GLYCINE A-AMIDATING MONOOXYGENASE (PAM), APROTININ AND THROMBIN.

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Enzene Biosciences Pvt Ltd. Peenya Industrial Area, Bangalore-5600 058

Abstract

We have derived DZNU-Bm-16 from larval ovaries of the silkworm, *Bombyx mori* and characterized regarding its population doubling time, ploidy, infection susceptibility and transfection efficiency. We adapted Bm-16 cells in serum free media, Sf-900 II SFM.

As the bacmid generated by AcNPV, does not work for silkworm, it was essential to generate a system which readily infects silkworm *B. mori*. The BmNPV Bac-to-Bac provides a tool for expression of any gene in *B. mori* without time consuming and cumbersome screening procedures. Keeping this in view construction of a BmNPV Bac-to-Bac expression system applicable to silkworm *B. mori* and its cell lines was carried out.

The pFast Bac clones of PAM, Aprotinin and Thrombin and pFast Bac GFP were transformed into DH10 Bm Bac chemically competent cells. The recombinant bacmid DNA was isolated and was confirmed by PCR amplifications using gene specific primers.

Amplification with specific primers has given 2.5kb, 200bp and 1.9kb amplification for Bm bacmid PAM, Aprotinin and Thrombin respectively.

Key words: *Bombyx mori*, bacmid vector, BmNPV



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Effect of plant derived silver nanoparticles on 3T3L1 cells.**Dr. Utpal Dongre**Head, Assistant Professor, Department of Biochemistry and Biotechnology, Dr Ambedkar College,
Deekshabhoomi, Nagpur.(9730398751, utpal24dongre@gmail.com)**ABSTRACT**

Nanotechnology is an emerging field in medical diagnostics and therapeutics. At present this technique has been used tremendously to solve various biological enigmas. However, use of nanotechnology in the field of cancer and obesity has attended much prominence in the last few decades. Obesity is a metabolic disorder affecting millions of people through-out the globe. In India, if urgent preventive steps are not taken then obesity will be the worst situation to handle in Indian population. There are various ways to target obesity at clinical level, while the use to nanotechnology to reduce body fat level could help to achieve this goal more realistically. Plant derived nanoparticles plays a significant role in targeting such clinical, pathological and etiological parameters of any disease. Study of plant derived metal nanoparticles like silver in In-Vitro obesity studies could give a better understanding about the combined role of plant and nanoparticles. 3T3L1 is a better In-Vitro model to study such effect for obesity. This cell line is a mouse embryonic audiogenic cells, which can differentiate from pre-adipocyte to mature adipocytes using, dexamethasone, insulin and IBMX. These properties make this cell line a better option to study effects of plant derived nanoparticles for anti-obesity potentials.

Keywords: Nanoparticles, Plants, 3T3L1 cell line, In-Vitro studies etc.

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“Screening of 36 leafy vegetables of Chhattisgarh for VA Mycorrhizal association.”

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ABSTRACT

VAM Fungi, an obligate symbiont assist the plants to absorb mineral nutrients from the soil, especially Phosphorus (P). They are found to increase plant resistance during various stresses like water logging, drought, salty and heavy metal toxicity. The symbiosis is characterized by bi-directional movement of nutrients and VAM can affect the Agro ecosystem in variety of ways (Francis & Read, 1994)

Biodiversity a term to describe variability between organism and the composition of plant community may affect fungal community (Giovannetti et al 1988). The present study was under taken to examine the colonization, abundance, species richness and diversity of VAM fungi associated with common Leafy vegetable plants of Durg District,(C.G.).

The roots of common fertile lands vegetable plants collected from different areas were analyzed at earliest for percent root VAM colonization .A very wide range i.e. 10-100% of VAM colonization was recorded in *Amaranthus gangeticus* L , *Vigna unguiculata* respectively.

The maximum percentage VAM colonization was found in Pyaj Bhaji 93%, Methi Bhaji 88% and minimum percentage VAM colonization on Jhurga Bhaji 61%, Jari Bhaji.

Out of 36 famous Bhaji vegetables of Chhattisgarh we got infection of VAM in 28 Bhajis 48% colonization with all the four stages in different proportions that id Mycelium, arbuscle, vesicle and spore stage .All the spores recovered belong to genus Glomus and Gigaspora, Glomus showing its dominance.



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PLANT DEFENCE REINFORCEMENT AGAINST FUNGAL PHYTOPATHOGENS THROUGH DEFENCE-RELATED GENES EXPRESSION

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Abstract

Being a nutrient-reservoir, plants are always a soft target for wide range of fungal pathogens. Activation of defence-related genes by the application of beneficial bacteria or using resistant varieties provides protection against such pathogens through defence reinforcement. The present research provides the insight about the activation of various defence genes in soybean and wheat plants against fungal phytopathogen *Fusarium oxysporum* and *Bipolaris sorokiniana* respectively. *F. Oxysporum* is responsible for the Fusarium wilt and necrosis of root and lower stem of soybean while *B. sorokiniana* causes spot blotch of wheat. In our study on soybean, the seeds treated with the bio-control agent *Bacillus* spp. SJ-5 shown significant increase in plant growth parameters along with enhanced expression of defense-related enzymes peroxidase, phenylalanine ammonia lyase, lipoxygenase, polyphenol oxidase, chitinase, beta 1,3- glucanase upon *F. oxysporum* challenge inoculation as well as higher accumulation of JA observed which is required for elicitation of ISR. Gene expression study using qPCR technique of all the plants also confirmed the findings of enzyme activity assay. In another study on wheat varieties, the expression of eight defense-related genes in wheat were found highly expressed in resistant genotype Chirya 7 as compared to susceptible cultivars with highest up-regulation of chitinase gene. These studies suggest the role of defence related genes in plant defence reinforcing.

Key words: Soybean, Wheat, Jasmonic acid, Biocontrol, *Fusarium oxysporum*, *Bipolaris sorokiniana*, Defence-related genes



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Isolation of lytic bacteriophage against phytopathogenic *Ralstonia solanacearum* of potato crops in Hassan District, Karnataka : A case study

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ABSTRACT

Ralstonia solanacearum is a Gram negative bacteria causing devastating lethality in most of the *solanaceous* plants including potato and ginger, resulted in economic losses world-wide. The chemical method of control of this bacterium is difficult because of its drug resistance. The use of alternative bactericidal agents is now prevalent over antibiotics and synthetic chemicals. This study was aimed to find natural antimicrobial agents specifically kill the bacterial population and results in reduction of pathogenicity. *R. solanacearum* strains were isolated from wilting potato crops in Hassan district, Karnataka and were characterized by biochemical test and PCR based detection. Further DNA was subjected to 16s ribosomal sequence analysis using 16S rRNA FU8 universal primers (16s rRNA F-5'AGAGTTTGATCCTGGCTCAG 3', 16s rRNA R-5'ACG GCTACCTTGTTA3') and phylogenetic analysis were used molecular relatedness of the isolated animal pathogenic bacteria. 16S rRNA sequences were submitted to GenBank, NCBI and Accession number were allotted. The obtained 16S rRNA sequences were subjected in-silico analysis by genomics workbench software. Pathogenicity test was conducted with tomato and chilli seedlings. Isolates were subjected to antibiotic sensitivity test and all strains were exhibited antibiotic resistance. Bacteriophage δ HMPM22-2023 was isolated against *R. soalanacearum*. The potency of phage activity was checked in laboratory condition. The lytic phage morphology was studied with scanning electron microscopy and partial molecular analysis of isolated phage was done. The results of the study greatly anticipated the use of bacteriophages as potent antimicrobial agents against phytopathogenic *R. solanacearum* and they can be used as natural bio-control agents for plant protection.

Key words: *Ralstonia solanacearum*, Phage, 16s rRNA sequence and bio-control agents.



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