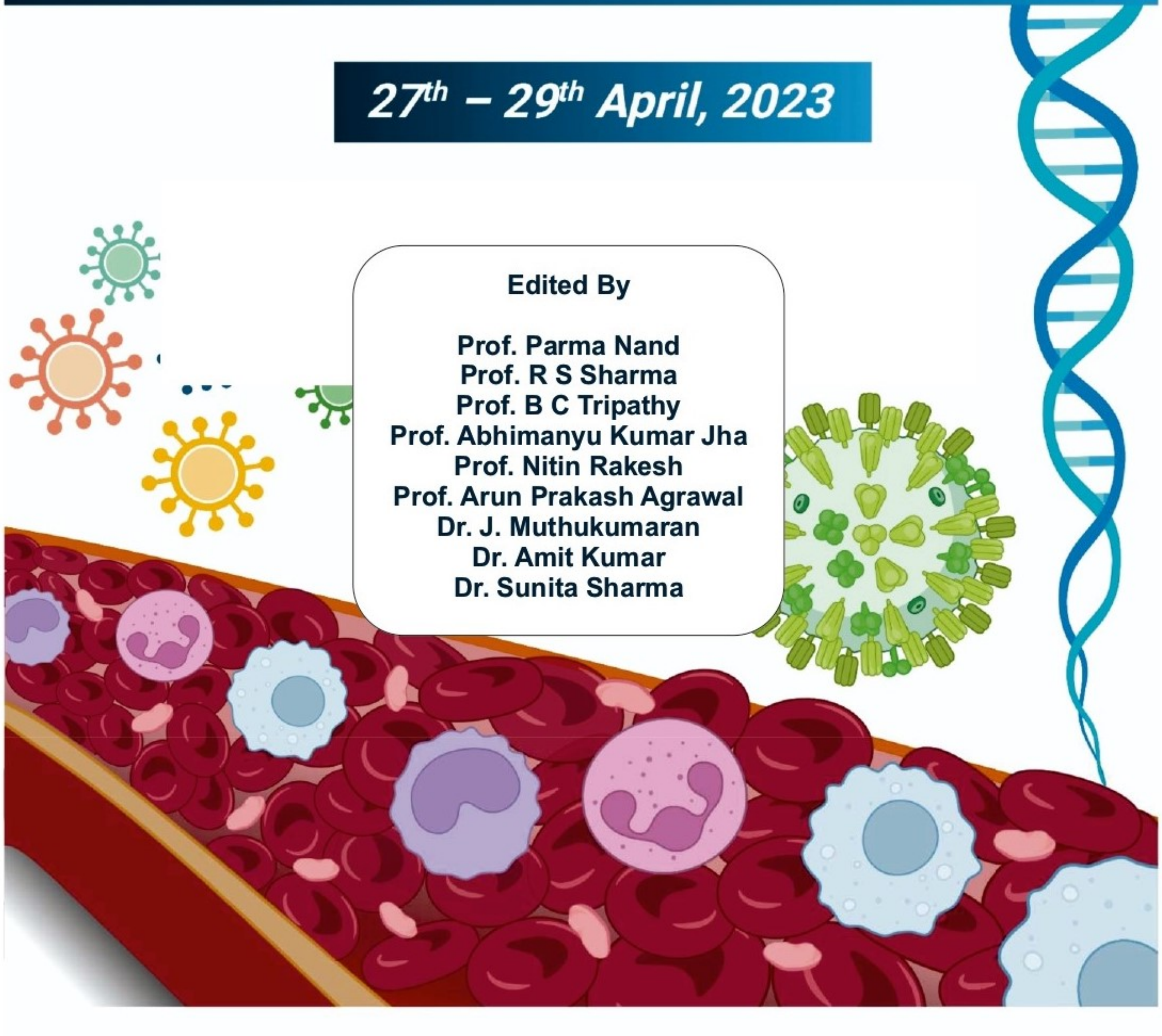
SHARDA UNIVERSITY
Beyond Boundaries

SERB INDIA

DST@50 1971-2021 DEPARTMENT OF SCIENCE & TECHNOLOGY

International Conference on Recent Trends in Biotechnology and Applied Bioinformatics

27th – 29th April, 2023



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Dr. Sunita Sharma

Organized by

Department of Biotechnology in association with
Departments of CSE & CSA, Sharda School of Engineering & Technology, Sharda University, Greater Noida, India

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Abstract Book

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International Conference on Recent Trends in Biotechnology and Applied Bioinformatics

27th - 29th April, 2023

Sharda University, Greater Noida, Uttar Pradesh, India

SSB

Selective & Scientific Books
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International Conference on Recent Trends in Biotechnology and Applied Bioinformatics

27th - 29th April, 2023

Sharda University, Greater Noida, Uttar Pradesh, India

ICRTBAB – 2023

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Prof. B C Tripathy
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Anandiben Patel
Governor, Uttar Pradesh

सत्यमेव जयते

Raj Bhavan
Lucknow - 226 027

13 April, 2023

Message

I am glad to know that the Department of Biotechnology and the Department of Computer Science at Sharda University will be hosting a combined international conference on **'Recent Trends in Biotechnology and applied Bioinformatics'** from 27th to 29th April, 2023.

Biotechnology and bioinformatics are two fast growing areas that are receiving considerable interest from experts in India and throughout the world. Hence, it is essential to evaluate the current level of research in these areas of agricultural, medicinal, and industrial significance in order to make effective strategies for future research in the areas of Biotechnology and Bioinformatics.

Best wishes for success of the international conference.

Anandi Patel

(Anandiben Patel)

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Yogi Adityanath

CHIEF MINISTER
UTTAR PRADESH

Azadi Ka Amrit Mahotsav

Lok Bhawan,
Lucknow - 226001
No : G-108/CM-2/2023

21 APR 2023

Message

I am happy to know that Sharda University, Greater Noida is organizing an International Conference on 'Recent Trends in Biotechnology and Applied Bioinformatics' from 27th to 29th April, 2023. A Souvenir will also be published on this occasion.

Biotechnology has applications in many areas, which include medicine, agriculture, crop production and environment etc. Bioinformatics helps to organise and analyse the biological data for optimal use. Thus, Biotechnology & Bioinformatics are fundamentally connected in multidisciplinary areas of research. In this perspective the Conference assumes much significance.

I hope that the deliberations during the event would be fruitful and the Conference would successfully achieve its objectives.

My best wishes for the entire endeavour.

(Yogi Adityanath)

आज़ादी का अमृत महोत्सव

अश्विनी कुमार चौबे
Ashwini Kumar Choubey

सत्यमेव जयते
आहारशुद्धौ सत्त्वशुद्धिः
स्वच्छ भारत
एक कदम स्वच्छता की ओर

राज्य मंत्री
पर्यावरण, वन एवं जलवायु परिवर्तन
उपभोक्ता मामले, खाद्य और सार्वजनिक वितरण
भारत सरकार
MINISTER OF STATE
ENVIRONMENT, FOREST AND CLIMATE CHANGE
CONSUMER AFFAIRS, FOOD & PUBLIC DISTRIBUTION
GOVERNMENT OF INDIA

दिनांक : 20 अप्रैल, 2023

मुझे यह जानकर हर्ष है कि **शारदा विश्वविद्यालय, ग्रेटर नोएडा** के **बायोटेक्नोलॉजी, कंप्यूटर साइंस एंड इंजीनियरिंग और कंप्यूटर साइंस एंड एप्लीकेशन** विभागों द्वारा संयुक्त रूप से 27 से 29 अप्रैल, 2023 तक **"बायोटेक्नोलॉजी और एप्लाइड बायोइनफॉरमैटिक्स"** पर संयुक्त रूप से अंतर्राष्ट्रीय कान्फ्रेंस आयोजित किया जा रहा है।

जैव प्रौद्योगिकी के भारत के विशिष्ट क्षेत्रों ने भविष्य में वैयक्तिक चिकित्सा, जीनोम इंजीनियरिंग, मानव जीन थेरेपी, जैव निर्माण, जैव ईंधन, पर्यावरण उपचार और सूखा प्रतिरोधी पौधों की आनुवंशिक इंजीनियरिंग, सिंथेटिक जीव विज्ञान जैसे संभावित अनुप्रयोगों के क्षेत्र में आशा की किरण है। जैव प्रौद्योगिकी और जैव सूचना विज्ञान दोनों ही विज्ञानों में नित नए आयाम बन रहे हैं और विश्व में इन क्षेत्रों में बहुत अनुसंधान हो रहा है।

यह कान्फ्रेंस इस क्षेत्र में नवीनतम अध्ययनों, उनके अनुप्रयोगों और उनसे संबंधित तकनीकों के ज्ञान एवं अनुभवों को साझा करने का अवसर प्रदान करेगा। तीन दिन के विचार-विमर्श के बाद इसके निर्णय एवं इस क्षेत्र की नवीनतम तकनीकों के उपयोग का ज्ञान हमें सामाजिक और आर्थिक विकास में अधिक सक्षम बनाएँगे।

बायोटेक्नोलॉजी एवं बायोइंफोर्मेटिक्स दोनों विज्ञान आज उन क्षेत्रों में से हैं, जो हमारे परिवेश की भावी समस्याओं के निराकरण की तरफ बढ़ रहे हैं। इन दोनों के क्षेत्रों में होने वाली तकनीकी प्रगति के प्रयोग बिना LIFE जैसी जीवन शैली अपनाने की कल्पना करना कठिन है। इसलिए हमें इनके अनुप्रयोगों के बारे में जानने और समझने की नितांत आवश्यकता है। यह कान्फ्रेंस विश्व में इन विज्ञानों के क्षेत्र में हुए अनुसंधान व उनके उपयोग को जानने का सुअवसर है। इनके अनुप्रयोग से हम लोगों के जीवन में सकारात्मक परिवर्तन ला सकते हैं।

मैं **शारदा विश्वविद्यालय के आयोजकों और अंतर्राष्ट्रीय कान्फ्रेंस** के प्रतिभागियों को बधाई देता हूँ। कान्फ्रेंस अपने अभीष्ट लक्ष्य को प्राप्त करे, इसके लिए साधुवाद।

(अश्विनी कुमार चौबे)

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डॉ. एस. चंद्रशेखर
Dr. S. Chandrasekhar

सचिव
भारत सरकार
विज्ञान एवं प्रौद्योगिकी मंत्रालय
विज्ञान एवं प्रौद्योगिकी विभाग
Secretary
Government Of India
Ministry of Science and Technology
Department of Science and Technology

17th April, 2023

MESSAGE

It gives me immense pleasure to note that **Sharda University, Greater Noida** is organizing an **International Conference on "Recent Trends in Biotechnology and Applied Bioinformatics"** during April 27 – 29, 2023.

This International Conference will serve as an excellent platform for scientists and students from different disciplines of Biotechnology, Bioinformatics, and Life Sciences to come together and deliberate on the progress made recently, as well as to share ideas and approaches to solve existing problems in this niche area. The conference will go a long way to foster long-lasting interdisciplinary and inter-institutional collaborations involving experts, scientists and academicians and further explore possibilities of innovation.

I extend my best wishes to the organizing team at Sharda University, Greater Noida and welcome all participants.

I wish the International Conference a grand success.

(S. Chandrasekhar)

सीसीएमबी CSIR CCMB

कोशिकीय एवं आणविक जीवविज्ञान केन्द्र
(वैज्ञानिक तथा औद्योगिक अनुसंधान परिषद)
उप्पल रोड, हैदराबाद - 500 007, भारत

डॉ. विनय कुमार नंदिकूरी
निदेशक

CENTRE FOR CELLULAR AND MOLECULAR BIOLOGY
(Council of Scientific & Industrial Research)
Uppal Road, Hyderabad - 500 007, India

Dr. Vinay Kumar Nandicoori
Director

MESSAGE

I would like to take this opportunity to welcome everyone for the International Conference on Recent Trends in Biotechnology and Applied Bioinformatics at Sharda University.

I hope this will serve as a great meeting place for researchers and students from all areas of biotechnology, bioinformatics, and the life sciences to discuss recent developments, collaborate on solutions to pressing issues, and discover untapped avenues for innovation. This could also a forum where academicians and researchers may connect with one another to create enduring partnerships across disciplines and institutions. I anticipate stimulating discussions and scientific presentations. I hope that the Conference will also produce some actionable suggestions.

I hope everyone has a wonderful time at the conference.

Date: 12-04-2023

[Vinay K Nandicoori]

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Message

It is my pleasure to inform that the Departments of Biotechnology and Computer Science of Sharda University will co-host an international conference on April 27-29, 2023. There are many promising applications for biotechnology that have yet to be realised.

Experts in India and across the globe are putting a lot of time and energy into expanding the fields of biotechnology and bioinformatics. So, in order to establish successful plans for future research in the fields of Biotechnology and Bioinformatics, it is necessary to assess the existing level of research in these areas of agricultural, medical, and industrial relevance.

I appreciate and wish success organising this conference. I hope everyone has a great experience.

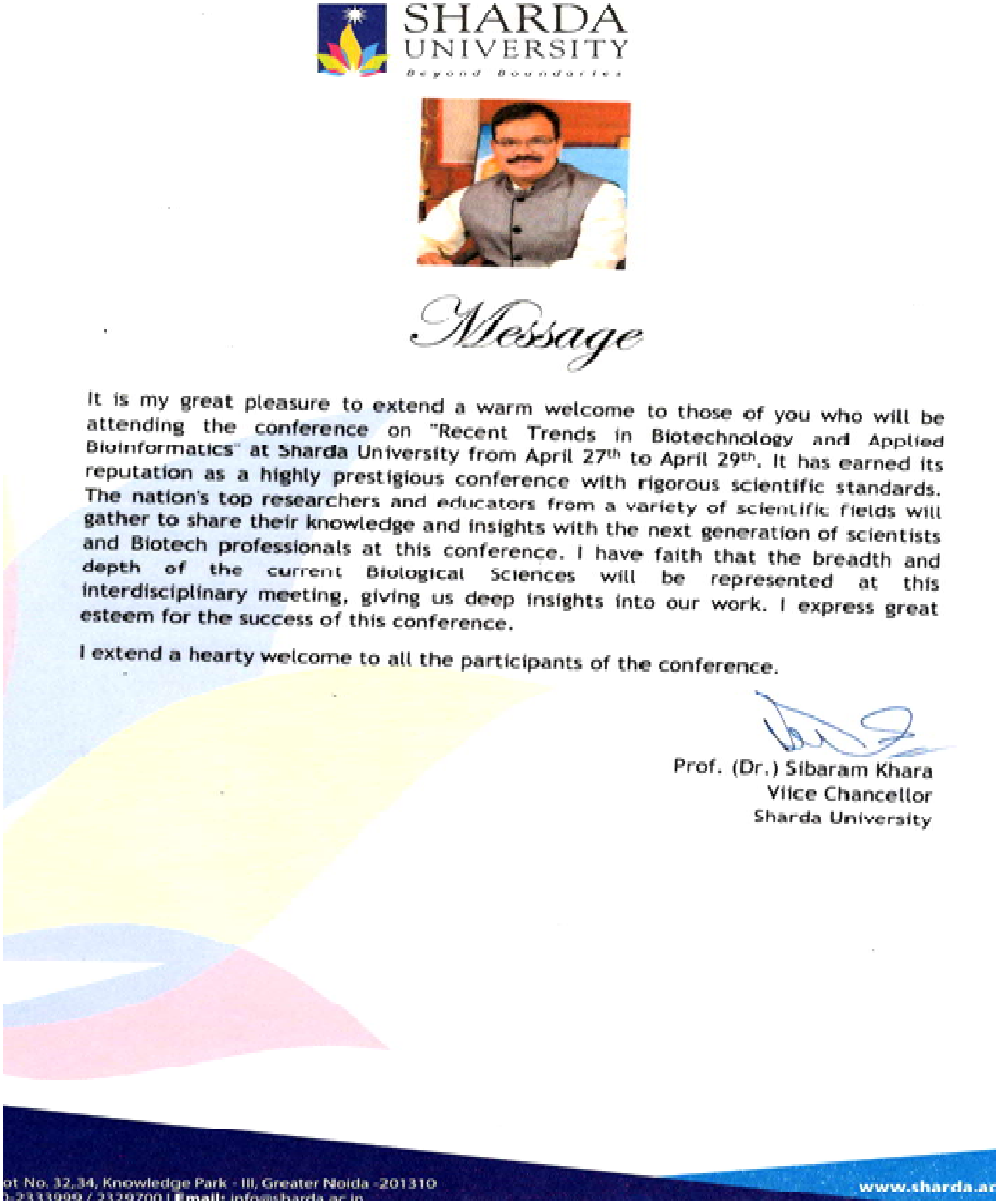
(Shri Pradeep Kumar Gupta)

Chancellor, Sharda University

Message

If you want to learn from and network with the finest in your field, then you should attend the International Conference on Recent Trends in Biotechnology and Applied Bioinformatics in Sharda University. The knowledge you get at a conference like this will equip you to deal with scientific developments in the real world. We are India's first truly international institution, and we bring together the brightest minds in academia and the industry for your benefit. This is a meeting place for persons who may then build enduring partnerships inside and beyond disciplines and institutions. I hope there will be interesting discussions, new ideas, and exciting demonstrations of cutting-edge research. I hope that the Conference will provide some actionable suggestions. Best wishes for a successful event.

(Yatendra Kumar Gupta)
Pro-Chancellor, Sharda University



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Message

It is my great pleasure to extend a warm welcome to those of you who will be attending the conference on "Recent Trends in Biotechnology and Applied Bioinformatics" at Sharda University from April 27th to April 29th. It has earned its reputation as a highly prestigious conference with rigorous scientific standards. The nation's top researchers and educators from a variety of scientific fields will gather to share their knowledge and insights with the next generation of scientists and Biotech professionals at this conference. I have faith that the breadth and depth of the current Biological Sciences will be represented at this interdisciplinary meeting, giving us deep insights into our work. I express great esteem for the success of this conference.

I extend a hearty welcome to all the participants of the conference.

Prof. (Dr.) Sibaram Khara
Viice Chancellor
Sharda University

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SHARDA UNIVERSITY
Beyond Boundaries

SU/SSET/Dean/2023/001 Date: 20.04.2023

Sharda School of Engineering and Technology

MESSAGE

This International Conference will feature distinguished speakers, informative talk sessions, interactive poster sessions, seminars, and discussions. It is an ideal way for aspiring students to network with seasoned academics and advance in their pursuit of their goals.

Both biotechnology and bioinformatics are prospering fields of study, attracting the attention of scientists in India and around the globe. In order to formulate informed strategies for future research in the disciplines of Biotechnology and Bioinformatics, it is necessary to evaluate the current state of research in these areas of agricultural, medicinal, and industrial significance.

Kind compliments to Sharda University for hosting this conference, and best wishes for a successful event to all delegates from around the globe.

Prof. (Dr.) Parma Nand
Dean, SSET and Dean, Academic Affairs

Dean
Sharda School of Engineering & Technology
Sharda University
Greater Noida

Dean Academic Affairs
Sharda University, Greater Noida
(U.P.) 201310

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Message

I am delighted to know that Sharda University, Greater Noida, Delhi-NCR, India, is organising an international conference on advances in biotechnology and bioinformatics.

Biotechnology and bioinformatics are two areas, which bear a significant lot of attention from scientists all around the globe. In the present scenario, life sciences and bioinformatics research need to be prioritised. In this context, it's the need of the hour to take stock of the state of current status of the subject matter. Educative talks from eminent speakers, interdisciplinary technical sessions, interactive poster sessions, workshops and discussions shall form important platform for researchers to establish possible collaborations.

The scheduled conference will provide a wider platform for innovative creativity and deeper deliberation upon extensive subjects encompassing contemporary issues and trends in life science and bio-informatics. Needless to say, this will serve as a foundation, which in turn, will result in multiple advantages in the holistic development of life sciences domain leading to a great degree of service to the society.

My warmest wishes to the organizers for grand success of this conference.

Prof. (Dr.) Bhuvnesh Kumar
Dean Research, Sharda University

SHARDA UNIVERSITY
Beyond Boundaries

Dr. Radhey Shyam Sharma, Ph.D, FAMS
Distinguished Professor
Dept. of Biotechnology, Sharda University &
Former Sr. DDG, Head & Scientist-G,
Division of RBMCH, ICMR, New Delhi

Email: radheyss@gmail.com,
radheyshyam.sharma@sharda.ac.in
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Message

I am pleased to extend a warm welcome to distinguished dignitaries, speakers, chairpersons' delegates and guests participating in the International Conference on Recent Trends in Biotechnology and Applied Bioinformatics being organized by the Department of Biotechnology in association with Departments of Computer Science & Engineering and Computer Science Applications, School of Engineering and Technology, Sharda University, Greater Noida, Utter Pradesh, India during April, 27th-29th 2023.

In this conference special attention and care has been taken to invite young, mid-carrier scientists, researchers and faculty from various reputed Institutions of the country and from different parts of the World. To generate interest in research, efforts have been made to invite large number of young scientists, Ph.D. scholars, postgraduate and undergraduate students from various Institutions and Universities of the Country. The International Conference is also expected to provide an excellent opportunity for young researchers and students to update themselves on various issues on the subject and interact with their peers at national and international level.

The Sharda University always encourage research on various areas with special reference to Biotechnology, Bioinformatics Engineering Basic Sciences, Medical Sciences etc. The outcome of the International Conference would be of great used in initiating new area of research in these disciplines in addition to augmenting the efforts already going on. The discussion and presentations of the International Conference will help the experts from various disciplines in understanding the problems related with Biotechnology and Bioinformatics and will come out with a strategic plan to resolve to these problems. The Organizing Committee extends its appreciation and thanks to the invited chairpersons, speakers and delegates for their participation and contribution to the success of the conference.

On behalf of Organizing committee and on my behalf, I thank all the Govt. and non-Govt. sponsors for their financial, the Administrative, Accounts and Engineering staff of the Sharda University for their cooperation and help. I am thankful to my colleagues and Ph.D scholars & students of the Departments of Biotechnology, CSE & CSA School of ET for their unstinted help and support.

I wish all the delegates splendid memories of the conference.

RSharma

(Prof. Radhey Shyam Sharma)
(Chairman-ICRTBAB-2023)

Sharda University
Plot No. 32-34, Knowledge Park III,
Greater Noida, Uttar Pradesh, India-201310

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Message

It gives me immense pleasure to write a message for "International Conference on Recent Trends in Biotechnology and Applied Bioinformatics" being held in Sharda University from April 27-29, 2023.

The Climate change occurring in Earth due to geological and anthropogenic events poses a catastrophe before us. We do not have any control over geological events; however, we can certainly regulate the anthropogenic ones that will favour human and ecological resilience. Climate change will ultimately bring slow but massive changes including temperature rise, increase of sea level, massive inaundation of land mass by saline water of sea forcing human beings to move to higher elevations, crop loss and severe loss of biodiversity. To build a harmonious Earth where human beings, animals, plants and microorganisms will be able to continue to sustainably coexist harmoniously and peacefully in all the time to come will require Himalayan effort and immense scientific wisdom. The deliberations in the Biotechnology conference organized in Sharda University shall endeavor to address these issues by thought provoking scientific approach. I am sure, presentation and discussions that shall follow during the conference should be able to suggest a way out of the catastrophe our future generation going to face in near future.

Professor Baishnab Charan Tripathy

Conference Chair
Department of Biotechnology
Sharda University, Greater Noida 201310

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Message

It gives me an immense pleasure to extend a warm welcome to all of you as the Convener of the DST-SERB sponsored International Conference on "Recent Trends in Biotechnology and Applied Bioinformatics (ICRTBAB)-2023." The conference is scheduled to take place from 27th-29th April 2023, providing an excellent opportunity for participants from all over the world to come together and share their knowledge, ideas, and latest research findings.

The International Conference "Recent Trends in Biotechnology and Applied Bioinformatics" encompasses a wide range of topics including Cancer Biology, Animal Biotechnology, Genetic Engineering Neuro-oncology, Microbiology, Molecular Biology as well as the use of bioinformatics and computational studies to study biological systems and processes.

The conference will feature keynote lectures, plenary sessions, invited talks, oral presentations and poster presentations, all of which will provide a platform for the participants to share their research and engage in fruitful discussions with other researchers in their respective fields.

This conference will provide a platform for industry professionals, technocrats, and academia to come together and discuss the effective application of the latest research and recent innovations in the field of Biotechnology and Applied Bioinformatics.

We have invited renowned scientists and experts in the field of Biotechnology and Applied Bioinformatics for the deliberations in this conference, which will provide valuable insights and perspectives on the latest developments in the field.

I thank DST-SERB and all the sponsors who have agreed to sponsor this conference as well as the speakers who have agreed to spare some time from their busy schedule for igniting the young minds and budding scientist. I would also like to thank the higher management of Sharda University for their kind support and motivation. In addition to that, I would like to appreciate the hard work of the organising committee members as well as the volunteers for this conference.

I invite all participants to take advantage of this unique opportunity to exchange ideas and establish new collaborations that will help drive research and innovations in the field of Biotechnology and Applied Bioinformatics.

I look forward to welcoming you all to this knowledgeable and enlightening conference.

Prof. (Dr.) Abhimanyu Kumar Jha
Convener, ICRTBAB-2023
&
Head, Department of Biotechnology,
Sharda School of Engineering and Technology,
Sharda University, Greater Noida, India.

Prof. (Dr.) Nitin Rakesh's Message
Convener
Head, Department of Computer Science & Engineering

On behalf of the Department of Computer Science & Engineering, I am delighted to welcome you all to International Conference on Recent Trends in Biotechnology and Applied Bioinformatics, 27th - 29th April, 2023, Sharda University, Greater Noida, Uttar Pradesh, India.

This conference aims to provide a platform for researchers, practitioners, and experts to share their knowledge, experiences, and ideas in the fields of biotechnology and applied bioinformatics.

The conference will cover a wide range of topics, including but not limited to Computational Genomics, Artificial Intelligence and Diseases, Next-generation sequencing data analysis and many more. We are pleased to have a distinguished panel of keynote speakers who will share their insights and expertise with us. This will be an excellent opportunity to learn about the latest research and developments in the field, and to network with colleagues from around the globe.

To all the presenters, I want to congratulate you for your hard work in preparing your presentations. I look forward to learning from your research and engaging in meaningful discussions.

Lastly, I want to wish all the delegates a productive and enjoyable conference. Let us use this opportunity to learn, network, and collaborate to advance our shared goals.

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International Conference on Recent Trends in Biotechnology and Applied Bioinformatics

Scientific Programme

27th – 29th April, 2023

Venue: Sharda University, Greater Noida, Uttar Pradesh, India

Day 1
27th April2023, Thursday, Anand Swaroop Auditorium

09:00 AM to 10:00 AM	**Registration**
10:00 AM -11:30 AM	**Inaugural Function**
High Tea (11:30 AM – 12:00 PM)	
Keynote Addresses	
Chairpersons: Prof. Vinod Joshi & Prof. B.C. Tripathy	
12:00 PM - 12:30 PM	**Prof. R N K Bamezai**, GAP Health Foundation, New Delhi Metabolic convergence despite genomic-epigenomic heterogeneity in cancer with a therapeutic potential
12:30 PM – 1:00 PM	**Prof. (Dr.) Anil Kumar Suri**, NII, New Delhi Newer frontiers of cancer immunotherapy in reproductive cancers
1:00 PM – 1:30 PM	**Prof. Bernhard Grimm**, Institute of Biology AG Plant Physiology, Berlin, Germany Multiple regulatory effects on the synthesis of 5-aminolevulinic acid by auxiliary and regulatory factors
Lunch (1:30 PM – 2:15 PM)	
Session Continuing	
2:15 PM – 2:45 PM	**Prof. Suhel Parvez,** School of Chemical and Life Sciences, Jamia Hamdard, New Delhi Dopamine Agonists Target Mitochondrial Permeability Transition Pore in Alzheimer's Disease
2:45 PM - 3:15 PM	**Dr Roya Rozati,** MHRT andShadan Institute of Medical Sciences, Hyderabad An exploration of the proteomic landscape of unexplained female infertility using bioinformatics
3:15 PM – 4:30 PM	Poster Presentation
Tea Break (4:30 PM – 5:00 PM)	
5:30 PM – 7:00 PM	Cultural Program
7:00 PM Onwards	Dinner

Day 2
28th April 2023, Friday
APJ Abdul Kalam Auditorium and Visvesvaraya Auditorium

Keynote Address (APJ Abdul Kalam Auditorium)		Keynote Address (Visvesvaraya Auditorium)	
Chairperson: Prof. RS Sharma		**Chairperson: Prof. Pitam Chandra**	
9:30 AM – 10:00 AM	**Dr G Taru Sharma**, Director, NIAB, Hyderabad Bench to bedside to brass tacks research: opportunities and challenges	9:30 AM – 10:00 AM	**Prof. Govindjee**, University of Illinois, Urbana, IL, USA Photosynthesis research - A historical perspective

Plenary Lecture (APJ Abdul Kalam Auditorium)		Plenary Lecture (Visvesvaraya Auditorium)	
Chairperson: Prof. Abhimanyu Kumar Jha& Dr Pankaj Taneja		**Chairperson: Prof. Nasreen Zafar Ehtesham& Dr. Arpita Roy**	
10:00 AM – 10:30 AM	**Dr Hisashi Ito**, Hokkaido University, Sapporo, JAPAN Structural and functional analysis of chlorophyll metabolic enzyme for application to plant biotechnology	10:00 AM – 10:30 AM	**Prof. M. Z. Abdin**, Jamia Hamdard, New Delhi A molecular approach for the production of modified stevia sweetener with enhanced sweetening index
10:30 AM – 11:00 AM	**Prof. AngamuthuSelvapandiyan**, Jamia Hamdard, New Delhi Comprehensive proteomic profiling of the host and the gene-deleted leishmania parasites towards the parasite's efficacy as a potential vaccine candidate	10:30 AM – 11:00 AM	**Prof. B C Das**, AIMMSCR, Amity University, Noida, Uttar Pradesh Novel Curcumin-Folate Conjugates; Targeted Drug Delivery for Cervical Cancer
11:00 AM – 11:30 AM	**Prof. S S Chauhan**, AIIMS, New Delhi Diagnostic, prognostic and therapeutic significance of RNA binding proteinHnRNPD in head and neck cancer	11:00 AM – 11:30 AM	**Prof. Dhruv Kumar**, UPES, Dehradun Autophagy-metabolic axis in head and neck cancer

Tea Break (11:30 AM – 12:00 Noon)

11:30 AM – 12:00PM	**Prof. Abhisheka Bansal,** JNU, New Delhi Combination of reverse genetics and biochemical approaches to identify novel intervention strategies for control of malaria	11:30 AM – 12:00PM	**Prof. Anju Shrivastava,** University of Delhi, Delhi Neutrophils in host-tumor crosstalk: Role in systemic deterioration
12:00PM – 12:30 PM	**Prof. D B Sahu,** University of Delhi, New Delhi Seaweeds and their biotechnological applications	12:00PM – 12:30 PM	**Dr Mohd. Ashraf Ganie,**Sher-i-Kashmir Institute of Medical Sciences, Srinagar, J&K Molecular Pathogenesis of Polycystic Ovary Syndrome (PCOS)
12:30 PM – 1:00 PM	**Prof. Nelson Saibo**, Institute of Chemical & Biological Technology, Lisbon, Portugal	12:30 PM – 1:00 PM	**Dr Deena Hassan Elsori**, Rabdan Academy

	Phytochromes and Phytochrome Interacting Factors regulate rice development: from coleoptile elongation to flowering		Abu Dhabi, UAE Non-steroidal anti-inflammatory drugs and Biomarkers: A new paradigm in Colorectal Cancer
1:00 PM – 1:30 PM	**Prof. Margarida Oliveira**, Catedrático Institute of Chemical & Biological Technology, Lisbon, Portugal Setting-up biotech tools to uncover the molecular regulation of cork development	1:00 PM – 1:30 PM	**Dr ShowkeenMuzamil,** Khalifa University, Abu Dhabi Decellularized extracellular matrix-based nanoemulgel system for full-thickness wound healing

Lunch (1:30 PM – 2:15 PM)

Session 1: **Medical Biotechnology, Cancer Biology and Computational Biology** **(APJ Abdul Kalam Auditorium)** **Chairpersons:** **Prof. Anju Shrivastava, Dr Rani Astya & Dr Sunita Sharma**		**Session 2:** **Environmental Biotechnology, Genetic Engineering, Plant Biotechnology and Virology** **(Visvesvaraya Auditorium)** **Chairpersons:** **Prof. M. Z. Abdin & Dr Amit Kumar Singh**	
2:15 PM – 2:35 PM	**Dr Rupesh K. Srivastava,** AIIMS, New Delhi, India Utilizing the Immunoporotic Potential of Bregs under Inflammatory bone loss in Osteoporosis: *Bench-to-Bedside*	2:30 PM – 2:50 PM	**Dr Rajeev Singh,** Jamia Milia Islamia, New Delhi Non-ionizing electromagnetic radiation and Human Health
2:35 PM – 2:55 PM	**Dr Nirmala Jagadish,** Mahatma Gandhi Medical College & Hospital, Jaipur (Rajasthan) SPAG9: A Novel Potential Therapeutic Target in Ovarian Cancer	2:50 PM – 3:10 PM	**Dr Ravi Datta Sharma,** Amity University, Gurgaon, Haryana Prediction of numbers and concentration of Alternative splicing based transcriptional biomarkers using RNA-Seq data
2:55 PM – 3:15 PM	**Dr Rakesh Kumar,** SMVDU, J&K New Breast Cancer Hotspot Mutation of ANKLE1 and its direct role in DNA Damage and Repair in Mammalian Cells	3:10 PM – 3:30 PM	**Dr M. Iqbal R. Khan,** Jamia Hamdard, New Delhi Phytohormones mediated defense mechanisms under different environmental stress regimes
3:15 PM – 3:35 PM	**Dr Pallavi Singh,** Graphic Era Deemed to be University, Dehradun, Uttrakhand, India Targeting GSK-3β for the development of potential Therapeutics against Neurodegenerative Diseases	3:30 PM – 3:50 PM	**Dr Neeti Sanan Mishra,** ICGEB,New Delhi ARMOUR for plant development and response to stress

Tea Break (3:35 PM – 4:00 PM)

Session 1 Continuing (APJ Abdul Kalam Auditorium)		Session 2 Continuing (Visvesvaraya Auditorium)	
4:00 PM – 4:20 PM	**Dr Niti Puri,** JNU, New Delhi A Proteomics approach to find novel therapeutic targets for allergic diseases by deciphering the spatial and temporal regulation of protein traffic in mast cells during allergen challenge.	4:00 PM – 4:20 PM	**Dr Ramesh NamdeoPudake,** Amity University, Noida Deploying a rhizospheric microbes to abiotic stress tolerance in finger millet
4:20 PM – 4:40 PM	**Dr Anil Kumar,** NII, New Delhi Inflammatory and deleterious role of gut microbiota-derived trimethylamine on colon cells	4:20 PM – 4:40 PM	**Dr Anuja Krishnan,** Jamia Hamdard, New Delhi Enhanced generation and characterization of dengue viral-like particles

Day 3
29th April 2023, Friday, APJ Abdul Kalam Auditorium

Plenary Lecture

Chairpersons: Prof. Syed Ehtesham Hasnain &Prof. Bhuvnesh Kumar

9:30 AM – 10:00 AM	**Prof. (Dr.) Ashwani Pareek,** NABI, Mohali Making Rice STRONGER
10:00 AM – 10:30 AM	**Dr Niranjan Chakraborty,** NIPGR, New Delhi Application of organellar proteomics in biotechnology
10:30 AM – 11:00 AM	**Dr Harpreet Singh,** ICMR, New Delhi, India Genome Disparities in Pathogens: Implications for Global Health and Policy - A Case Study of Mycobacterium Tuberculosis

Tea Break (11:00 AM – 11:30 AM)

Session 3: Plant Biotechnology (APJ Abdul Kalam Auditorium) Chairperson: Dr Saleem Siddiqui, Dr SachinTeotia & Dr Vishal Jain		Session 4: Microbiology and Industrial Biotechnology (Visvesvaraya Auditorium) Chairperson: Prof. Parma Nand, Dr Tripti Bhatnagar & Dr Amit Kumar	
11:30 AM – 11:50 AM	**Prof. Girish Mishra,** University of Delhi, Delhi Emphasis on lipid metabolism and lipid-mediated signaling in plants	11:30 AM – 11:50 AM	**Dr Neetu Kumra Taneja,** NIFTEM, Sonipat Probiotic Bacteria as Vitamin Biofactories-Biotechnological approaches to combat micronutrient deficiencies
11:50 AM – 12:10 PM	**Prof. Renu Deswal,** University of Delhi, Delhi Digging Brassica cuticle leads to surprises	11:50 AM – 12:10 PM	**Dr Tripti Bhatnagar,** Codon Biotech, Noida
12:10 PM – 12:30 PM	**Dr NiralaRamchiary,** JNU, New Delhi Structural and functional conservation of genetic loci governing morphological and yield component traits	12:10 PM – 12:30 PM	**BD Biosciences** Role of flow cytometry in Biotechnology
		12:30 PM – 12:50 PM	**IAS Medicare ART Bank** The best Egg Donor and ART Bank of India

Lunch (12:50 PM – 1:30 PM)

APJ Abdul Kalam Auditorium

Oral Presentation

Session 5 **(APJ Abdul Kalam Auditorium)** **Chairpersons:** **Dr. Garima Chauhan, Dr. Monika Jain** **& Dr. Niraj Kumar Jha**		**Session 6** **(Visvesvaraya Auditorium)** **Chairpersons:** **Dr. Arun Agarwal, Dr. Saurabh Kr. Jha** **& Dr. J. Muthukumaran**	
1:30 PM – 1:40 PM	**Dr Tarana Sarwat-** Sharda University, UP, India C-reactive protein as a prognostic marker in coronavirus disease-2019	1:30 PM – 1:40 PM	**KetkiGwalani** - Hislop College, Nagpur, India Optimization of culture conditions for callus induction and in vitro plant regeneration of Coleus forskohlii, an endangered medicinal plant
1:40 PM – 1:50 PM	**Rajesh Kumar**- Gautam Buddha University, Greater Noida, UP, India Transcription Activator-Like Effector Nucleases (TALENs) based genome editing for increased fruit size of tomato	1:40 PM – 1:50 PM	**Shweta Chaudhary** - Gautam Buddha University, Greater Noida, UP, India Effects of cytokinins on in vitro flowering of nodal explant of Vitex negundo (L.): an important medicinal plant
1:50 PM – 2:00 PM	**Priyanka Babuta** - Department of Botany, University of Delhi, Delhi Genome-wide identification and characterization of NADPH-dependent thioredoxin reductases from Brassica juncea	1:50 PM – 2:00 PM	**Jaskirat Kaur Sohal** - Chandigarh University, Punjab, India The Impact of the COVID-19 Pandemic on the Early Onset of Polycystic Ovary Syndrome (PCOS) and Polycystic Ovary Disorder (PCOD) in Young Women: A Cross-Sectional Survey Analysis using RStudio
2:00 PM – 2:10 PM	**Ajeet** – Indian Council of Medical Research (ICMR), New Delhi, Delhi, India Influence of RFR emitted from Cell Phone on Common Mental Disorders of North Indian Population	2:00 PM – 2:10 PM	**Archana Prajapati** - Gautam Buddha University, Greater Noida, UP, India CRISPR/Cas9 mediated gene editing against Powdery Mildew disease to mimic natural ol-2 mutation in Solanum lycopersicum
2:10 PM – 2:20 PM	**Garima Gangwar**, Gautam Buddha University, Greater Noida, UP, India Role of target of rapamycin (TOR) in Candida auris growth and pathogenesis.	2:10 PM – 2:20 PM	**Jyoti Singh** - Sharda University, Greater Noida, UP, India Survey of major allium viruses infecting Indian shallot (*Allium cepa var. aggregatum*) cultivars and their detection with multiplexed RT-PCR
2:20 PM – 2:30 PM	**Soumya Sharma** - Amity University, Noida, UP, India Candida rugosa lipase immobilization on biopolymer-based nano gel and its morphological characterization	2:20 PM – 2:30 PM	**Naveen Kumar** - Sharda University, Greater Noida, UP, India Targeted gene mutations using CRISPR-Cas9 technique affects production of seed oil content in Brassica juncea (Indian mustard)

2:30 PM – 2:40 PM	**DahirSagir Idris** - Sharda University, Greater Noida, UP, India Eco-friendly synthesis, characterization, and application of silver-copper bimetallic nanoparticles	2:30 PM – 2:40 PM	**Pardeep Yadav** - Sharda University, Greater Noida, UP, India Repurposing of FDA approved viral drugs against RNA-Dependent-RNA-Polymerase of Japanese Encephalitis Virus
2:40 PM – 2:50 PM	**Zainab Mirza** - Jamia Millia Islamia, New Delhi, Delhi, India Molecular Aspects Of Arsenic-Iron Give-And-Take To Alleviate Arsenic Stress In Rice	2:40 PM – 2:50 PM	**Taniya Bargoti** - Gautam Buddha University, Greater Noida, Uttar Pradesh, UP, India Genome editing for reversing the evolutionary loss of anthocyanin accumulation in tomato (Solanum lycopersicum L.)
2:50 PM – 3:00 PM	**Rishab Tyagi** Secure and Efficient Medical Image Storage with Deep Learning and Significance-based Encryption and Compression.	2:50 PM – 3:00 PM	**Ajay Arya** AI based models for predicting DNA-binding residue from sequence
3:00 PM – 4:00 PM	**Valedictory Function**		
4:00 PM	**High Tea**		

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Oral Presentations

Poster Presentations

Keynote Lectures

(KN)

KN1

Metabolic Convergence despite Genomic-Epigenomic Heterogeneity in Cancer with a Therapeutic Potential

RNK Bamezai

Former Professor and Dean School of Life Sciences and School of Computational and Integrative Sciences, JNU, New Delhi ; Former VC, SMVDU, Katra, J&K and Former Hon. Director, Delhi School of Public Health, Institution of Eminence, University of Delhi

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Identifying precise molecular etiology for efficient diagnosis, prognosis, prevention and cure in cancer continues to remain a challenge, despite substantial progress made in diagnosing and treating many a cancers. Mutation or risk providing variation-based diagnosis, prognosis of response and recovery, and possible intervention, direct or designed, based on chemical or immune based drugs, vaccines, or stem cell- and gene-therapies, has benefited the patients largely. Adopting emerging approaches of epigenetic sequences and targeting of drugs to chromatin has added another dimension to cancer research.

Our studies on genomic-epigenomic-heterogeneity in sporadic breast cancers and understanding of cancer cell metabolism unraveled an event of a metabolic-convergence towards the formation of stable dimers of pyruvate-kinase isoform-M2 (PKM2) with considerably low activity when compared to its homo-tetramer-enzyme. This feature, first observed in cancer-prone Bloom syndrome and later noticed across cancer types, prevailed despite diverse variations at genomic, epigenomic, and mitochondrial levels. Insulin, known to be tightly associated with cancer progression, enhanced metabolic capacities of cancer cells by dual regulation: of upregulated PKM2 (tetramer) expression through PI3K/mTOR-HIF1-alpha pathway, resulting in enhanced glucose uptake and lactate production; and a significant drop in its activity by subunit dissociation and dimerization of PKM2 through insulin-induced ROS, resulting in glycolytic and NADPH pooling. The latter generating a pro-proliferation condition for cancer cells. Independent experiments of mitochondrial ROS generated in the background of germline or somatic ND3/ND5/CoI - subunit mutations also downregulated the activity of PKM2 and influenced the expression epigenetically of apoptotic/anti-apoptotic genes towards cancer-cell-survival.

These observations suggested a role for relatively inactive PKM2 dimer in tuning cancer cells towards a pro-proliferation state. Additionally, an alternatively spliced form of PKM gene, PKM1, was upregulated under hypoxic-low-vascularized-low nutrition conditions, through LKB-AMPK pathway. Such cells depicted low proliferation and relatively quiescent-survival with a probable cancer-stem cell like features. Apparently, pro-proliferation and pro-survival metabolic signals guided by the two isoforms of PKM in cancer cells depended on the cellular state and neighboring environment, despite the presence of aberrant genetic, epigenetic and mitochondrial cellular background.

Unlike others, we observed co-expression of PKM1 and PKM2 in cancer tissues and cell lines, raising a possibility of the formation of multiple hetero-tetrameric cross-oligomers, all contributing to the differential glycolytic activity to yield ATP in a cancer cell; also indicating that PKM1 was not necessarily a bystander, in addition to AMPK mediated energy metabolism rewiring protecting cancer cell viability. Targeting the observed metabolic tuner(s) in initial experiments with and without AMPK has shown promise for therapeutic intervention across diverse cancer types, requiring additional studies.

KN2

New Frontiers in Cell-Based Immunotherapy of Cancer

Anil Suri

Centre for Cancer Immunotherapy (CCI), Sri Ram Cancer &SuperspecialityCenter,
Mahatma Gandhi Medical College & Hospital, Jaipur, India

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Immunotherapy using dendritic cell (DC)-based vaccination is an approved approach with the potential of a patient's own immune system to eliminate tumor cells. DCs, often referred to as “Nature's adjuvant” have been recognized as the most potent antigen-presenting cells (APCs), capable of activating both naive and memory immune responses and are essential in immunity owing to their role in activating T cells, hence promoting antitumor responses. In their resting state, DCs are considered to be immature but primed to acquire antigens *in situ* through a variety of receptors and mechanisms. Upon exposure to activating stimuli, DCs undergo a complicated series of phenotypic and functional changes. The process of DC activation is an intricate and tightly controlled differentiation process that is closely associated with antigen acquisition. DCs take up antigens through phagocytosis, micro- or macro-pinocytosis, and endocytosis using Fc receptors, integrins, C-type lectin receptors, apoptotic cell receptors, and scavenger receptors. Upon maturation, DCs migrate to the secondary lymphoid tissues where they come in contact with T and B cells. There is only one DC based vaccine that has been granted FDA approval. Sipuleucel-T (Dendreon) was accepted in 2010 for the treatment of metastatic, castration-resistant prostate cancer. Creative DC-targeted therapeutic strategies will be highlighted, including cancer vaccines and how current approaches to apply DC vaccines in the clinic could be improved to enhance anti-tumor immunity.

KN3

Multiple Regulatory Effects on the Synthesis of 5-Aminolevulinic Acid by Auxiliary and Regulatory Factors

Bernhard Grimm

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(Building 12), 10115 Berlin

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Tetrapyrrole biosynthesis (TPB)in plants consists of more than twenty enzymatic steps and is tightly controlled because of the synthesis of photoreactive intermediates and the different spatio-temporal demands of their end-productschlorophyll and heme.The two enzymes glutamyl-tRNA reductase (GluTR) and glutamate-1-semialdehyde aminotransferase (GSAT) ensure the synthesis of 5-aminolevulinic acid (ALA), the precursor of tetrapyrroles. ALA synthesis is the rate-limiting step at the beginning of the TPB pathway and is tightly controlled by multiple posttranslational control mechanisms to ensure a balanced metabolic flow in TPB on the level of activity, stability, oligomerisation and subplastidal compartmentation of the participating enzymes. In recent years, we successfully unraveled the complex control of ALA synthesis during daytime, nighttime, and changing light intensities. The presentation summarizes these different regulatory strategies to control the activity of ALA synthesis by regulatory and supporting factors.

KN4

Dopamine Agonists Target Mitochondrial Permeability Transition Pore in Alzheimer's Disease

Suhel Parvez

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Increasingly recognized as significant pathogenic processes for neurodegenerative illnesses, such as aging and Alzheimer's disease, oxidative damage and mitochondrial dysfunction are two key pathological hallmarks of AD. The purpose of the current study was to investigate the effects of pramipexole (PPX) medication given for an extended period after amyloid beta (Aβ1–42)-induced cognitive deficits, oxidative stress, and mitochondrial dysfunction in a Wistar rat model. In the Morris water maze, we found that PPX (1.0 mg/kg, b.wt.) reduces the cognitive deficits caused by Aβ1–42-infused rats. At the same time, PPX reduced the oxidative damage caused by Aβ1–42 and increased reduced-glutathione levels, decreased lipid peroxidation rates, and inhibited acetylcholinesterase activity, demonstrating antioxidant benefits.

In addition, PPX therapy in Aβ1–42 rats reduced the production of reactive oxygen species in the mitochondria and restored mitochondrial membrane potential, oxidative phosphorylation, and ATP levels. Moreover, PPX therapy prevented the translocation of Bax and Drp-1 to mitochondria and the release of cytochrome-c into the cytoplasm while also reducing bioenergetic loss and dynamics changes. A fundamental component of the mitochondrial fusion process, mitofusin-2 protein expression, was likewise increased by PPX. We conclude that the protective effects of PPX may contribute to the development of AD by reducing oxidative damage and mitochondrial disruption that are altered in Aβ1–42 rats.

KN5

An Exploration of the Proteomic Landscape of Unexplained Female Infertility using Bioinformatics

Roya Rozati

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Female unexplained infertility is a multifactorial disorder with poorly understood pathogenesis with underlying mechanisms. Around 50% of infertility cases are caused solely by female factors, with 15-20% having no identifiable cause, making it a primary challenge for reproductive medicine experts for decades. Among all omic procedures, proteomics is now being widely used in the field of human reproduction. In recent years, the literature on the proteome database connected to various reproductive tissues in males and females has been enhanced by the availability of improved proteomic methods and databases. Further, Network and pathway analysis using bioinformatic tools has now provided a more scholastic and comprehensive view of the potential pathways connected to the significantly elevated DEPs (Differentially Expressed Proteins) to identify their relevance to specific infertility circumstances.

This study investigated differential tissue proteome profiles in patients with unexplained female infertility and healthy fertile controls and explored the association between their tissue proteomes. Paired samples of ten patients with unexplained infertility and ten healthy fertile controls during their mid-secretory phase (LH +7) were obtained for optimized quantitative tissue proteomics analysis. High-resolution two-dimensional gel electrophoresis (2-DE) analysis was used for comparing patterns of protein expression, and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry was used to identify protein spots on 2-DE gels (MALDI-TOF MS). The presence of upregulated DEPs were then validated against their respective primers using the qPCR technique. To interpret and analyze the collected data in light of their biological function, pathway, and interaction network, bioinformatic software and tools, including UniProt, Genecards (v.4.8.2), KEGG, Reactome, and STRING were utilized (version 10.5). Using PANTHERS 14.0, the genes corresponding to differentially expressed proteins were mapped to multiple gene annotation data and the biological pathway. Molecular function, biological process, cellular location, and protein class was done.

The history of infertility, age of menarche, OCP and other drug use history, menopausal status and baseline parameters like age and BMI were evaluated for patients from both groups. All participants provided their informed consent after the Institutional Review Board of the study institute authorized the protocol. The study's subjects were under-40-year-old females with regular menstrual cycles (27–35 days), a typical double-phase basal body temperature, normal serum prolactin levels and a male partner with ≥5 million motile sperms. The cause of infertility was investigated according to the minimum propaedeutic procedure for infertile couples: hormone and biochemistry profile, testing for sexually transmitted diseases, imaging examinations, investigation of genetic and/or immunological abnormalities, semen analysis of the partner, hysterosalpingography, hysteroscopy and laparoscopy. If none of these examinations revealed an abnormality, infertility was considered unexplained. Women who did not achieve pregnancy after at least six natural or induced cycles following laparoscopy were considered infertile. All fertile women with a history of parity and no uterine abnormalities were taken as controls. We identified twelve proteins differentially expressed in Infertility when compared with healthy controls, including Ankyrin repeat domain-containing protein 36A (ANKRD36), Zinc finger protein 658 (ZNF658B), MAM and LDL receptor class A domain containing 1(MALRD 1) and proline-rich coiled-coil 2A (PRRC2A).

In addition, we noted several proteins involved in receptor and cell signaling pathways with distinct expression patterns in patients with unexplained Infertility, suggesting an upregulated Integrin signaling pathway which can play a major role in the pathomechanism of unexplained infertility. A better understanding of the underlying causes and the mechanistic pathways of unexplained female infertility is needed to better comprehend the disease and its management.

KN6

Bench to Bedside: Opportunities and Challenges in Stem Cell Research

Taru Sharma

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A chronic wound is defined as the one in which the normal healing process is disrupted at one or more points in the phases of hemostasis, inflammation, proliferation, and remodelling. In diabetes mellitus, wounds remain in a chronic inflammatory state and fail to heal quickly and orderly. The continual influx of inflammatory cells and sustained production of their inflammatory mediators cause imbalances in wound proteases and their inhibitors, preventing extracellular matrix synthesis (ECM) and remodeling that is essential for normal wound healing. The standard approach for the treatment of diabetic ulcers includes measures to assess the vascular status and optimize glycemic control, extensive debridement and infection elimination by antibiotic therapy based on wound pathogen cultures, the use of moisture dressings, and offloading high pressure from the wound bed.

Mesenchymal stem cells (MSCs) appear to be an attractive cell type for cell-based therapy to promote dermal regeneration. In addition to their differentiation potential, MSCs exhibit substantial trophic support to regenerating tissues, accelerate wound closure, enhance wound repair quality, and increase collagen composition, resulting in healed tissue with increased tensile strength. MSCs are ideal for allogeneic and xenogeneic use due to the lower expression of major histocompatibility complex (MHC) molecules. Therefore, the hypo-immunogenicity property exhibited by MSCs makes them an ideal candidate for cross-species applications. This work was executed to evaluate the healing potential of canine bone marrow-derived mesenchymal stem cells (BMSCs) in experimental full-thickness cutaneous wounds in diabetic rats.

The wound healing potential of canine bone marrow-derived mesenchymal stem cells (BMSCs), collected aseptically from the iliac crest of healthy canine donors, was evaluated in the excisional wound of streptozotocin-induced diabetic rats. Full-thickness experimental wounds were created on the dorsum of adult healthy Wistar white rats and randomly assigned to three treatment groups: control, BMSCs injected into the wound margins on days 0, 7, and 14 and BMSCs injected into the wound margins on days 7, 14, and 21 post-wounding. The degree of wound healing was evaluated based on macroscopical, hemato-biochemical, histopathological, and histochemical parameters.

The results indicated granulation tissue formation with reduced exudation and peripheral swelling in the MSCs treated groups with significantly higher degree of wound contraction compared to control. The transplantation of BMSCs resulted in early drying of wounds, granulation tissue appearance, and enhanced cosmetic appearance. Thus suggested great therapeutic potential of xenogeneic mesenchymal stem cell therapy in managing diabetic wounds.

Plenary Lectures
(PL)

PL1

Structural and Functional Analysis of Chlorophyll Metabolic Enzyme for Application to Plant Biotechnology

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Chlorophyll a and bare primary photosynthetic pigments in land plants. Understanding the chlorophyll metabolic enzymes is essential to improve photosynthesis productivity. However, they are still not characterized well. Chlorophyll a oxygenase (CAO) oxidizes the methyl group of chlorophyll a to produce chlorophyll b. Mg-dechelatase catalyzes the committed step of the chlorophyll degradation pathway by removing central Mg from chlorophyll. To elucidate the regulatory mechanism of the chlorophyll metabolic pathway, we predicted the structures of these enzymes and investigated their reaction mechanisms.

CAO structure was computationally predicted. Mg-dechelatase structure was determined by X-ray crystallography and its enzymatic activity was examined using recombinant proteins.

The conserved motif of the plant monooxygenase family was found in the predicted CAO structure. Structural and biochemical analysis ofMg-dechelatase suggested that Mg of chlorophyll is coordinated by the side chain of aspartate residue in cooperation with the neighboring histidine residue, resulting in destabilization and extraction of Mg.

Our study can potentially improve plant photosynthesis by modifying pigment metabolism. Furthermore, metal ion extraction from organic molecules achieved by Mg-dechelatase is a rare enzymatic reaction. The elucidation of Mg-dechelatase reaction mechanism will provide important information on enzyme research.

PL2

A Molecular approach for Production of Modified Stevia Sweetener with Enhanced Sweetening Index

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For hundreds of years stevia has been known for its sweet characteristics. With the advent of modern lifestyle, the problems like obesity, diabetes, and other linked comorbidities are becoming more prevalent. To address these issues, the global public policies are recommending manufacturing the food items with reduced sugar. Owing to higher risk associated with artificial sweeteners, the low-and no-calorie sweeteners such as stevia are gaining popularity among consumers and food manufacturers. Stevia featuring many anti-diabetic and anti-oxidant properties is approximately 300 times sweeter than sugar. Stevia also has zero calories, which makes it highly beneficial for people seeking to lower their glucose levels.As a result; industries have focused on the use of natural sweeteners like steviol glycosides (SGs), which have become increasingly important in the food industry. Despite the fact that industries are switching to this plant-based sweetener, they are unwilling to sacrifice taste, which is still the most important factor influencing purchasing decisions. Stevia sweeteners have thus been on a quest to achieve the best possible taste profile. The bitter aftertaste that is commonly associated with early generation stevia products has been one of the most difficult challenges that ingredient makers have faced in recent years. It is being said that the sweetest and purest compound in its leaves is rebaudioside-A, whereas the stevioside is responsible for the bitter aftertaste.The key metric of sweetness quality is the ratio of rebaudioside-A to stevioside; the higher the rebaudioside-A content, the better the organoleptic quality. Thus, to make use of this natural sweetener, a new variety of *S. rebaudiana*with higher SGs content and a higher rebaudioside-A to stevioside ratio is needed. In our lab, miRNAs targeting genes of SGs biosynthetic pathway has been identified. Based on their targets and expression profiles, the two miRNAs i.e., miR319g and miRStv_11 were selected and validated for their function and impact on SGs contents.A total of eleven miRNAs was found to target the genes of SGs biosynthesis. The over-expressionand knock-down constructs of miR319g and miRStv_11were prepared and it was showed that miR319g downregulated, while miRStv_11 upregulated their target genes in *S. rebaudiana*. Further, miRStv_11 and anti-miR319gwere overexpressed together, which resulted in significant increase in stevioside (24.5%) and rebaudioside-A (51%) contents. Development of such trait specific novel variety will help to achieve the target of producing natural sweetener with best possible taste profile.

PL3

Comprehensive Proteomic Profiling of the Host and the Gene Deleted *Leishmania* Parasites towards the Parasite's Efficacy as a Potential Vaccine Candidate

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With no efficient vaccine, *Leishmania* continues to create havoc in third world countries. To counter this, a cell division specific gene deleted live attenuated *L. donovani* parasite (*LdCen1*$^{-/-}$) has been developed, that exhibits a selective growth arrest as axenic amastigotes and is being widely anticipated as a probable vaccine candidate. *LdCen1*$^{-/-}$ challenge is known to activate the Th1 arm, with remarkable increase in IFN-γ secreting CD4^{+} and CD8^{+} T cells, thus exhibiting a protective proinflammatory immune response. Towards understanding the physiology of infection, and prediction of disease interceptor or vaccine biomarkers, as well as attaining valuable insight into molecules and pathways identification in *Leishmania*-macrophage infection studies, both labelled and label free proteomics approach have been employed. Various Th1 stimulatory proteins responsible for the immunogenic role of these knockout parasites are reportedly upregulated in mutant parasites. Proteins known to be host protective, like Glyceraldehyde-3-phosphate dehydrogenase (GAPDH), cytochrome *c*, calreticulin and those responsible for inducing immune response, namely tubulins, HSP70 and tryparedoxin, are modulated in these parasites.Tryparedoxin has been adjudged as a probable biomarker of *in vitro* growth attenuation in *Leishmania* parasites.Further, proteomic modulation after mutant in vitro infection suggested elevated annexin A6 in host, potentiating its immunological capacity and curtailing the infection promotion. Besides, S100A8 and S100A9 known to maintain a homeostatic balance in regulating the inflammatory response, has been observed to be upregulated with infection propogation. This further supports our understanding of *LdCen1*$^{-/-}$ being able to activate and release pro inflammatory cytokines. Inhibitory clade of serpin known to inhibit cysteine proteases have been found to be upregulated in host cells after 48h of infection. This is reflected in the diminished expression of Cysteine protease C in *Leishmania* amastigotes as the infection progresses. Such global proteome analysis of a mutant parasite itself and its mediated manifestations in host, towards identifying any drift from the usual pathogen induced host conduct, holds great significance in ascertaining its efficacy as a vaccine candidate, and predicting potential markers in future vaccine development strategies for leishmaniasis and other related diseases.

PL4

Novel Curcumin-Folate Conjugates; Targeted Drug Delivery for Cervical Cancer

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Cervical cancer (CaCx) is the most common cancer in women around the world. The incidence and mortality of CaCx in women rank second in low-and middle-income countries including India. The principal etiologic agents that cause cancer of the uterine cervix in women is persistent infection of high-risk Human Pappillomaviruses (HR-HPVs), but HPV alone is not sufficient to cause cancer. Though there are three prophylactic HPV vaccines and also an indigenous Indian HPV vaccine, Cervavac, but no therapeutic vaccine is available. Though more than 110 countries world over introduced HPV vaccine successfully in their national programme but in India in-spite of high annual incidence of cervical cancers and associated deaths, there is no national immunization programme in India for HPV vaccination in women. HR-HPV E6/E7 is responsible for tumorigenic transformation and their expression depends on the availability of host cell transcription factor (AP-1), which binds to the upstream regulatory region (URR) of HR-HPVs and act as a signallingepicentre for cervical cancer. It is also known that a small sub-population (1-2%) of cancer stem cells (CSCs) are responsible for tumor initiation, progression, metastasis, multidrug resistance and cancer relapse even after successful treatment. Current conventional chemotherapy usually results in poor prognosis with low treatment efficacy and severe side effects because of weak targeting specificity and fast elicitation of multidrug resistance.

Thus, novel multidrug codelivery system provides a promising method to improve the clinical outcome of CaCx patients. In this work, we developed a novel triple-conjugate drug for targeted delivery to cancer and cancer stem cells without affecting the normal cells which otherwise cause serious adverse/toxic side effects. Our data shows that HPV16-E6 is found to be differentially upregulated in CSCs and is responsible for maintenance of stemness through upregulation of Hes1, a downstream gene of stemness marker NOTCH1. Overexpression/activation of transcription factor, AP-1 contributes to chemo-radio resistance of CSCs which can be sensitized if FRA-1 (Fos related antigen 1), one of the family proteins of AP-1 is upregulated. A triple-conjugate drug comprising curcumin-folic acid -cancer drug (Doxorubicin) has been synthesized as a non-toxic, small molecular weight, novel drug which will specifically be taken out by the cancer and CSCs via receptor-mediated internalization due to over-expression of high-affinity folate receptor in cancer cells thereby improving the bioavailability and targeted delivery of the drug. While folic acid serves as a targeting ligant, curcumin chemoradiosensitizes the CSCs and also reduces the toxicity and adverse effects thus making the cancer treatment most effective and relapse free. Our *in-vitro* cytotoxicity assays and cellular uptake results revealed that our novel triple-conjugate provide satisfying therapeutic efficacy to improve the treatment outcome of drug resistant cancers. Taken together, the novel Curcumin-Folate and doxorubicin conjugate potentially ensure sensitization of CaCx-CSCs making the cancer treatment most effective.

Diagnostic, Prognostic and Therapeutic Significance of RNA Binding Protein HnRNPD in Head and Neck Cancer

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Our proteomic analysis revealed heterogeneous nuclear ribonucleoprotein D (hnRNPD) overexpression in oral dysplasia as compared with normal mucosa. However, its role in oral carcinogenesis remained unknown. So we determined the hnRNPD associated protein networks and its clinical significance in oral squamous cell carcinoma (OSCC). Immunoprecipitation (IP) followed by tandem mass spectrometry was used to identify the binding partners of hnRNPD in oral cancer cell lines. hnRNPD expression was analyzed in 183 OSCCs, 44 oral dysplasia and 106 normal tissues using immunohistochemistry (IHC) and correlated with clinico-pathological parameters and follow up data over a period of 91 months. Protein-protein interactions of hnRNPD with 14-3-3ζ, hnRNPK and S100A9 were confirmed using co-IP-western blotting. IHC analysis showed significant overexpression of nuclear hnRNPD in oral dysplasia [$p = 0.001$, Odds ratio (OR) = 5.1, 95% CI = 2.1-11.1) and OSCCs ($p = 0.001$, OR = 8.1, 95% CI = 4.5-14.4) in comparison with normal mucosa. OSCC patients showing nuclear hnRNPD overexpression had significantly reduced recurrence free survival [$p = 0.026$, Hazard ratio = 1.95, 95% CI = 1.0-3.5] by Kaplan-Meier survival and Cox-multivariate-regression analyses and has potential to define a high-risk subgroup among OSCC patients with nodal negative disease.

Our findings suggest novel functions of hnRNPD in cellular proliferation and survival, besides RNA splicing and stability in oral cancer. Association of nuclear hnRNPD with poor prognosis in OSCC patients taken together with its associated protein networks in oral cancer warrant future studies designed to explore its potential as a plausible novel target for molecular therapeutics.

PL6

Autophagy-Metabolic axis in Head and Neck Cancer

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Autophagy and metabolic alterations are the key hallmarks of cancer. Due to its continuous proliferation and high-energy demands, cancer cells undertake increased glucose uptake, resulting in the production of enough amount of energy for their replication and survival. While autophagy plays critical role in maintaining cellular homeostasis by breaking down macromolecules and utilizing the metabolites as energy. This allows cells to maintain efficient ATP levels and promote cell survival by recycling macromolecules or dysfunctional organelles. Totally different from the normal cell metabolism, even at aerobic conditions, cancer cells undergo glycolysis rather than oxidative phosphorylation. These glycolytic events in cancer cells elevate the expression of enzymes responsible for glucose metabolism, such as hexokinase, pyruvate kinase, and lactate dehydrogenase-A, c-MET/HGF, FGF/FGFR etc. In addition, increased glucose metabolism in cancer cells leads to the formation of necessary amino acids, lipids, purines, and pyrimidine via the inter-branching biosynthetic pathways such as pentose phosphate pathway, serine biosynthesis, and glutaminolysis. The underlying mechanism of autophagy is regulated by specific genes, primarily known as autophagy-related genes (ATGs). Although autophagy is critical for normal cell maintenance, cancer cells utilize autophagy to eliminate the demanding metabolic stress that is put on the cells allowing them to continue to grow and divide. Cancers with elevated autophagy activity are able to regulate important proliferative signaling pathways, including the PI3K/AKT/mTOR. In general, the cross-talk of autophagy and metabolism lead to the growth and progression, also, induces drug resistance in cancer. Therefore, targeting/modulating autophagy and metabolic switches can be used to develop therapeutic solutions for cancer and to resolve drug resistance problems.

Combination of Reverse Genetics and Biochemical Approaches to Identify Novel Intervention Strategies for Control of Malaria

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Malaria is one of the major infectious diseases transmitted through bite of infectious mosquitoes. Effective treatment options are available to cure clinical cases however, incidences of treatment failure against front-line anti-malarial drugs are hugely worrisome. We have shown that disruption of mutant calcium dependent protein kinase 1 (CDPK1) through CRISPR mediated gene targeting inhibits the parasite growth during asexual as well as sexual stages of parasite development. CDPK1 disrupted parasites show reduced invasion of red blood cells by Plasmodium merozoites and are also deficient in establishing infection in mosquitoes. In the absence of CDPK1, the mutant parasites do not form viable male and female gametes leading to block in the sexual development inside the mosquito. Global transcriptomics of CDPK1 null parasites show increased expression of raf kinase inhibitor protein (RKIP). RKIP is a major regulator of MAPK signalling pathway in multicellular eukaryotes. Interestingly, the classical components of MAPK pathway are not represented in malaria parasite suggesting unconventional role of RKIP in the parasite biology. Biochemical experiments suggest that recombinant CDPK1 and RKIP interact with each other and RKIP regulates the kinase activity of CDPK1. Importantly, here we have shown the interaction of CDPK1 and RKIP inside the parasite through cellbased assays that confirm the existence of the bimolecular complex in the parasite. We have further shown that a specific inhibitor of human RKIP inhibits the asexual growth of malaria parasite in dose dependent manner. Interesting, at low concentrations, the inhibitor increases the interaction of CDPK1 and RKIP suggesting that it locks the interaction of CDPK1 and RKIP perhaps sequestering CDPK1 as an inactive protein. Screening of compounds that can stabilize the interaction of CDPK1 and RKIP represent a novel strategy to target the asexual growth of malaria parasite that may inhibit its replication inside the red blood cells.

PL-8

Neutrophils in Host-tumor Crosstalk: Role in Systemic Detoriation

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Cancer is known to have systemic impact by targeting various organs that ultimately compromises the overall physiology of the host. Several reports have demonstrated the role of neutrophils in cancer wherein the focus has been drawn on the elevated neutrophil count in blood or at tumor loci. However, their role in mediating systemic effects during cancer progression has not been deciphered so far. Therefore, it is worthwhile to explore whether and how neutrophils contribute to systemic deterioration in cancer. To discern their systemic role, we evaluated neutrophil count and function at different stages of tumor growth in Dalton's Lymphoma mice model. Notably, our results displayed a gradual increase in Ly6G+ neutrophils in peripheral blood and their infiltration in vital organs including liver, lungs, spleen, kidney, lymph nodes and peritoneum of tumor bearing host. We showed remarkable alterations in histoarchitecture and serum enzyme levels that aggravated with tumor progression. We next examined neutrophil function by assessing its granular cargoes including neutrophil elastase (NE), myeloperoxidase (MPO), and matrix metalloproteinases (MMP-8 and MMP-9). Interestingly, blood neutrophils of tumor bearing mice exhibited a marked change in morphology with gradual increase in NE and MPO expression with tumor growth. In addition, we observed upregulated expression of NE, MPO, MMP-8 and MMP-9 in the vital organs of tumor bearing host. Taken together, our results demonstrate heightened infiltration and function of neutrophils in vital organs of tumor bearing host which possibly account for gradual systemic deterioration during cancer progression. Our findings thus implicate neutrophils as a potential therapeutic target that may help to reduce the overall fatality rate of cancer.

PL9

Phytochromes and Phytochrome Interacting Factors Regulate Rice Development: from Coleoptile Elongation to Flowering

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Rice is the staple food for more than half of the world population, which is growing fast and demands higher crop yields. To improveplant yield, it is important to better understand the molecular mechanisms underlying plantresponse to light, a key determinant of growth and development. Phytochromes (Phys), the red/far-red light photoreceptors, play an important role in plant architecture, stress tolerance, and productivity, and Phytochrome-Interacting Factors (PIFs) act as central hubs in the integration of external stimuli to regulate plant development (Cordeiro*et al.,* JXB2022). We have producedCRISPR/cas9 knockout mutants for all rice PIFs and Phys andinvestigated how theyare involved in different stages of ricedevelopment. We have, forinstance, shownthat OsPIF15 and OsPIF16 are the main PIFs regulating coleoptile growth in the dark and arealso involved in the regulation of de-etiolation. OsPIL15 and OsPIL16 work together to regulate rice coleoptile elongation and to repress light-induced genes. We have also shown that phyBplays an essential role in the regulation of rice flowering time by the photoperiod through the Evening Complex (EC) (Andrade *et al.,* PNAS2022). Rice mutants in the EC genes *LUX ARRYTHMO (LUX)* and *EARLY FLOWERING3 (ELF3)* paralogs do not flower, as EC directly binds andsuppresses the expression of flowering repressors, including PRR37 and Ghd7. We also demonstrated that light acts via phyB to cause a rapid and sustained post-translational modification of ELF3-1, thus modulating its activity and consequently flowering time. These resultswill be very useful for future breeding programs.

PL10

Molecular Pathogenesis of Polycystic Ovary Syndrome (PCOS)

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An unfavourable metabolic environment may unmask genetic traits of ovarian dysfunction and endocrine derangement which could further aggravate the metabolic disarray leading to hyperandrogenism, anovulation and insulin resistance which lie at the pathophysiological core of PCOS. The hypermethylation of tumor necrosis factor (*TNF*) and the hypomethylation of aldo-keto reductase 1 C3 (*AKR1C3*), calcium-sensing receptor (*CASR*), growth hormone-releasing hormone receptor (*GHRHR*), resistin (*RETN*) and mastermind-like domain 1 (*MAMLD1*) lead to hyperandrogenism, that is crucial for the pathogenesis of PCOS (1). Luteinizing hormone (LH), luteinizing hormone receptor (LHR) and FSHR (follicle stimulating hormone receptor) genes show variants strongly related to PCOS phenotypes (2), causing an impaired oocyte maturation, anovulation and consequent infertility (3). DNA methylome profiling of granulosa cells recently has revealed an altered methylation in genes regulating pivotal ovarian functions in PCOS (1). However, PCOS being multifactorial needs further evaluation of the potential genes/cell signaling cascades involved in the disease pathogenesis for the treatment of the disease.

PL11

Non-steroidal Anti-inflammatory Drugs and Biomarkers: A New Paradigm in Colorectal Cancer

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Colorectal cancer is a sporadic, hereditary, or familial based disease in its origin, caused due to diverse set of mutations in large intestinal epithelial cells. Colorectal cancer (CRC) is a common and deadly disease that accounts for the 4th worldwide highly variable malignancy. For the early detection of CRC, the most common predictive biomarker found endogenously is KRAS and ctDNA/cfDNA along with SEPT9 methylated DNA. Early detection and screening for CRC are necessary and multiple methods can be employed to screen and perform early diagnosis of CRC. Colonoscopy, an invasive method is most prevalent for diagnosing CRC or confirming the positive result as compared to other screening methods whereas several non-invasive techniques such as molecular analysis of breath, urine, blood, and stool can also be performed for early detection. Interestingly, widely used medicines known as non-steroidal anti-inflammatory drugs (NSAIDs) to reduce pain and inflammation have reported chemopreventive impact on gastrointestinal malignancies, especially CRC in several epidemiological and preclinical types of research. NSAID acts by inhibiting two cyclooxygenase enzymes, thereby preventing the synthesis of prostaglandins (PGs) and causing NSAID-induced apoptosis and growth inhibition in CRC cells. This review paper majorly focuses on the diversity of natural and synthetic biomarkers and various techniques for the early detection of CRC. An approach toward current advancement in CRC detection techniques and the role of NSAIDs in CRC chemoprevention has been explored systematically. Several prominent governing mechanisms of the anti-cancer effects of NSAIDs and their synergistic effect with statins for an effective chemopreventive measure have also been discussed in this review paper.

PL12

Setting-up Biotech Tools to Uncover the Molecular Regulation of Cork Development

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Cork oak (Quercus suber) is an very important species from the Fagaceae family, playing a critical role at economic and ecologic levels in Portugal and the Mediterranean area. Cork forests contribute to fight social desertification and the sector contributes to create employment. Cork is sustainably produced and harvested only once every 9 years. It has numerous applications that exploreitselasticity, low density, hydrofobicity, acustic insulation and slow combustibility, among other traits(e.g., cork stoppers, insulating coverings). Portugal leads in cork production and processing. Cork is a protective layer resulting from secondary growth. The phellogen (cork cambium) produces an outer layer -phellem or corkmade up mainly of suberin-rich dead cells. The cork industry is being threatned by climate change and our work has been focusing on developing genomic and biotechnological tools to address the challenges. In this talk we will cover aspects of our initiatives to raise a national effort to develop transcriptomics, genomics and biotech tools, to uncover the molecular regulation of cork development. Furthermore, sincethecorkkey component is suberin (a polymer made of monomersderived from phenolics and fatty acids), we have also characterized related stress-responsive genes.To accelerate our studies, we also exploredother biological modelsusing roots as models. By gathering data from transcriptomic analyses and gene regulatory networks, as well as from histological, physiological and chemical studies, we have demonstrated thatheat and osmotic stresses modulate the initial development and suberization of phellem.Our key goal is to uncover the genetic pathways acting on the cross-talk between cork development and abiotic stress adaptation to be able to screen genotypesfor improved resilience and productivity and thus contribute to establish more resilient production forests.

Decellularized Extracellular Matrix-based Nanoemulgel System for Full-Thickness Wound Healing

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Extracellular matrix (ECM) that has been decellularized has been utilized extensively to treat wounds. When free radical levels are high and biofilm production is taking place at the wound site, however, the ECM was unable to integrate the tissue and restore appropriate function to the tissue. Here, nanoemulgel systems were created using a combinatorial strategy that included goat small intestine submucosa ECM gel and nanotechnology (nanoceria and curcumin nanoemulsion). To improve bioavailability in terms of antibacterial, antioxidant, sustained release, and penetration at the wound site, the curcumin was encapsulated in the nanoemulgel technology. To improve the generated nanoemulgel formulation's antibacterial, antioxidant, and wound-healing qualities, nanoceria was also added. All of the formulations had improved wound healing rates and were porous, hydrophilic, biodegradable, antioxidant, antibacterial, hemocompatible, and biocompatible. The DG-SIS/Ce/NC formulation displayed the better efficacy (DG-SIS/Ce/NC) and demonstrated the highest full-thickness wound contraction (97.33% in 14 days) and the highest collagen synthesis at the wound site (1.61 g/mg in 14 days), as well as the highest free radical scavenging capacity and antibacterial property. Curcumin release was prolonged (62.9% in 96 h), and skin permeability was increased (79.7% in 96 h). The study's findings indicated that the formulation (DG-SIS/Ce/NC) might be used as a nanoemulgel system for full-thickness wound healing.

PL14

Genome Disparities in Pathogens: Implications for Global Health and Policy - A Case Study of Mycobacterium Tuberculosis

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Genomic sequence databases of pathogens are a valuable resource for developing diagnostics and therapeutics. However, the usefulness of these databases is significantly impacted by disparities in their content. One such disparity is the underrepresentation of countries with a high disease burden. Therefore, it is essential to quantitatively measure these disparities to fully utilize the potential of the information in genomic databases.

To develop and validate an indicator for evaluating Geographical disparity

In this study, we aimed to address the issue of geographical disparities in genomic sequence databases of pathogens, which can impact the development of diagnostics and therapeutics. To achieve this, we introduced a novel indicator called the Genome Disparity Index (GDI), which quantitatively measures the number of genomes sequenced per infected individual for a given country. The GDI is calculated using the number of sequenced genomes available in the public domain (Gid) and the number of active and relapsed cases (Nid) for a specific disease in a particular country. It is calculated as:

Genome Disparity Index (〖GDI〗 _id)=G_id/N_id

For disease d in country i, Gid is the number of sequenced genomes available in the public domain, and Nid is the number of active and relapsed cases.

To validate the effectiveness of our GDI, we chose Mycobacterium tuberculosis as our test case. We gathered data from publicly available sources, such as the NCBI biosamples and WHO TB report, on November 1, 2022. We then developed a Python script to parse the XML-formatted biosamples file.

The Genome Disparity Index (GDI) measures geographical bias in genomic data to identify regions where more genomic data is required. The GDI was used to divide countries into four quadrants, based on the availability of genomic data and the reported cases of Mycobacterium tuberculosis. The first quadrant (Portents) contains countries with low reported cases and sequenced genomes, which may be at risk of a future outbreak. The second quadrant (Challengers) contains countries with a high burden of tuberculosis but limited availability of genomic data. The third quadrant (Leaders) contains countries with high reported cases and a substantial number of sequenced genomes. Finally, the fourth quadrant (Explorers) contains countries with high availability of genomic data, but a low burden of tuberculosis. The GDI provides a tool for tracking progress in addressing geographical bias in genomic data, and ensuring all regions have access to information needed to develop medical solutions for infectious diseases.

To sum up, the Genomic Disparity Index (GDI) introduced in this study provides a novel approach to measure the gap between expected and observed numbers of sequenced genomes for each country based on its population size and disease burden. The variation in genomic representation for Mycobacterium tuberculosis genomes across countries highlights the need for more effective policies and research programs to combat tuberculosis. The GDI is a valuable tool that can guide countries in maximizing the benefits derived from genome sequences in combating various diseases and can be extended to other pathogens or diseases that have genomic data available. However, there is a need to improve the GDI by incorporating more relevant parameters to capture multiple factors that influence the spread/outbreak of diseases. Overall, genome sequencing is a powerful tool for studying TB and holds great promise for improving the diagnosis, treatment, and prevention of this deadly disease.

Invited Lectures

(IL)

IL1

Utilizing the Immunoporotic Potential of Bregs under Inflammatory Bone Loss in Osteoporosis: *Bench-to-Bedside*

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Our group established the field of "Immunoporosis” i.e. Immunology of Osteoporosis to unravel the pivotal role of immune system in the pathophysiology of osteoporosis. In continuation, recently, our group has discovered the inhibitory role of regulatory B cells (Bregs) on osteoclastogenesis and in ameliorating inflammatory bone loss under postmenopausal osteoporosis (PMO). Recent studies highlighted that Gut microbiota (GM) has a very crucial role in shaping the development of Bregs. In addition, our group along with others has demonstrated that dysbiosis of the GM may be one of the contributing factors to the pathogenesis of inflammatory bone loss diseases including osteoporosis. However, whether dysbiosis of GM influences the function of the Bregs in osteoporosis remains unknown.

In the present study, we elucidated the nexus between GM and Bregs in osteoporosis. Further, we interrogated the immunoporotic potential of candidate bacterial species and their metabolites that would enhance bone health under physiological conditions such as osteoporosis. To determine the same, firstly, we employed 16S ribosomal RNA (rRNA) gene sequencing to screen the candidate bacteria that might be associated with the estrogen deficiency-induced bone loss in the osteoporotic mice model. Our in-depth data analysis revealed that *Bifidobacterium longum* (BL) is the candidate bacteria, and its deficiency might be promoting inflammatory bone loss in osteoporosis. *Bifidobacterium* species are known to produce indole derivatives. Surprisingly, our metabolomic analysis too revealed a significant reduction in the levels of indole-3-lactic acid (ILA) in the serum of osteoporotic mice model in comparison to the control group, thereby pointing towards the role of BL in bone loss under estrogen deficient conditions. Moreover, we observed that levels of ILA were found to be negatively correlated with the bone mineral density (BMD) and Bregs (CD19+IL-10+) population in osteoporosis. Moving ahead in our study, we tested whether the transplantation/administration of BL or its indole derivate (ILA) could rescue the observed inflammatory bone loss in a pre-clinical mice model of osteoporosis (Ovx). For the same, we carried out *in vivo* studies and analyzed various osteo-immune parameters via several cutting-edge technologies such as SEM, AFM, µCT, FACS, and ELISA. Interestingly, we observed that administration of BL (109 CFU) and ILA (50 mg/kg) prevented inflammatory bone loss in osteoporosis, assessed by enhanced bone mineral density and bone micro-architecture in the Ovx groups treated with BL and ILA. Of note, our flow cytometry data demonstrated that administration of BL and ILA significantly enhanced Bregs population along with its tendency to produce IL-10 cytokine via the aryl hydrocarbon (AhR) receptor.

The present study thus for the first time highlights the potential of BL and its metabolite i.e. ILA as a novel osteoprotective agent in the treatment and management of bone-related diseases including osteoporosis.

IL2

Non-ionizing Electromagnetic Radiation and Human Health

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The increasing penetrance of non-ionizing radiation both through medical diagnostic or environmental sources in the population is becoming a major epidemiological concern world-wide and the mechanisms how non-ionizing radiation act and the potential long-term health consequences need to be thoroughly investigated. Since the immune system promotes internal protection and promotes continued health and survival, interactions between the immune system and the reproductive system are of particular interest because the reproductive system is distinct in that its primary function is to ensure the continuity of the species. Although several studies have been published on the health effects of RFR but no satisfactory agreement has been reached.

The aim of this study was to determine whether exposure to Non-ionizing electromagnetic radiation emitted from mobile phone would affect the innate immune responses and reproductive health in the cell specific manner.

Cells were exposed to Non-ionizing electromagnetic radiation for different time durations in controlled manner. After irradiation, cells were processed for various functional assays.

The non-ionizing electromagnetic radiation significantly induced apoptosis and reactive oxygen species production, as compared to the control. Unlike this, the non-ionizing electromagnetic radiation reduced the phagocytic activity in cells. Furthermore, alteration in the levels of proinflammatory cytokines, Nf-kB, cell cycle kinetics was observed. DNA damage increased insignificantly with longer exposure duration. Cell viability did not affected significantly. The data indicated modulatory role of non-ionizing electromagnetic radiation.

IL3

SPAG9: A Novel Therapeutic Potential Target in Ovarian Cancer

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SPAG9 is a novel tumor associated antigen, expressed in variety of malignancies. However, its role in ovarian cancer remains unexplored. SPAG9 expression was validated in ovarian cancer cells by real time PCR and Western blot. SPAG9 involvement in cell cycle, DNA damage, apoptosis, paclitaxel sensitivity and epithelial- mesenchymal transition (EMT) was investigated employing RNA interference approach. Combinatorial effect of SPAG9 ablation and paclitaxel treatment was evaluated in *in vitro*.Quantitative PCR and Western blot analysis revealed SPAG9 expression in A10, SKOV-3 and Caov3 compared to normal ovarian epithelial cells. SPAG9 ablation resulted in reduced cellular proliferation, colony forming ability and enhanced cytotoxicity of chemotherapeutic agent paclitaxel. Effect of ablation of SPAG9 on cell cycle revealed S phase arrest and showed decreased expression of CDK1, CDK2, CDK4, CDK6, cyclin B1, cyclin D1, cyclin E and increased expression of tumor suppressor p21. Ablation of SPAG9 also resulted in increased apoptosis with increased expression of various pro- apoptotic molecules including BAD, BID, PUMA, caspase 3, caspase 7, caspase 8 and cytochrome C. Decreased expression of mesenchymal markers and increased expression of epithelial markers was found in SPAG9 ablated cells. Combinatorial effect of SPAG9 ablation and paclitaxel treatment was evaluated in *in vitro* assays which showed that ablation of SPAG9 resulted in increased paclitaxel sensitivity and caused enhanced cell death. *In vivo* ovarian cancer xenograft studies showed that ablation of SPAG9 resulted in significant reduction in tumor growth. Present study revealed therapeutic potential of SPAG9 in ovarian cancer.

IL4

Prediction of Numbers and Concentration of Alternative Splicing based Transcriptional Biomarkers using RNA-Seq Data

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AS plays a pivotal role in complex genomes. Based on AS events and by utilizing information of associated meta-features, we have developed a pipeline, Finding Alternative Splicing Events (FASE), as the R package (https://github.com/harshsharma-cb/FASE). FASE provides a comprehensive method for analyzing RNA-sequencing data, predicting the transcript structures expressed in different conditions, and estimating transcript concentration. Hence, FASE can target novel transcript structure/s expressed in given conditions which are otherwise missed in transcript-level analysis.FASE focuses on precision and accuracy of results by minimizing the false positives. It accepts data as the input in multiple formats and generates robust and reproducible results. We validated prediction of FASE using RT-PCR. Moreover, FASE can be applied selectively from a single gene to simple or complex genome even in multiple experimental conditions for the identification of differential AS-based biomarkers, prognostic targets and novel therapeutics.

IL5

New Breast Cancer Hotspot Mutation *of ANKLE1* and Its Direct Role in DNA Damage and Repair in Mammalian Cells

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Breast cancer is one of the leading Cancers in India and has replaced cervical cancer as being the most common and having the highest mortality among women in India. DNA damage and repair is very critical process regarding *ANKLE1* is the human orthologous of LEM-3 and is involved in DNA damage response and DNA repair. *ANKLE* gene is conserved among organisms during evolutionary succession and is a member of LEM family proteins in lower metazoans and is involved in critical functions in the nuclear architecture, gene expression and cell signalling. Whole Exome Sequencing (WES) of paired breast cancer samples was performed and *ANKLE1* was found to be a new possible hotspot for predisposition of breast cancer. The mass array genotyping for breast cancer variant rs2363956 further confirmed the *ANKLE1* association with the studied population of breast cancer. To elucidate the role of *ANKLE1* in DNA damage, it was knocked down in MCF-7 breast cancer cell line and the expression of γH2AX was assessed. *ANKLE1* knockdown cells displayed elevated levels of γ-H2AX foci in response to the cisplatin induced replication stress. The localization pattern of *ANKLE1* further emphasized the role of *ANKLE1* in DNA repair process. We observed that *ANKLE1* is required for maintaining genomic stability and plays a role in DNA damage and repair process. These findings provided a molecular basis for the suspected role of *ANKLE1* in human breast cancer and suggested an important role of this gene in controlling breast cancer development among women in India.

IL6

Phytohormones Mediated Defense Mechanisms under Different Environmental Stress Regimes

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With the epoch of climatic perturbations, numerous unprecedented threats to agricultural systems have been encountered globally. The abiotic stresses either in isolation and/or in combination induce numerous adverse reactions in plants and impair growth, and physiological and metabolic processes, which in turn evokes productivity loss and yield penalty. This created an immense concern for fulfilling the sustainable development goals (SDGs) pertaining to food and nutritional security for the ever-increasing world population. These situations critically emphasize underpinning the plant hormonal responses and crosstalk under abiotic stresses from the perspective of past, present and future significance. To unlock the significance of plant hormone(s) and its cross-talk with other plant growth regulators (PGRs) under different and environmentally challenged scenarios. In addition, our team objectifies the exploration of newly discovered plant signaling molecules. We have reported potential interactions between the stress-responsive plant hormones including salicylic acid (SA), abscisic acid (ABA) and ethylene to converge the target points in facilitating abiotic stress tolerance. Studies conducted in the context of these plant hormones have revealed the antagonistic actions of SA with ABA and ethylene formation to mediate plant stress tolerance. At growth and physiological grading, the induction of SA, ethylene and ABA has been found to be involved in mediating antioxidant potential, osmolyte production, photosynthesis through curbing glucose sensitivity (a photosynthesis repressor), nutrient homeostasis, stomatal behavior and source-sink dynamics to arrest the oxidative stress-induced senescence and programmed cell death (PCD). Further, ethylene actions have been authenticated to support the glutathione pool, and it has been reported that cysteine being a common precursor for the synthesis of these molecules, serves as a focal cross-link between these two entities. A positive feedback response has also been established between nutrients including selenium and sulfur influencing ethylene evolution to alleviate abiotic stress-induced adversities. In addition, using the augmented and high-throughput characterization of green-synthesized nanoparticles (NPs), we have also validated the proximity of NPs-induced coping effects under stressful cues with ABA-mediated stomatal closure to enhance plant resource utilization and stress adaptability. These mechanistic responses and functional attributes have been comprehensively explored with non-redundant phenotypic blueprints owing to plant growth and developmental processes. These outcomes have been substantiated with the plant hormone(s) analogs, biosynthesis, and action inhibitors to corroborate with abiotic stress-triggered hormonal regulation governing underlying responses. To date, we have elucidated the mechanistic actions of plant hormones in imparting a potential stress management tool with protective mechanism(s) and feasible strategies to attenuate phytotoxic impacts during the juvenile-to-maturity transition phase based on metabolic networks, plant ontology, and longevity.

IL7

Targeting GSK-3β for the development of potential Therapeutics against Neurodegenerative Diseases

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Neurodegenerative diseases are a major threat to global health. These disorders currently have no effective treatment options and therapeutic intervention is required to develop effective drugs to prevent and combat these disorders. It is fatal when these conditions cause central nervous system cells to malfunction and severely deteriorate the brain activity of the patients. Despite the diversity and complexity of neurodegenerative diseases, they have similar molecular signalling pathways and, therefore, similar treatment options can be developed which target the root cause. Glycogen synthase kinase-3 (GSK-3) is a highly conserved serine-threonine protein kinase enzyme which has been implicated in a pivotal role in several different biological processes affecting the survival of neurons & behavioral regulation. Various biological functions, including cell division, proliferation, adhesion, and differentiation are regulated by GSK-3 enzyme. Unregulated functioning of GSK-3 enzyme is linked to different neurological disorders including Parkinson's disease (PD), Alzheimer's disease (AD), bipolar disorder (BPD), type 2 diabetes, and cancer. GSK-3α and GSK-3β are two isoforms that have similar regulation but are expressed by separate genes. Both isoforms are highly expressed in the cerebellum, cerebral cortex and hippocampus regions of the Brain. Nevertheless, GSK-3β is more highly expressed than the other isoforms. Emotion, mood, social abilities, and schizophrenia-like behaviours have all been shown to be affected by changes in GSK-3 activity (either excessive activation or inhibition).

Research Studies have shown that GSK-3 affects three signaling pathways in neurodegenerative disorders which include mitochondrial dysfunction, the autophagy axis/mammalian target of rapamycin (mTOR), and cytoskeleton organization. Inhibiting GSK-3 activity is a potential strategy for treating neurodegenerative and psychiatric illnesses. A master growth regulator, mTORC1 is activated by nutrition and growth hormones to increase the synthesis of cellular proteins and alter the level of nucleic acids and lipids. Our research investigations have found out some crucial lead molecules against GSK-3β in Alzheimer’s disease wherein the repurposing and pharmacophore modelling of anti-cancerous drugs was done to develop some novel conformers followed by computational biology approaches to estimate their binding affinity, key residues involved in interaction and structural stability of these conformers. RMSD and RMSF values have shown good binding between these ligands and GSK-3β, prominent Hydrogen bond interactions wherein the RMSD of bound ligand and GSK-3β enzyme were obtained in the range of 2.4Å to 2.6Å. We propose novel potential drug ligands against Glycogen synthase kinase-3 (GSK-3) beta enzyme based on our research studies to develop effective therapeutics against Alzheimer's disease.

IL8

ARMOUR for Plant Development and Response to Stress

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The microRNAs (miRNAs) comprise a novel class of regulatory species that have added a new dimension to the genetic management module within living cells.The regulatory action of the miRNAs is typically inhibitory in nature and itmay operate at both transcriptional and post-transcriptional levels. The miRNAs are involved in regulating the vital and specialized aspects of plant biology including growth of cells, development of organisms and maintaining the integrity of genomes. The development programming of plants is greatly influenced by a wide range of environmental factors. Among these increasing temperatures and soil salinity have emerged as the primary cause for limiting rice production. The stresses are normally multigenic in nature so, it is important to understand the genetic machinery that is activated in response to stress. To explore the role of miRNA networks involved in orchestrating plant development under normal and stressed environments, we adopted the approach of deep sequencing several small RNA libraries of endogenous (indica) rice varieties. During the analysis of sequencing data we identified several known and novel miRNAs and captured their expression patterns. This data was compiled and developed as a web server, ARMOUR, which is now being used to select miRNAs for functional analysis.

IL9

A Proteomics Approach to Find Novel Therapeutic Targets for Allergic Diseases by Deciphering the Spatial and Temporal Regulation of Protein Traffic in Mast Cells during Allergen Challenge

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Due to changing lifestyles and increase in pollution allergic diseases are increasing in developing countries like India. Around 20-30% of Indians suffer from allergic ailments. Allergies are incurable and only options are strict avoidance of allergens or continuous medication, which can be expensive and also have undesired side effects. Other than interfering with normal functioning, in severe cases such hypersensitivities can also lead to life threatening anaphylactic shock. Hence, it is imperative to look for affordable novel common therapeutics for allergic diseases. This will be possible if we explore in detail and identify the important pathways involved in release of inflammatory mediators like histamine during an allergic response. Mast cells are innate immune tissue resident cells that release various inflammatory mediators like cytokines, and histamine upon allergen activation. Our previous work revealed that Synaptosomal-associated protein of 23 kDa (SNAP-23) is a t-SNARE present in mast cells, which plays a major role during mast cell exocytosis. Our recent cellular and molecular studies have revealed a very interesting dynamicity of SNAP-23 in terms of intracellular localization and phosphorylation that has a tremendous role in mast cells exocytosis and can be targeted as a potential therapy against allergy. With this aim we are targeting to unravel by a proteomic approach, the SNAP-23 post-translational modification dependent protein traffic pathways involved in the release of inflammatory mediators from mast cells; that are the root cause of all the nasty allergy symptoms. We would then try to discover affordable and specific drugs for this disease, by targeting these proteins and their specific interactions.

IL10

Deploying a Rhizospheric Microbes to Abiotic Stress Tolerance in Finger Millet

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Recent climate changes are expected to cause more frequent and severe drought affecting major field crops.Finger millet (*Eleusine coracana* L.) is an arid crop having soils with poor water holding capacity. Therefore, it is difficult for the plants to obtain water and mineral nutrients from such soil to sustain life. Like other cultivated field crops millets have a symbiotic association with the arbuscular mycorrhizal fungi (AMF) which is present in rhizosphere of these crops. Members of these classes of fungi have been found to be colonizing roots and forming an association with field crops for mutual benefits of both the partners. This symbiosis is known to help the plant to tolerate drought with the positive effects on plant growth. To understand the role of mycorrhizal symbiosis in water and mineral up-take from the soil, we studied the role of *Rhizophagusintraradices* colonization and its beneficial role for drought stress tolerance in finger millet seedlings. Our studies provide an overview of possible biochemical and genetic mechanism involved in AMF assisted drought tolerance in finger millet. The improved water and nutrient absorption with the help of extraradical hyphal growth of AMF is one the important factor in helping plants to avoid the ill effects of drought. Along with this, by increased concentration of many biomolecules like amino acids, polyamines, hormones ; osmotic adjustment with the help of total soluble sugar (TSS), proline, ascorbic acid, and removing reactive oxygen species through antioxidant enzymes and antioxidants; AMF helps plant to reduce the effects of drought. Besides this, the results of some studies have given new exciting genetic perspectives including cellular water transport by mycorrhized roots.

IL11

Inflammatory and Deleterious Role of Gut Microbiota-Derived Trimethylamine on Colon Cells

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Trimethylamine (TMA) is produced by the intestinal microbiota as a by-product of metabolism of dietary precursors. TMA has been implicated in various chronic health conditions. However, the effect of TMA in the colon and the underlying mechanism was not clear. In this study, TMA exhibited toxic effects in vitro as well as in vivo. TMA-induced oxidative stress causes DNA damage, and compromised cell membrane integrity leading to the release of LDH outside the cells which ultimately leads to cell death. Besides, TMA also exhibited pronounced increase in cell cycle arrest at G2/M phase in both HCT116 and HT29 cell lines. TMA was found to be genotoxic and cytotoxic as the TMA concentration increased from 0.15 mM. A decreased ATP intracellular content was observed after 24 h, 48 h, and 72 h treatment in a time and dose-dependent manner. For in vivo research, TMA (100 mM, i.p. and intra-rectal) once a week for 12 weeks caused significant changes in cellular morphology of colon and rectum epithelium as assessed by H & E staining. TMA also significantly increased the infiltration of inflammatory cells in the colon and rectal epithelium indicating the severity of inflammation. In addition, TMA caused extensive mucosal damage and distortion in the epithelium, decrease in length of small intestine compared to control mice. In conclusion, these results highlight the detrimental effects of TMA in the colon and rectal epithelium.

IL12

Enhanced Generation and Characterization of Dengue Viral-Like Particles

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Viral-like particles (VLPs) due to their non-infectious and high immunogenic properties have important biomedical applications in diagnostics, drug delivery, and vaccine production. They also serve as an attractive model system to study virus assembly and fusion processes. Dengue virus (DENV) is not very efficient in the production of VLPs on the expression of DENV structural proteins. Our goal was to find elements that would promote the production of particles. It is known that stem region and transmembrane region (TM) of G protein of Vesicular Stomatitis virus (VSV) alone are sufficient for budding. We generated chimeric VLPs replacing regions of stem and transmembrane domain (STEM) or only transmembrane domain (TM) of Envelop (E) protein of DENV-2 with corresponding regions of VSV G protein. Both chimeric proteins secreted VLPs at higher levels than the wild type (2-4 folds) without any significant change in the expression in the cell. They were also found to interact with dengue-infected patient sera effectively thus implying that their antigenic determinants are preserved. In addition, they were able to bind to its putative receptor, heparin with similar affinity as the parent counterpart thus retaining its functional property. However, cell-cell fusion revealed that there is no significant increase in the fusion ability of chimeras as compared to the parent clone, whereas VSV G protein displayed high cell-cell fusion activity. Moreover, we found that co-transfection with capsid protein promoted VLP production. Overall, this study suggests that chimeric dengue VLPs can be taken forward for their likely potential as vaccine production and serodiagnosis.

Probiotic Bacteria as Vitamin Biofactories- Biotechnological Approaches to Combat Micronutrient Deficiencies

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Vitamins are important micronutrients that are often precursors to enzymes, which all living cells require to perform biochemical reactions. Yet, as most vitamins are not produced by humans, they must be taken from outside sources. The use of vitamin-producing microbes could be an environmentally friendly and commercially viable alternative to the chemical synthesis of pseudovitamins, permitting the development of foods with higher vitamin levels that could lessen adverse side effects. Probiotic bacteria can de novo synthesise and provide the human body with vitamins, as can commensal bacteria like *Lactobacillus* and *Bifidobacterium* that are naturally present in the human gut. In humans, the majority of the water-soluble B vitamins, including cobalamin, folates, pyridoxine, riboflavin, and thiamine, are also produced by the gut flora. However, the growing micronutrient deficiencies in humans has instilled the desire to explore and harness natural processes of the microbes to fulfil the human needs. Vitamin producing lactic acid bacteria (LAB) attracted much attention of researchers to enhance level and bioavailability of vitamins in the food. We investigated the ability of riboflavin producing lab. isolates *L. plantarum* strains (MTCC 25432, 25433, and 25434) to improve riboflavin content in yogurt and techno-functional feasibility thereof. The strains used were isolated and characterized on the basis of riboflavin production ability and probiotic properties, optimized for enhanced vitamin production, evaluated for safety and preparation of riboflavin enriched food products.

Oral Presentations

(OP)

OP-01

C-Reactive Protein as a Prognostic Marker in Coronavirus Disease-2019

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Coronavirus disease-2019 (COVID-19) is a recently emerged viral disease, for which currently no definitive treatment. It is, therefore, necessary to determine biomarkers to know the extent of disease severity so that timely action can be taken to reduce mortality. We aimed to determine the usefulness of C-reactive protein (CRP) levels in assessing COVID-19 disease severity and correlate them with mortality due to the same.The objective of the study was to determine the potential role of CRP in outcome prediction of patients with COVID-19.Data for COVID-19 were retrospectively collected and analyzed from May 2020 to October 2020. The CRP value was correlated with disease severity using Karl Pearson's correlation coefficient. A logistic regression model was adopted to analyze the association between mortality and related factors. Out of 642 patients enrolled, 22 died while 620 recovered. Most of the non-survivors were male. Multivariate analysis showed that age, diabetes, hypertension, and CRP values were significantly associated with mortality. CRP showed a strong positive correlation with disease severity and, hence, mortality.In patients with COVID-19, CRP correlated with disease severity and tended to be a good predictor of adverse outcome.

OP-02

Transcription Activator-Like Effector Nucleases (TALENs) based Genome Editing for Increased Fruit Size of Tomato

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Numerous studies have been focusing on wild types tomato plants with increased fruit size, considering its positive effects of fruits on the visual and functional properties. Wild type tomato has all the necessary features like enhanced nutritional content, vitamin C content, high lycopene content etc. In this regard, the genome editing tools such as Transcription Activator-Like Effector Nucleases (TALENs), which is a highly specific and highly efficient technology that can be exploited to explore the genetic resources for the improvement of tomato fruits. Objective is to increase the fruit size of wild type tomato using Transcription Activator-Like Effector Nucleases (TALENs) based genome editing.

Transcription Activator-Like Effector Nucleases (TALENs) based knockout of Clavata and Wushel genes to increase fruit size.

Transcription Activator-Like Effector Nucleases (TALENs) vectors and plant transformation system to increase wild-type tomato fruit size was developed. Transcription Activator-Like Effector Nucleases (TALENs) vectors and plant transformation system can be effectively used for increasing the fruit size of wild-type tomato.

OP-03

Genome-Wide Identification and Characterization of NADPH-Dependent Thioredoxin Reductases from *Brassica Juncea*

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Nitric oxide-dependent cell signaling is mainly mediated by S-nitrosylation/ denitrosylation, a well-known post-translational modification switch. Other than S-nitrosoglutathione reductase, thioredoxin (TRX)–thioredoxin reductase (NTR) is also considered a crucial enzymatic system involved in the mechanism of denitrosylation plants. TRXs are small thioldisulfide oxidoreductases that also act as transnitrosylases in a cell. Protein-SNOs are denitrosylated by reduced TRXs resulting in the formation of TRX-NO, that are in turn converted back to its oxidized form again by releasing NO/HNO. NTR regulates denitrosylation by reducing thioredoxins in the presence of NADPH as cofactor. There are three types of NTRs present in the plants viz. NTRA (cytosolic), NTRB (mitochondrial) and NTRC (plastid). The present study was aimed to systematically identify and analyze NTR genes in *B. juncea*. Genome-wide identification and syntenic relationship showed the presence of a total of 12 NTR (4 each of NTRA, NTRB, and NTRC) genes in *B. juncea* were attributed to whole genome triplication (WGT) and tandem duplications. The phylogenetic analysis revealed clustering *B. juncea*NTRs with their Arabidopsis homologs suggesting high sequence similarity within groups. Multiple sequence alignment and domain analysis of BjNTRs showed the variation among BjNTRs were mainly because of variations outside NTR domain. As expected, BjNTRCs contained TRX domain at C-terminal along with the NTR domain. Cis-regulatory elements analysis in the promoter region using PlantCARE database suggested the regulation of denitrosylases by light, phytohormones and environmental stresses. These outcomes were validated by performing total NTR activity assays. Etiolated seedlings showed a 10.3% increase in NTR activity in comparison with light-grown seedlings. Phytohormone treatment showed a reduction of 60 % (auxin) and 55% (abscisic acid) in NTR activity. Low temperature and dehydration stress showed 30% reduction and 36.4 % increase in NTR activity, respectively. The present work provides an understanding of the evolution and functional analysis of multiple copies of NTR genes and suggested the involvement of NTRs in plant growth and stress responsiveness in *B. juncea*.

OP-04

Influence of RFR emitted from Cell Phone on Common Mental Disorders of North Indian Population

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The wireless technology has been introduced without fully establishing its safety. The objective of the study is to find out the clear association based on research; in the present investigation first time the efforts have been made to study the effect of RFR emitted from cell phone on CMD of North Indian population.

Healthy male volunteers age from 18-45 years after fulfilling the exclusion and inclusion criteria in Delhi-NCR have been included in this study and were divided under six categories-based duration of exposure. The demographic, lifestyle profiles and CMD criteria’s of all the subjects were recorded through a prescribed proforma in questionnaires form.

The 1170 subjects have been enrolled. Though majority of both male and female subjects enrolled under moderate and heavily exposed groups were charging their cell phone twice in a day but percentage is higher under heavy exposed group both in male and female subjects. Almost 100% enrolled subjects of both male (99%) and female (100%) under heavily exposed groups and around 53-54% male and female subject under moderately exposed groups reported more than 8 CMD scores. More than 70% male and 66% female subjects under heavily exposed group reported somatic symptoms whereas more than 64% female subjects under heavily exposed group reported anxiety and depression in comparison to 50.86% male

subjects under this category. 59.75% male subjects under moderately exposed group reported anxiety and depression. More than 70% heavily exposed female subjects reported Cognitive Items in comparison to 50% male subjects under this category. The association was significantly high (p=0.001) between in moderately exposed male subjects taking coffee and CMD. The study showed an association between CMD and heavy cell phone users which are also linked with lifestyle factors and this association are synergistically enhancing the adverse effect of RFR on CMD in highly exposed group.

OP-05

Crispr/Cas9 Mediated Gene Editing against Powdery Mildew Disease to Mimic Natural Ol-2 Mutation in Solanum Lycopersicum

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Powdery Mildew (PM) disease caused by fungus *Oidium neolycopersici*affects both field-grown and greenhouse tomato crops. PM infection can be prevented by selective inhibition of Mildew Resistance Locus O genes (SlMLO) that expresses the heptahelical transmembrane domains serving as receptors for fungal infections. *Solanum lycopersicum* var. *cerasiforme* contains a 19 base pair natural loss-of-function mutation in SlMLO1 gene locus (ol-2 mutants) that confers PM resistance. Introgression of resistance genes to susceptible varieties through breeding can introduce resistance but this is a labor-intensive process and is limited by linkage-drag. CRISPR/Cas9 technique, however, provides rapid and precise editing at the target gene locus. In this study, CRISPR/Cas9 technique used to determine the efficiency and specificity of deletion that replicates the ol-2 mutation present in wild tomatoes. CRISPOR web-based tool used to design 35 potential guide RNAs (gRNAs) against the SlMLO1 locus. To maximize on-target specificity and to minimize the off-target cleavage, top five gRNAs were selected based on the MIT specificity score, proximity to the 19 bp natural ol-2 mutation, gRNA secondary structure, and the least free energy. These gRNAs were later employed to introduce deletions identical to natural ol-2 mutants in tomatoes for conferring resistance against PM disease.

OP-6

Candida Rugosa Lipase Immobilization on Biopolymer-based Nano Gel and Its Morphological Characterization

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A versatile approach to entrap relatively small enzymes in hydrogels allows their diverse biotechnological applications. Nanogels of controlled composition, structure, size, and shape characteristics have raised widespread interest due to their unique engineered properties and technological functions. Molecular self-assembly is a rapid and simple method for fabricating nanosized materials with novel supramolecular architectures and various biological applications. Self-assembly of amphiphilic polymers in selective solvents is one of the most important techniques in materials science due to its potential to produce well-defined particles with various ordered structures, which depend on the chemical structure of the polymers as well as the self-assembly conditions such as pH, temperature, and ion concentrations. To prepare biopolymer- based nano gel for efficient immobilization of Candida rugosa lipase.

We have prepared alginate nanoparticles in the aqueous phase of water-in-oil (W/O) nanoemulsions. This method allows the preparation of finely dispersed emulsions without a large input of mechanical energy, with alginate concentrations of 2 wt. % in the aqueous phase, emulsions showed good stability and narrow, monomodal distributions of droplets with radii ~112 nm. Gelation of the alginate was induced by the addition of aqueous salt solution of various Fe+3 to the emulsions under stirring, and particles formed were collected using a simple procedure. The final particles were characterized using scanning electron microscopy (SEM) and dynamic light scattering (DLS). These methos are used for preparation of biocompatible nanoparticles has been further exploited for the encapsulation of sensitive biomacromolecules i.e., lipase enzyme from Candida rugosa. In addition, the morphological characteristics of alginate nano gels have been studied and compared.

The nano gel showed elongated-rice shaped morphology, and size varied from 100-112 nm. An efficient support matrix for the encapsulation of lipase enzyme from Candida rugosa is prepared with enhanced enzyme activity, thermal stability, and reusability. Conclusions: This research demonstrates the potential application of a new nano-encapsulation method employed to enhance the stability, biocompatibility and bioavailability of bioactive molecules for biotechnological applications.

OP-07

Eco-friendly Synthesis, Characterization, and Application of Silver-copper Bimetallic Nanoparticles

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Bimetallic nanoparticles are nanoparticles made up of two different types of metal elements in the nanoscale range (1-100nm). They possess unique characteristics and properties which differ from the individual components thereby, making them useful for application in various fields including biomedical fields. As such, this paper aims to describe an eco-friendly method for synthesizing silver-copper bimetallic nanoparticles using domestic/industrial waste of orange (citrus Aurantium Dulcis) peel extract as the reducing and stabilizing agent. The synthesized bimetallic nanoparticles were characterized using various characterization techniques including UV-Vis, DLS, FTIR, FESEM, and XRD. Due to the synergy that exists between the two metals, the bimetallic nanoparticles have been found to exhibit good catalytic activity. The objective of this paper is to synthesize bimetallic nanoparticles using domestic waste, characterize and study the catalytic activity of the synthesized bimetallic nanoparticles.

Extract preparation: Orange peels were obtained domestically. The peels were washed and dried in a hot-air oven at 70-80 Â°C. The peels were then crushed to powder using a mortar and pestle. 1g of the orange peel powder was added to 25 ml of double distilled water and boiled for 3-4 minutes. The solution was allowed to cool down and filtered with Whatman's filter paper. The extract was collected and stored at 4Â°C for further use. Synthesis: In a typical experiment, 10ml of the extract was added to 90ml of 5mM of AgNO3 and CuSO4.5H2O on a ratio of 1:9. The mixture was heated on a heating mantle at 80-90Â°C for 30-40mins. A visible color change was observed.

A constant dark color was observed even after heating for 1hr, suggesting the formation of bimetallic nanoparticles. UV-Vis, FTIR, FESEM, EDX, and XRD were used to characterize the bimetallic nanoparticles. The bimetallic nanoparticle was also tested for catalytic activity and was found that the bimetallic possesses good activity.Bimetallic nanoparticles have shown remarkable properties which can be used for industrial application.

OP-08

Molecular Aspects of Arsenic-Iron Give-and-Take to Alleviate Arsenic Stress in Rice

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Arsenic (As) is a significant environmental element that restricts the growth and production of rice plants. Its toxicity, propensity for bioaccumulation, and protracted persistence in the ecosystem has emerged as a severe environmental issue on a global scale. Rice is a suitable target for as, due to its bioavailability in paddy soils. There is evidence that the as speciation and mobility in the environment are affected by the presence of certain minerals. Among them, using iron (Fe) to reduce as toxicity has received a lot of attention. Although the significance of Fe in rice's ability to sequester as is well understood, the molecular mechanism underlying As-Fe interaction is yet unknown.The present study focused on WRKY Transcription factors (TFs) and their interaction with MAPK in As-exposed seedlings, for a better understanding of the molecular aspects of As-Fe give-and-take.

We performed in-silico gene expression analysis of the WRKY Transcription factor gene family and analyzed their expression. Additionally, mRNA levels of MAPK genes and Fe transporters were investigated. Molecular docking and protein-protein interaction assays were performed to explore the underlying mechanism. Further, the positive effects of Fe supplementation in as and Fe accumulation and morphological traits were evaluated as plants modify these responses to endure severe environments.

When OsWRKY76 is activated by MAPK signaling, it inhibits the gene expression of Fe transporters OsIRT1 and OsYSL2, which reduces the amount of Fe accumulated. However, MAPK signaling and OsWRKY76 remain down-regulated during Fe supplementation with as, which subsequently encourages the up-regulation of OsIRT1 and OsYSL2. This result in greater Fe content, decreased as accumulation, and improved morphological traits in rice varieties. These results together suggest the role of OsWRKY76 in Fe-mediated as stress alleviation.

OP-09

Optimization of Culture Conditions for Callus Induction and In Vitro Plant Regeneration of *Coleus Forskohlii*; an Endangered Medicinal Plant

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Coleus forskohlii is an important medicinal plant. It has a long history of use in heart disease and respiratory disorders. Its medicinal uses have also been reported in the treatment of spasmolysis, constipation and certain cancers. The plant is valued for the production of diterpenoid forskolin which is used in the treatment of various disorders like eczema, asthma, psoriasis, and hypertension. Rampant collection due to increase in demand has resulted in the rarity of the species and the plant is now listed under endangered species category.

There is a need for rapid mass propagation of this plant. The present study was therefore carried out to develop an efficient protocol for callus induction and *in vitro* regeneration of the plant *Coleus forskohlii.* Plants of *Coleus forskohlii* were collected, identified and maintained under greenhouse conditions. Young leaves and nodal segments were used as explants. MS medium supplemented with 3% (w/v) sucrose and vitamins was used for experiments. The surface sterilized explants were inoculated on MS medium containing growth regulators 2,4D, NAA, BAP, IAA and Kinetin in different combinations and concentrations.

An efficient and simple protocol for the callus induction in *Coleus forskohlii* is described in the present study. The callus cultures can further be used for indirect organogenesis and can be evaluated for production of active ingredients particularly diterpenoid forskolin in suspension cultures. Direct organogenesis using nodal explant was also successful in the present study with optimal hormone concentrations which gave maximum number of shoots in the explants. The direct organogenesis method is suitable for large scale cultivation of this endangered plant

concentrations which gave maximum number of shoots in the explants. The direct organogenesis method is suitable for large scale cultivation of this endangered plant.

OP-10

Effects of Cytokinins on In-vitro Flowering of Nodal Explant of Vitex Negundo (L.): An Important Medicinal Plant

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Vitex negundo L. (Verbenaceae) is an important medicinal plant in India and widely used in the Indian system of medicine. *V. negundo* is a woody aromatic and medicinal shrub or a small tree. There are very few reports on the micropropagation of V.negundo. Sahoo and Chand reported callus-free multiple shoot formation from axillary meristem explants in MS medium with BAP and GA3. In-vitro flowering and an efficient micropropagation protocol developed by in vitro culture of the nodal segment of mature plant.

Literature-based study for the selection of explant of *V. negundo* for in vitro flowering. Study the effects of natural and synthetic cytokinins for rapid multiplication through axillary buds. Study the effects of cytokinins on in vitro flowering. Review the literature and collect the details of different steps of plant tissue culture protocol for in vitro flowering of V.species which will help to design new and detailed experiment layout of our work. Young and actively growing shoots or branches with shoot tip and nodal explants with dormant axillary bud being the first choice. Collection of experimental plant material then the establishment of aseptic cultures or sterilization of explants. To study the effect of synthetic cytokines on axillary proliferation, multiplication, and in vitro flowering.

Murashige and Skoog (MS) medium supplemented with BAP (Benzylamino purine), NAA (Nepthaline acetic acid), and DPU(Diphenylurea) were found to develop fully functional flowers. MS medium supplemented with 2.0 mg/l BAP,1.0mg/l NAA and 1.5mg/l DPU induced an average of two shoots per nodes and was the best for axillary bud proliferation. Subsequent culture and enhance the number of shoots. The highest percentage (94.5%) of flowering was noticed from nodal explant cultured on MS medium supplemented with 1.5mg/l DPU and 1.0mg/l NAA combination.

OP-11

The Impact of the COVID-19 Pandemic on the Early Onset of Polycystic Ovary Syndrome (PCOS) and Polycystic Ovary Disorder (PCOD) in Young Women: A Cross-Sectional Survey Analysis using RStudio

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Polycystic Ovary Disease (PCOD) and Polycystic Ovary Syndrome (PCOS) are endocrine disorders in women that lead to severe health conditions such as infertility, diabetes, etc. COVID-19 may affect women's reproductive health as the enzyme responsible for cell penetration, ACE2, has been found in ovarian granulosa cells. Recent studies have shown that COVID-19 infection or vaccination may lead to temporary irregular menstrual cycles, but these changes eventually revert back to normal. To investigate the post impact of the COVID-19 pandemic on women's reproductive health, specifically by examining whether it has resulted in the early onset of PCOD and PCOS in young adults using cross-sectional survey analysis method with RStudio. An analytical cross-sectional study was conducted with young adults as non-probability sample targets. The anonymous questionnaire was circulated through social media networks to get responses from students. The survey had five sections: socio-demographic factors, disorder diagnosis and history, COVID 19, a symptomatic quiz-assessing the likelihood of having the condition, and consent. The collected data was refined, analyzed, and visualized using RStudio. Based on 420 responses recorded, north zone had maximum responses, i.e., 70% (294 of 420). Majority of respondents were of age 18 to 23. 65 participants, i.e., 15.5% were already diagnosed whereas the rest, i.e., 84.5% (355 of 420) attempted the symptomatic quiz. The survey results show that 46.2% of the affected were diagnosed after the pandemic. The study found that a high proportion (46.2%) of the participants with PCOD or PCOS were diagnosed after the pandemic, indicating a possible link between the COVID-19 pandemic and the onset of disorders. However, the study also suggests that other factors, such as genetics, stress, changes in diet, sleep, and lifestyle during the pandemic, may also play a role in the development of these disorders. It is essential to note that this study has limitations, and further research is needed to fully understand the potential impact of the COVID-19 pandemic on women's reproductive health.

OP-12

Role of Target of Rapamycin (TOR) in *Candida Auris G*rowth and Pathogenesis

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Candida auris is an emerging multidrug-resistant fungal pathogen becoming a worldwide public health. Unlike other fungal pathogens, its thermotolerant, high salt resistant, and drug-tolerant. It can survive desiccation and can survive on hospital surfaces for a longer duration, causing a threat to immunocompromised patients and patients with a prolonged hospital stay. This newly emerged pathogen's growth, pathogenesis, and drug tolerance mechanisms are largely unknown. Target of Rapamycin (TOR) plays crucial role in regulation of cell growth and fungal pathogenesis. The role of TOR in growth, pathogenesis and drug tolerance of *Candida auris* is largely unknown. In-silico analysis showed that Tor kinase, components of TORC, and downstream components in *C.auris*are highly conserved. The established Tor inhibitors rapamycin and torin2 inhibits the growth of *C.auris*at 20μM concentration of torin2 and 15 nM concentration of rapamycin. Inhibition of Tor leads to cell cycle arrest at the G1 phase with a defect in cytokinesis. The exposure of biofilm to rapamycin and torin2 at different phases of growth, 4th, 8th and 12th hour, showed a prominent inhibition of biofilm formation. Treatment of cells with rapamycin results in downregulation of of efflux pumps (CDR1, MDR1). TOR inhibition suppresses growth of *Candida auris* significantly. It causes cytokinesis defect and G1 growth phase arrest. Inhibition of TOR influence pathogeneses as reduces the formation of biofilm

OP-13

Survey of Major Allium Viruses Infecting Indian Shallot (*Allium Cepa Var. Aggregatum*) Cultivars and their Detection with Multiplexed RT-PCR

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Shallot (*Allium cepa* var. *aggregatum*) is also known as small onion/multiplier onion. It is one of the oldest bulb crops known to mankind and extensively grown and consumed in Southern states of India. Several different viruses from the *Potyvirus*, *Carlavirus*, and *Allexivirus* genera frequently co-infect shallots. These viruses are currently prevalent around the world, producing symptoms that are remarkably similar, making it difficult to distinguish them using electron microscopy (EM) or immunological detection techniques. As a result, crop yields and crop quality are adversely affected. The identity and distribution of these viruses were studied in different shallot accessions from various geographical locations of India. To detect these viruses early and reliably, virus-specific primer sets, including species- and genus-specific primers, were developed. For the simultaneous detection and identification of OYDV, SLV and Allexivirus infected shallot accessions in India, a multiplex reverse transcription (RT)-PCR method was developed. Multiplex PCR methods detected particular targets up to a dilution series comparable to monoplex reverse transcription (RT)-PCR. Allexiviruses were found in all accessions, while SLV and OYDV were observed only in a few accessions. The allexiviruses in the infected shallot plants were identified by sequence analysis of the projected *Allexivirus*amplicons as being Garlic virus X (GarV-X) and Shallot virus X (ShVX) which shared 84.71–90.83% and 78.6-89.8% sequence identities with various isolates from the world, respectively. Sequence analysis of OYDV and SLV sequences revealed 85.94-99.09% and 80.5-82.09% sequence identities respectively with other OYDV and SLV isolates present in NCBI from all over the world, respectively. We draw the conclusion that the simultaneous detection system developed during this work is able to distinguish between mixed viral infections in shallots with high accuracy.

OP-14

Targeted Gene Mutations using CRISPR-Cas9 Technique Affects Production of Seed Oil Content in *Brassica Juncea* (Indian Mustard)

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Fatty acids and lipids obtained from plants serve as potent energy source for many organisms. Majority of the plant lipids are stored in the form of triacylglycerols (TAGs) in oilseed plants. TAGs contribute upto 50% of dry weight of seed that makes oil quality improvement a major research goal. *Brassica juncea* (Indian mustard) is one of the major seed oil crops grown on a large scale in India as well as in other parts of the world. Here, we are using CRISPR-Cas9 technique in order to create targeted mutation in genes involved in fatty acid biosynthesis in *Brassica juncea*. CRISPR Cas9 construct were designed for BJuBDCP1, BJuBDCP2 and BJuBDCP3 genes, which negatively regulate the enzyme Acetyl CoA Carboxylase (ACCase) involved in fatty acid biosynthesis. Agrobacterium-mediated transformation was performed and targeted mutations in BJuBDCP1, BJuBDCP2 and BJuBDCP3 genes were obtained. These targeted mutations are expected to be transmitted to successive generations and provide a range of homozygous mutant lines. It is hypothesized that these mutations may functionally inactivate BDCP genes and elevate the seed oil content and its composition in mutant lines which will indicate the redundant roles of these genes in *Brassica juncea.*

OP-15

Repurposing of FDA Approved Viral Drugs against RNA-Dependent-RNA-Polymerase of Japanese Encephalitis Virus

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Japanese encephalitis virus (JEV) is a severe vector born disease which affects the central nervous system. The non-structural protein known as RNA-dependent RNA polymerase (RdRp) binds to the 3′UTR and 5′UTR to initiate RNA synthesis, promote viral growth, and control viral genome replication and translation. Patients with JEV infection cannot be treated with medication. The aim of this study is to find the FDA-approved pharmaceuticals for JEV therapy that have the fewest adverse effects, are most effective, and have a stable dynamic mechanism. Using the FDA database, a ligand library made up of FDA-approved viral medicinal molecules was prepared. Molecular docking was perform with PyRx and Chimera. The GROMACS programme was utilized to deploy the docked complexes with the highest binding affinities and lowest energy to a molecular dynamic simulation. SwissADME was also utilised to research ADME, drug-likeness, and medicinal chemistry friendliness. Docking data of the study indicates that sixteen compounds out of five hundred thirty four shows less than -11 Kcal/mol binding energy and the commercially available ligands Paritaprevir, Ledipasvir, Amentoflavone, and Hypericin have the efficient docking scores and the strongest binding affinities for catalytic site of RNA-dependent RNA polymerase. The molecular dynamics analysis shows that the structures have improved their stability while using less energy with respect to time. The molecular interaction of lead compounds with RdRp suggest that all ligands are the optimal lead compound and holds the potential to be used as an effective drug for the treatment of JEV. Paritaprevir, Ledipasvir, Amentoflavone, and Hypericin FDA approved viral compound, can be used as an effective drug for the treatment of JEV. In conclusion, the study provides valuable insights into the potential therapeutic options for JEV viral infection. Repurposing existing FDA-approved drugs can be a viable option for the treatment of this debilitating disease. The study's findings can pave the way for future research into developing more effective drugs to combat Flavivirus infections.

OP-16

Genome Editing For Reversing the Evolutionary Loss of Anthocyanin Accumulation in Tomato (*Solanum Lycopersicum* L.)

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The study on the genetic basis of *Aft* (*Anthocyanin fruit*) locus has revealed that it encodes a master regulator called *SlAN2like* (R2R3 MYB encoding gene) that controls the anthocyanin biosynthesis pathway. However, cultivated tomatoes contain non-functional alleles of *SlAN2like,* resulting in the failure to produce anthocyanin. Fortunately, the anthocyanin biosynthesis pathway can be activated in cultivated tomatoes with the utilization of CRISPR-Cas9-mediated genome editing targeting the *SlAN2like^{aft}* locus. By utilizing the CRISPR-Cas9-mediated homologous recombination mechanism, the engineered master regulator *SlAN2like^{Aft}* gene (from *Aft* fruit tomato) under the control of fruit-specific *SlE8* promoter, can be integrated at the inactivate *SlAN2like^{aft}* locus of cultivated tomato, which will result in the induction of anthocyanin biosynthesis.

OP-17

Secure and Efficient Medical Image Storage with Deep Learning and Significance-based Encryption and Compression

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Cloud computing has gained significant traction in the healthcare industry due to its potential for improving patient care, reducing costs, and enhancing operational efficiency. However, the use of cloud-based technologies in healthcare also raises concerns regarding the security and privacy of sensitive medical data. This paper discusses the unique security challenges faced by healthcare organizations when storing and processing medical data in the cloud, including compliance with industry regulations. The paper employs a deep learning technique for the purpose of classifying images according to their significance, with the consequential encryption and preservation of important images and the compression of non-important ones. The extensive experimental analysis shows that the proposed scheme outperforms recent methods.

OP-18

AI Based Models for Predicting DNA-Binding Residue from Sequence

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Proteins that interact with DNA play crucial roles in many biological processes, such as DNA replication, transcription, and repair. Predicting which amino acids are involved in these interactions can provide valuable insights into protein function and aid in the design of new drugs that target specific proteins. AI-based approaches use machine learning algorithms to analyze large amounts of protein sequence and structure data to identify patterns that are indicative of DNA-binding. These methods have shown promising results in accurately predicting DNA-binding sites observed in known protein-DNA complexes. Most such predictions are currently based on evolutionary profiles of protein sequences. However, it is not clear whether such profiles contain information about interactions sensitive to small changes in amino acids, not reflected in evolutionary profiles. The objective of the study is as follows: bjectives: 1. Introducing specificity determining behaviour of protein sequences by creating a database of Transient Residues Transient Binding (TRTB) residues. 2. Benchmarking sequence versus evolutionary profiles based AI-methods to predict TRTB residues.In order to accurately study DNA-binding proteins, a high resolution and non-redundant dataset is created. This dataset included the annotation of DNA-binding residues to identify the specific amino acid positions responsible for binding DNA. Additionally, pairing of closely related proteins has been done for each representative protein that aids in the analysis of conserved versus transient residues. Structural and biophysical labelling of residues were done and analysed to provide further insights into the functional significance of each amino acid position. In order to generate predictions, a predictive machine learning model is trained and cross-validated using a variety of methods, such as PSSM versus sequence features on single amino acid positions. Finally, treatment of residue types is important for performance measure estimates and should be taken into consideration when interpreting the results of the predictive model. By following these steps, researchers can gain a deeper understanding of DNA-binding proteins and the specific amino acid residues that play a critical role in their function.We created pairs of closely related DNA-binding proteins (DBPs) to group their DNA-binding alignment positions into four categories based on whether the residue bindings were conserved or transient. In this way, we investigated a class of DNA-binding residues that are

sensitive to single substitutions and thus difficult to predict from an evolutionary profile. While the binding label in such positions is difficult to predict using current methods, single sequence information can still predict such binding with modest accuracy. The study aimed to understand the overall sequence properties and predictability of DBPs with transient versus conserved DNA-binding residues. The study identified general patterns of DNA binding being lost when substitution occurs from aromatic to aliphatic, longer to smaller side chain, or from positive to negative residues. The conclusion of the study is as followss: 1. Evolutionary profiles (PSSM) are best features for sequence-based prediction of general DNA-binding residues on proteins. 2. A novel class of DNA-binding residues viz. TRTB is difficult to predict from an evolutionary profile; single sequence information can still predict such bindings. 3. Change in physiological properties of TRTB residues has an impact on their gain/loss of binding. 4. Aromatic-aliphatic substitution, longer-to-shorter side chain, and positive-to-negative residues have been shown to affect DNA binding, of which aromatic-aliphatic changes seem to be the most emphatic.

Poster Presentations

(PP)

PP-01

Evaluation of Phytocompounds from *Centella Asiatica* against Multiple Sclerosis

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There is a rapid spread of multiple sclerosis (MS) disorder across the globe. There are around 2.8 million cases of multiple sclerosis worldwide; among them, 1 million are just present in the US. Many drugs have been tested on MS patients, but there has been no effective treatment for MS till now. Many inhibitors, such as dronabinol and nabilone, have been used to treat MS but have many challenges.

This study evaluated binding interactions through molecular docking calculations against the 1PY9 receptor. 22 phytochemicals from *Centella asiatica* were selected and gone under molecular docking, and some of them showed positive responses against MS.

This study found that betulinic acid, asiatic acid, rosmarinic and terminolic acid have the potential to inhibit the 1PY9 receptor, and their binding energies are -7.81 kcal/mol, -9.93 kcal/mol, -8.53 kcal/mol and -8.88 kcal/mol respectively. Based on the bioavailability radar studies, asiatic acid and terminolic acid are two bioactive compounds that can be further used for dynamics studies. To find the more effective compound, these compounds can be taken in *in vitro* studies.

PP-02

A Comprehensive Review cn Subtractive Proteomics and Its Applications towards Drug Target Identification from Various Bacterial Pathogens

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Proteomics is the branch of Omics Technology. Proteomics is a field in which we study proteins concerning sequence, structure and function. The subtractive proteomics approach is the perspective in which we take a large scale of data which ultimately gets subtracted; hence we need to study only summarized data and work get systemized. The subtractive proteomics approach is the method in which we recognize the novel drug target through various proteomics and bioinformatics means.This study aims to present a review of the importance of the subtractive proteomics approach concerning identifying drug targets from bacterial pathogens.

In this study, we have used text mining approaches with the aid of the PubMed database to identify the appropriate research or review papers related to subtractive proteomics and how they are used to identify novel targets from various bacterial pathogens.

In this study, we have presented a comprehensive review of the importance of subtractive proteomics and applications towards identifying drug targets from various bacterial pathogens.In the present study, we have utilized a subtractive proteomics approach to identify and prioritize the potential drug target. This will be further used to identify the potential inhibitors against the pathogen. The present study opens the gateway for a promising therapeutic route against the disease.

PP-03

Probiotics in Inflammatory Bowel Disease

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Microbes exist within the host (human) specifically in the intestine and express a mutual association with the host and hold important role in the several functionalities such as physiology, nutrition and regulation of responses related to the immune system. This microbial interaction within the host sometimes leads to the inflammation in the intestine including both the large and the small, which leads to a group of autoimmune diseases alias inflammatory bowel disease. In this type of disease host's immune system itself starts attacking the elements of the digestive system, thus generating an auto-immune response. The major form of the IBD is Crohn's Disease that has no major target and can affect anywhere in the digestive track while the second major form of the IBD is the ulcerative colitis which severely affects the colon lining of the large intestine. Several medications are being used for the treatment of IBD such as anti-inflammatory drugs Mesalazine, Remicade that work against cytokines responsible for the inflammation but the application of these drugs are limited due to their side effects such as anemia, nausea, peripheral neuropathy respectively. If medication procedures fail, the last option is to undergo colectomy an operative method in which colon region is removed. Surgical procedure shows a success in the ulcerative colitis as it dominantly affects the large intestine but reoccurrence in the case of Crohn's disease is seen even after a successful surgery. In the recent times the use of probiotics is being promoted as their beneficial effect is seen in treatment of digestive disorders with immunomodulation and minimum or no side effect. Probiotics have been progressively investigated for their beneficial effects in IBD. In this context, we summarize the advances made in field of IBD treatment and possibility, merits as well as demerits that probiotics can offer to treat IBD.

PP-4

Shedding Light on Structural and Functional Aspect of Survivin: A Unique Target for Cancer

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Survivin is the fifth key Inhibitor of the Apoptosis (IAP) Family member. Since its discovery more than two decades ago, it has been recognized as a significant cancer therapeutic agent due to its role in inhibiting apoptosis. However, several studies concluded that over-expression of Survivin being associated with tumor progression and further show resistance in the functioning of therapeutic procedures.For the last few years, various research studies have discussed on function of Survivin, mutations, inhibitors and other related aspects. However, a comprehensive conclusive study was missing that summarizes the sequential, structural, functional, inhibitory and mutational aspects. Therefore we have compiled till date available data in this study so that new strategies to tackle this protein can ultimately be devised through a better understanding using a different approach. This will bring us a step ahead in therapeutics against cancer.

In this study, we have used text mining approaches with the aid of the PubMed database and in silico tools to explore the comprehensive information on Survivin Protein.

In this study, we have presented the sequential, structural properties and essential mutations linked with cancer and reported available inhibitors/drug molecules against Survivin Protein. Currently, most cancer therapy protocols comprise a complex combination of surgery, chemotherapy, and radiotherapy, yet despite significant progress in this direction, patient survival rates have remained relatively unchanged. Despite this, there is a growing interest in developing novel therapeutic methods that target Survivin and in the future, this could become one of the most critical targets in cancer therapy.

PP-05

Indian Priority Pathogen List

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The Indian Priority Pathogen List (IPPL) is a comprehensive list of infectious agents that pose a significant threat to public health in India. The list was initially published in 2017 by the Indian Council of Medical Research (ICMR) as part of a broader attempt to increase the country's preparation for outbreaks and epidemics. The IPPL is separated into three categories according to the threat level they provide to human health: high, medium, and low priority. Pathogens with a high mortality rate, the potential to cause severe illness and ease of human-to-human transmission are considered to be of high priority. The Ebola virus, the Nipah virus, the virus that causes Crimean-Congo hemorrhagic fever, and the coronavirus that causes severe acute respiratory syndrome (SARS) are some of these pathogens. The pathogens with a medium priority can potentially lead to serious illness but are less contagious than those with a high priority. They include the Middle East respiratory syndrome (MERS) coronavirus, the Japanese encephalitis virus, and the Zika virus. Finally, low-priority pathogens have little potential to harm the public's health or cause significant sickness. They include the TB bacteria, the dengue virus, and the chikungunya virus. The severity of the illness each pathogen causes, its propensity for transmission, the availability of efficient therapies, and the possibility of an outbreak were among the criteria considered to determine the priority level of each infection. The publishing of the IPPL has been an enormous step forward for India's public health infrastructure, as it provides a roadmap for policymakers and healthcare professionals to prioritize resources and efforts to prevent and control infectious illnesses.

In order to reflect new dangers and scientific advancements, it will be crucial to keep updating and improving the IPPL. Moreover, efforts should be undertaken to develop India's public health infrastructure, including boosting laboratory capabilities, disease surveillance systems, and access to efficient medications and immunizations. Overall, the Indian Priority Pathogen List is a crucial instrument in the battle against infectious illnesses in India, and its continuous usage and refinement will be essential in defending the health of the Indian people.

PP-06

Comparative Study of Drug Targets against Enol-Pyruvyltransferases

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Enol pyruvyl transferase (EPT) is a target for the development of antibiotics and herbicides because it is involved in the manufacture of important amino acids in bacteria and plants. The literature survey was made based on the available research or review papers in PubMed database. Several comparable studies were examined, including in vitro testing of inhibitory efficacy against EPT, structural and functional comparisons of bacterial and plant EPT, and molecular docking simulations. Sulfonamides, thioureas, and substances containing a pyridine ring were among the possible inhibitors discovered in this research that had strong activity against EPT.

A number of comparable studies were examined, including in vitro testing of inhibitory efficacy against EPT, structural and functional comparisons of bacterial and plant EPT, and molecular docking simulations. Sulfonamides, thioureas, and substances containing a pyridine ring were among the possible inhibitors discovered in this research that had strong activity against EPT. As a result of comparative investigations of EPT, various prospective therapeutic targets for the creation of antibiotics and herbicides have been found as well as useful insights into the structure and function of this enzyme. These studies emphasize the value of comparative analysis in selecting and refining pharmacological targets for increased efficacy and selectivity. To create and evaluate these inhibitors in preclinical and clinical studies, more study is required.

PP-07

Role of Long Non-Coding RNA in Breast Cancer

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During the last decade, a significant role of long non-coding RNAs (lncRNAs) in breast cancer has been observed. These RNAs have shown both positive and negative effects in breast cancer cells like lncRNA TINCR (tissue differentiation-inducing non-protein coding RNA) enhances the expression of programmed death-ligand 1 (PD-L1) which leads to the progression of breast cancer. Another study revealed that lncRNA TMEM105 (Transmembrane protein) increases glycolysis in breast cancer cells and also promotes the breast cancer liver metastasis via sponging microRNA miR-1208 which directly regulates the expression of lactate dehydrogenase A. Likewise, lncRNA BCAR4 enhances metastasis and chemoresistance properties in breast cancer cells by down-regulating the expression of microRNA miR-644a. Apart from these, lncRNA BC069792 have shown inhibitory effect in breast cancer progression by sponging microRNA hsa-miR-658 and hsa-miR-4739. Similarly, lncRNA MBNL1-AS1 reduces proliferation, invasion, migration, and glycolysis of breast cancer cells by downregulating microRNA miR-889-3p. A study also revealed the potential of circulating lncRNA T376626 as a biomarker for breast cancer. These studies show that lncRNAs hold key properties for therapeutic applications in the treatment of breast cancer but still, a lot of things need to be done to find the right lncRNA target in breast cancer cells. Theobjective of the study is to understand the role of LncRNAs in Breast Cancer. In this study, we have made a literature survey based on available research or review papers from various resources.

LncRNAs have been found to influence the activity of Breast cancer cells in both positive and negative aspects. The lncRNAs are directly involved in regulating the metabolic activities of Breast cancer cells and could be a potent target molecule for various therapeutic agents related to Breast cancer cells in the near future.

PP-08

Antibacterial Activity of Essential Oils in Combination with Antibiotics against Methicillin-Resistant *Staphylococcus Aureus*

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Methicillin-resistant *Staphylococcus aureus* (MRSA) is a highly adaptive strain of commonly occurring *Staphylococcus aureus*, which is resistant to clinically available antibiotics. MRSA is considered a superbug due to its defiant activity against all antibiotics and available medications that are most used to treat major and minor infections. The continuous emergence of MRSA has been increasing attention to the search for an alternative drug from nature, such as phytochemicals, as a possible medicinal agent.The present study aims to focus on the MRSA threat, explore essential oils as alternative antimicrobials, and summarize the studies on synergistic combinations of essential oils and antibacterial antibiotics.

Medicinal plants are the natural reservoir of different biologically active compounds and have been used to treat infections caused by various pathogenic microbes for a long time. An effective solution is to combine the available antibiotics with adjuvants such as phytochemicals or essential oils. Essential oils from natural sources can be explored for their potential antimicrobial activity against MRSA. Essential oils contain various components such as carvacrol, cinnamaldehyde, cinnamic acid, eugenol, and thymol, which can have a synergistic effect in combination with antibiotics to enhance the efficacy and activity of antibiotics.

Several modes of action have been put forward by which antibiotics and the essential oil components may act synergistically by affecting multiple targets, such as physicochemical interactions and inhibiting antibacterial-resistance mechanisms. Combinations of synthetic drugs and plant essential oils can be a potent strategy to overcome the MRSA threat.

PP-09

Identification of Promising Molecules from *Aloe vera* - A combined Text Mining with the In-silico Study

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Aloe vera is a promising plant showing diverse biological activity including anti-bacterial activity against a diverse variety of bacteria like gram-positive and gram-negative bacteria including *E. coli, Pseudomonas aeruginosa, Methicillin-resistant Staphylococcus aureus* (MSRA), etc. After the identification of the plant, we used databases like PubMed, and IMPPAT to identify the ADMET properties and Lipinski drug-like properties which are important parameters for any molecule to act as a drug.The objective of the study is to identify the promising drug-like phytochemicals from *Aloe vera* followed by the preparation of an in-house library of promising drug-like phytochemicals.

In the present study, we have utilized text mining approaches with the aid of PubMed along with in silico tools and databases for the identification of promising phytochemicals from *Aloe vera*.

With the help of text-mining along with the in-silico screening, we have identified 7 molecules. The prioritized molecules from this study are as follows: IMPHY003500, IMPHY003999, IMPHY010728, IMPHY013885, IMPHY005416, IMPHY013885, IMPHY014895. Our ongoing work is directed towards identifying the crucial target from these molecules and understanding the interaction mechanism at the molecular level.

PP-10

Green Synthesis of Silver Nanoparticles Using Potato Peel Extract

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There are several uses for nanoparticles in industries including cosmetics, drugs, and agrochemicals, wastewater treatment and as antibacterial agents. It is incredibly effective, economical, practical and ecologically benign to synthesize nanoparticles using plant extract. When nanoparticles are created, a plant extract functions as a reducing agent.In the present study, synthesis of silver nanoparticles was done by using potato peels and further antibacterial activity has been investigated.

Potato peels were collected and then extract was prepared. For synthesis of silver nanoparticles, silver nitrate salt solution was utilized. The peel extract and salt solution were combined in a ratio of 1:9. The reduction of Ag ions into AgNPs, which produced a brown color was confirmed using a UV-vis spectrophotometer. Further antibacterial activity of synthesized nanoparticles was checked.

UV-vis analysis was used to find AgNP synthesis. The peak of AgNP was seen at about 450 nm. Further synthesized AgNPs were investigated for their antibacterial effectiveness against an E. coli gram-negative bacterial culture. After 24 hours of incubation, the results demonstrated the potential antibacterial activity of these AgNPs against E. coli. It has been found that when AgNP concentrations rise, the zone of inhibition expands. In 10 microliters of AgNP solution, the smallest zone of inhibition was discovered, while 30 microliters of solution revealed the largest zone of inhibition.One of the prospective ways that has attracted a lot of interest is the biological method of synthesizing nanoparticles. It creates innovative, economical, and environmentally friendly materials that have uses across a variety of industries. In this work, AgNP was synthesized from a potato peel extract. The plant extract functions as a reducing agent and gives nanoparticles stability. Synthesized AgNPs have proven antibacterial application therefore it can be used as antibacterial agent.

PP-11

Identification of Promising Phytochemicals from *WithaniaSomnifera* - A Text Mining Approach

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Cancer has been a significant cause of death for a large world population. It has been studied for decades, resulting in many technologies and therapies to treat cancer. Most involve chemicals, radiation, etc., that have been found to cause many adverse effects. These therapies and their side effects have been observed to have deteriorated patient's health. *Withaniasomnifera* (Solanaceae), commonly known as Ashwagandha, is a very well-known medicinal plant with ayurvedic properties known in abundance. The medicinal properties include anti-inflammatory, antioxidant, anti-stress, anti-arthritis, etc. Natural drugs obtained from the plant can be a safer and better route to treat the former disease.This review includes, considering the great potential of *W. somnifera*, an account of phytochemicals and molecules obtained from the plant and encapsulation of its anti-cancer effects found in various studies.

Various databases, like PubMed, Science Direct and Google Scholar, have been accessed for the literature study and to retrieve data involving the effects of the phytoconstituents found in the plant.

Various parts of *W. somnifera*, including root, stem and leaves, have shown the presence of constituents, majorly withanolides, including withaferins, withanolides and withanolides, which have been observed as active molecules showing anti-tumour and anti-cancer activities against various types of cancers like colon, pancreas, kidney, skin, etc.This Ayurvedic medical plant showing anti-cancer activities can be a great source of natural drugs that can treat various cancers through natural pathways with minimum side effects as with the combination of presently used therapies, or even no side effects if purely natural pathways are found.

PP-12

Review of Application and uses of Biosensors in the Prevention and Treatment of Breast Cancer

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Cancer is the second leading cause of mortality in poor nations and the leading cause in industrialised ones. Breast cancer affects women more than other malignancies. Reports indicate 2.3 million breast cancer cases worldwide every year. Breast cancer rates have risen over 30 years. HER-2 enriched, luminal-a, and luminal-b breast cancers exist. Cancer cells proliferate due to the protein HER2. Breast cancer risk depends on several factors. Invasive breast cancer covers a wide range of tumours that affect appearance, behaviour, and clinical presentation. Westernization, nutrition, artificial light, and chemical medications make women over 50 more susceptible to breast cancer. Stage and molecular subtype affect patient survival. The ability to divide indefinitely, increased antigenic potential (blood vessel development), resistance to growth-inhibiting signals, induction of own growth signals, and metastasis are the main mechanisms that enable cancer cell growth. Mutations and environmental factors cause cancer. Although not all tumors kill, many seriously affect well-being. Breast cancer is a common illness worldwide. Early identification and screening reduce breast cancer. Breast cancer treatment includes hormone therapy, surgery, radiation, and Biosensor. The objective of the study is as follows: (1). To analyze the different applications of biosensors in breast cancer diagnosis. (2). Different types of biosensors are used in the diagnosis of breast cancer. (3). Comparison of different biosensors with methods for detection of breast cancer

Because of the rapid nature with which cancer may spread, any novel techniques must be easy to evaluate, fast to test, and cheap. That's why label-free detection methods, like those used in biosensors, have been getting a lot of attention as of late. Its primary premise is that there is a causal connection between the bio recognition component and the target analyses. In order to enhance cancer prediction and therapy methods, there is an urgent need for efficient biosensors for fast analysis of cellular changes to discover significant biomarkers. Nevertheless, biosensor devices need to be continuously improved in order to tackle emerging issues, such as the multiplex analysis of many biomarkers, which would require the creation of arrays of sensors on a single chip. These devices may become particularly valuable in the field with the development of biomarkers, patterning software, and microfluidics biosensors.

PP-13

Long non Codingrnas and their Involvement in the Progression of Liver Cancer

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In the past few years, the long non coding RNAs (lncRNAs) have been demonstrated as a key biomolecule in controlling the metabolic activities of liver cells. These RNAs have mostly been found to upregulate the progression of liver cancer like lncRNA TLNC1 (tumorigenic long noncoding RNA on chromosome 1p13) enhances the growth and metastasis of liver cancer cell via modulating the activity of p53 through transporting it to cytoplasm. Another study revealed the involvement of lncRNA DSCR8 (Down syndrome critical region 8) in liver cancer progression by regulating miR-22-3p/ARPC5 (actin-related protein 2/3 complex subunit 5) axis. Similarly, lncRNA PNUTS (phosphatase 1 nuclear targeting subunit) target ZEB1 (Zinc finger E-box-binding homeobox 1) causing epithelial-mesenchymal-transition (EMT) that results in hepatocarcinoma metastasis. The knockdown studies have also supported the involvement of these RNAs in liver cancer progression like inhibiting the expression of lncRNA MIR44352HG resulted in a significant decrease in proliferation and metastasis of liver cancer cells. One more study reported that antisense oligonucleotide-mediated knockdown of lncRNA PURPL (p53-upregulated-regulator-of-p53-levels) not only inhibited the liver cancer progression via inducing apoptosis but it also increased the sensitivity of hepatocarcinoma cells towards chemotherapeutic agent doxorubicin. Likewise, lot of other studies also favours the involvement of lncRNAs in liver cancer progression and these not only make them a potential biomarker but also support the idea of desired target molecules for therapeutic agents. However, in order to make them a potential target in terms of clinical applications for treating liver cancer, a lot more studies need to be done. The objective of the study is to understand the involvement of long non-coding RNA in progression of liver cancer.

In this study, we have used PubMed and other literature databases to explore all possible information of LncRNA towards liver cancer.

It is observed that lncRNA influences the activity of liver cancer cells in both positive and negative aspects.lncRNA are directly involved in activities of regulating metabolic liver cancer cell and could be a potent target molecule for various therapeutic agents related to liver cancer cells in near future.

PP-14

Enterococcus Faecalis: An important Nosocomial Pathogen

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During the previous two decades, *Enterococcus faecalis* has emerged as responsible for up to 12% of hospital-related impurities, with mortality charges for bloodstream contaminations ranging from 20 to 68%, depending on the patient population. The *E. faecalis* can grow in an environment where ascorbate is found, such as plant material, and possibly most important, in the human body. E. faecalis is part of a large group of pathogens that cause nosocomial infections and are resistant to various antibiotics. Both *E. faecalis* and *E. faecium* are hazardous to humans since they resist various antibiotics, including daptomycin, vancomycin, etc. Moreover, *E. faecalis* forms biofilm on both hydrophobic and hydrophilic surfaces.The study's objective is to get comprehensive information on E. faecalis concerning various aspects related to infections, antibiotic resistance, biofilm-forming nature, etc.

In this study, we have used text mining approaches with the aid of the PubMed database to explore comprehensive information on *E. faecalis*.

Based on the information obtained from a detailed literature survey, drug target proteins will be identified from various critical pathways and facilitate designing potent inhibitors against them.This study concludes that *E. faecalis* resisted diverse classes of antibiotics. Moreover, they can develop biofilm on the surface of analytical and other medical strategies, which is one of its critical pathogenic aspects. Moreover, this pathogenic microorganism showed resistance against diverse classes of antibiotics, particularly vancomycin. Due to this bacterium's MDR (Multi-drug resistant), XDR (Extensive drug resistant) and biofilm-forming nature, this particular organism is considered a critical pathogen for further investigations on identifying target proteins and their inhibitors.

Unraveling the Regulation of Nutrient Use Efficiency in Wheat Cultivar under the Co-Impact of Drought and Arsenic

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Agricultural production is significantly impacted by drought (D) and arsenic (As) stress on a global scale, particularly in wheat, a staple crop with high consumption. These stresses lead to a loss of nutritional quality and biomass, highlighting the need to boost crop nutrient use efficiency (NUE) under stressful conditions. However, the mechanisms behind NUE regulation in wheat seedlings exposed to combined stress remain obscure.This study aimed to elucidate these mechanisms by examining the combined effect of D and As stresses with nitrogen (N) and phosphorus (P) supplementation at short and long exposures.

Growth responses and physiological, morphological, and biochemical parameters along with N and P-related enzyme activities were studied.

The results showed that dual stress hindered plant growth by interfering with essential metabolic mechanisms, reducing NP acquisition via declined root morphology. It also hampered N-assimilation via declined NO3- content, and impaired N-assimilating enzymes activity. However, enhanced NH4+ content at both exposures correlated with inclined oxidative damages and declined N accumulation. Dual stress also declined P-assimilation via P-assimilating enzymes, which is linked to P accumulation. Plants facing D stress performed better than those treated with As at 15 days. External NP supplementation improved nutrient content, growth-related functions, and N & P assimilating enzymes. This aids in the production of responsive protein and leads to reduced damage to the plants which is in correlation with the status of ROS scavengers.This work uncovered the involvement of N and P in enhancing the NUE-related mechanisms that let plants endure the combined effects of D and As stress.

PP-16

Utilization of *Ficus Auricualta* for the Making of Pickle and Its Physicochemical Analysis

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Our study aimed to fill a gap in the literature by documenting the traditional recipe of pickle made from Ficus auriculata (Timla), a non-conventional fruit that is often underutilized. The nutraceutical and pharmaceutical properties of Ficus genus make it a valuable fruit, but it is only available for a limited period of time, therefore it is necessary to make value-added products from this plant. In the current study, the physicochemical properties of the fresh fruit, edible mustard oil, stuffing material, and prepared pickle were analyzed.

The fresh raw fruits were pickled in salt, Vinegar, sugar, and Mixture (salt, oil, spices, and vinegar). The sensory attributes and titratable acidity of the pickle were evaluated during storage intervals of 15 days, the sample made with mixed method ranked the highest by the sensory panel. Changes in pH and acidity of the pickle were observed during storage.

The moisture content of the pickle was observed highest (60%) in the mixed sample and lowest (23%) in the vinegar-preserved sample on the other hand the fat content was only observed (17.5%) in mix pickled sample. The ash content for all the preserved samples was observed 10%, except for the mixed sample, which had a higher ash percentage of 30%.The overall finding of our study provides an approach for individuals who have access to this fruit to utilize the fruit and generate revenue from it while highlighting its potential as an ingredient in traditional pickle preparation. The study aims to promote the use of underutilized fruits and contributes to the sustainable use of natural resources for livelihood security.

Role of Epigenetics in Endometrial Cancer

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Endometrial cancer is a prevalent gynaecological cancer that affects women globally. Although genetic mutations have been identified as a major factor contributing to the development of endometrial cancer, recent studies have suggested that epigenetic modifications also play a crucial role in the initiation and progression of endometrial cancer. The main objective is to summarize the current knowledge regarding the role of epigenetic modifications in the development of endometrial cancer.

A comprehensive literature review was conducted using PubMed and Google Scholar databases. Relevant studies published between 2000 and 2021 were studied.

The literature review identified several epigenetic modifications that are involved in the pathogenesis of endometrial cancer, including DNA methylation, histone modifications, and non-coding RNAs. Dysregulation of these epigenetic modifications can lead to the aberrant expression of genes that are involved in key cellular processes such as cell proliferation, apoptosis, and DNA repair. Epigenetic modifications are important contributors to the development of endometrial cancer. Further studies are needed to fully understand the complex interplay between genetic and epigenetic alterations in the pathogenesis of endometrial cancer. The identification of specific epigenetic alterations may provide new diagnostic and therapeutic strategies for the treatment of endometrial cancer.

PP-18

Prediction with Computational Genomics

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Computer science and biology have been majorly focused on after the pandemic (COVID -19). The walk in this field was not seen before as it is now because of the increasing interest/curiosity of the students and researchers in 'COMPUTATIONAL BIOLOGY' as it gives purposeful results. Computational Biology or biocomputing is the combined use of mathematics, biology and technology. By adding the computer in all these branches, things get easier and more efficient to be solved in less time.

By using data chips, analysis, and statistics, devices and software (technologies) are made to solve certain issues in various fields like genomics, drug development, bioinformatics, neuroscience, medicines, machine learning and many more.

Here we will analyze certain topics in genomics like proteomics, epigenomics, transcriptomics and interactomics. The problems related to many fields can be solved using computational biology, like in the health sector, medicine, agriculture and many more, by developing new techniques and software accordingly. As a result, new technologies will be made, and more lives will be saved in time.

PP-19

Natural Tannin Biodegradation by *Aspergillus flavus* for Tannase Production

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Microbial tannases are important industrial enzymes with immense applications in food, feed, leather and pharmaceutical industries. Tannases (Tannin Acyl Hydrolase; E.C. 3.1.1.20) are the hydrolytic enzymes that catalyze the breakdown of tannins. Tannins are the most abundant biopolymer after cellulose and hemicelluloses and are found in leaves, fruit, galls and bark of many plants. It is, therefore, tannin biomass also contributes significantly to the agro- waste. The tannin-rich substrates can be substituted for costly tannic acid while large-scale production of the enzyme is to be attempted. The use of natural waste substrate makes the production of enzymes cheaper, ecofriendly and also suggests their beneficial utilization. The present study aimed to produce extracellular tannase using natural tannin substrate for tannase production from the selected fungal tannase producer Aspergillus flavus.

Evaluation of the natural tannin utilization efficiency of *Aspergillus flavus* using different tannin-rich substrates (1% w/v) as a carbon source in the production medium for tannase production. Optimizing different concentrations of tannin substrates and the incubation period enhanced the tannase production—qualitative determination of tannin utilization efficiency of Aspergillus flavus by Paper chromatography. Among the six tannin substrates, jamun leaves and spent tea induced higher tannase production than pure tannic acid. Further, different concentrations of the tannin substrates were tested for enhanced tannase production. The selected fungal strain utilized other natural tannin substrates, efficiently producing appreciable tannase yield. The optimization of the incubation period revealed that a higher incubation time was required for natural tannin utilization than the tannic acid used as control. Paper chromatogram also revealed the liberation of gallic acid from various natural tannins by *Aspergillus flavus*. The tannin biodegradation efficiency of the tannase produced by this fungal strain was studied by using natural tannin extract as the substrate for the enzyme. The significant biodegradation of natural tannin was observed qualitatively by paper chromatography and quantitatively by tannase assay. The tannin degradation efficiency of this tannase can be used as a powerful tool for a number of industrial applications like the treatment of tannery effluents, fruit juice debittering, wine clarification etc.

PP-20

Diagnosis and Treatment for Alzheimer’s Disease

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About 6.5 million people in the United States age 65 and older live with Alzheimer's disease. Among them, more than 70% are 75 years old and older. Of about 55 million worldwide with dementia, 60% to 70% are established to have Alzheimer's disease. We still do not have an effective treatment for AD despite it being the most common cause of dementia and impaired cognitive function—we developed machine learning models to determine the gene subset that best distinguishes between the AD samples from the healthy controls. The objective of the study is to determine the diagnosis and treatment for Alzheimer's disease.

Some biomarkers can detect the presence of plaques and tangles. There are so many tests to detect Alzheimer's disease by measuring the amyloid and tau protein in the fluid part of blood and cerebral spinal fluid: a blood test, magnetic resonance imaging, positron emission tomography test, and biomarker test, including a specific test in positron emission tomography scans. There is currently no cure or effective treatment for Alzheimer's disease. The treatment is the medicine that can help the patient to reduce the symptoms temporarily and not only medicine. There are innovation dementia care models; lifestyle and home remedies by which support is also available to help someone with the condition and their family cope with everyday life. The medicines are galantamine, donepezil and rivastigmine, prescribed for people with early to mid-stage Alzheimer's disease.

In the past AD was diagnosed only after death when looking brain with a microscope revealed plaque and tangles. Researchers are now able to diagnose Alzheimer's disease during a lifetime. AD is the most common of many causes of dementia, and its prevalence is increasing worldwide. Disease pathology starts years before noticeable symptoms. Neuropsychological, imaging, and spinal fluid tests can establish the diagnosis with high accuracy.

PP-21

Signaling Pathways and Therapeutic Intervention in Colorectal Carcinoma

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Colorectal cancer is the third most common disease diagnosed in both men and women worldwide. Genetic and environmental factors influence the risk of developing colorectal cancer (CRC). In 2023, approximately 1, 53,020 people will be diagnosed with CRC, and 52,550 will die. Nowadays, gastrointestinal cancer, especially CRC and gastric cancer, are the leading causes of cancer-related death. Several pathological, clinical, and therapeutic features of CRC have already been studied to identify patients' prognostic indicators. Laparoscopic surgery, radiotherapy, and chemotherapies are among the many primary and metastatic CRC treatments available. However, these treatment options had little effect on cure rates. This paper compasses the general aspects of CRC between the components of the PI3K/AKT/mTOR pathway and the AMPK pathway. The review paper includes all the co-relation and co-expression to reveal the control mechanism. The present review is aimed to showcase the anticancer activity of the AMPK pathway against the mTOR pathway. They further increased the level of pAMPK to suppress the mTOR pathway as a therapy in CRC.

The data were obtained from PubMed/Medicine databases, Scopus, and Google patent literature.

PI3K/AKT/mTOR pathway is an important event in colorectal carcinoma. In addition, it plays a significant role in cell proliferation and metastatic initiation in CRCs. Although, at the gene-level, AMPK pathways are potent inhibitors by effectively downregulating these pathways. Downregulation of the PI3K/AKT/mTOR signaling pathway has been successfully achieved by the AMPK pathway in CRC, rendering this pathway as a promising approach as a promising therapeutic target.

PP-22

Solution towards Sustainable Agriculture Development Goals - BIOINOCULANTS

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World population has been estimated to explode to nearly 9.4 billion by 2050, exerting pressure to boost agricultural production. After green revolution, though indiscriminate use of pesticides and chemical fertilizers drastically increased the agriculture production but has unknowingly posed a serious threat to ecosystem. Hence, it becomes important to protect, restore and promote sustainable use of terrestrial ecosystems and to warrant food security with good quality and all these have been defined under 17 sustainable development goals, an initiative by United Nations. Some sustainable development goals direct focus towards zero hunger, no poverty, sustainable consumption and production and Life on land. The eco-friendly solution to this is the application of microbial inoculants or bioinoculants which colonize near plant roots and improve plant growth and health by various indirect and direct mechanisms such as IAA production, N2 fixation, increased biotic and abiotic stress tolerance, nutrient acquisition, induced systemic resistance along with degradation of endocrine disrupting chemicals as pesticides, polyaromatic hydrocarbons, flame retardants etc. Now-a-days, bioinoculants are also being targeted as bio-fortifiers as they are known to provide nutrients such PO4, Zn, Fe, Se, N2 to plants. The role of bioinoculants as seed primers is also being explored to trigger nutritional enrichment in plants. The bioinoculants not only improves plant growth but also soil health by increasing nutrient mobility, availability and solubility. Hence, in the present industrial scenario, the key to agriculture and environmental sustainability is the formulation of robust bioinoculants with multiple plant and environment supporting traits.

PP-23

Electricity Producing Genetically Engineered Microorganisms

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Microorganisms have the potential to generate electricity since they can survive in extreme climates. Microorganism can be an excellent alternative renewable source for the electricity generation. They generate electricity both by the aerobic and anaerobic oxidation of organic as well as inorganic material. Microbial fuel cell (MFC) is attracting attention due to its ability to convert chemical or solar energy into electric energy with microorganism as catalyst. Unlike traditional fuel cells, microbial fuel cells produce electricity at a low cost since they do not require expensive catalysts at the anode. The ability of microbes to act as electrocatalyst at electrodes determines the practical usefulness of all microbes' electrode systems. They can have potential applications in the bioremediation, biosensing, and wastewater treatment. This review focuses on the classification, applications and future scopes of genetically engineered electricigen.

Mixed microbial communities used in MFC are unable to generate enough current to be utilized for industrial purpose. Strains of microorganisms of electricigen species are genetically manipulated by alteration of genes to produce higher current output.

Maximum current can be produced when flavin synthesis and cytochrome synthesis is increased. In addition, the thickness of biofilm formed also alters the electric output. Depleting availability and environmental pollution from non-renewal energy resources has encouraged researchers to look for alternative renewal energy sources. The use of electricigens is recent trend in the field of green energy. These microorganisms are capable of producing electricity but its industrial application has been limited due to small current and power output produced. The focus is on the technologies for enhancing the energy outputs for applications in the industrial sector. The use of genetic engineering techniques has been studied to increase the current output through enhancing electron transfer and power output. Various factors affecting the current output like biofilm thickness, EET transfer and MFC electrode material have provided a basis for production of mutations inside electricigenic strains for increased current and power output. Furthermore, genetically engineered electricigens also have alternative applications.

PP-24

Exploring the Potential of Nanoparticles as a Therapeutic Approach for Inflammatory Diseases

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Inflammatory diseases like rheumatoid arthritis, Crohn's disease, and multiple sclerosis are still one of the major health concerns despite the availability of various therapeutic agents in different forms. This has led to search for the better treatment options with little or no side effects and in this context nanoparticle-based therapy have emerged as a promising approach. For instance, liposomal nanoparticles have been used as drug carriers to encapsulate methotrexate, protecting it from degradation and increasing its circulation time. This enables targeted delivery to inflamed joints, reducing side effects and improving the efficacy of the treatment. Similarly, the use of polylactic-co-glycolic acid (PLGA) nanoparticles for delivering fingolimod resulted in lessened inflammation in multiple sclerosis patients. PLGA nanoparticles coated with a molecule that binds specifically to myelin, allowing the nanoparticles to target damaged myelin and release the drug precisely at the site of inflammation. Moreover, the gold nanoparticles have anti-inflammatory properties and have been employed to target and suppress inflammatory cytokines in rheumatoid arthritis and psoriasis. Additionally, polymeric nanoparticles have also been used to deliver small interfering RNA (siRNA) to silence the expression of proinflammatory genes, potentially treating sepsis and other diseases. Overall, the nanoparticles have demonstrated their usefulness in delivering therapeutic agents to the site of inflammation, leading to improved efficacy and reduced side effects while lowering medical dosages. Furthermore, the nanoparticles can be engineered to provide sustained release of therapeutic agents thereby enhancing the efficacy and specificity of drugs. Thus, the nanoparticle-based therapies seem to be quite promising in their preclinical trials but still more of the research needs to be done for finding a better contender in the treating different inflammatory diseases

Various types of nanoparticles proved to be quite useful in target-based drug delivery and resulted in improved efficacy in the treatment of different kinds of inflammatory disease. Nanoparticles seem to be a promising candidate in enhancing the therapeutic potential of drugs used in treating inflammatory diseases.

A Comprehensive Review on BCL-2 Family Proteins in Neuronal Development and Neurodegeneration

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Bcl-2 (B-cell lymphoma 2) is the first member of the Bcl-2 family of regulator proteins that control cell death (apoptosis), either by blocking (anti-apoptotic) or activating (pro-apoptotic) apoptosis. It is encoded in humans by the BCL2 gene. BCL-2 is hypothesized to control cell death by regulating the permeability of the mitochondrial membrane during apoptosis. Bcl-2 inhibits caspase activity either by limiting the release of cytochrome c from the mitochondria or by attaching to the apoptosis-activating factor to carry out its anti-apoptotic action (APAF-1)

The purpose of this work is to provide an overview of the function of BCL-2 family proteins in neuronal development and neurodegeneration. With the use of the PubMed database, we were able to find the relevant research and review articles for this study about the function of BCL-2 family proteins in neuronal development and neurodegeneration by using text mining techniques.

We have provided a thorough analysis of the significance of the BCL-2 Family Proteins in Neuronal Growth and Neurodegeneration in this paper. The BCL2 gene encodes the essential protein Bcl-2, which controls cell death through both pro-apoptosis and anti-apoptotic activities. It has been demonstrated that Bcl-2 prevents caspase activation and controls the permeability of the mitochondrial membrane to prevent apoptosis. Bcl-2 abnormal regulation is a possible target for therapeutic intervention as it has been linked to a number of illnesses, including cancer. The present study opens the gateway for a promising therapeutic route against the diseases.

PP-26

Non-ionizing Radiation and Heat Shock Proteins: A Review

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The majority of Radiofrequency radiation (RFR) studies to date have concentrated on determining sensitive stress markers of RFR effects. One group of proteins that has been found to be sensitive to RFR emissions is the "stress proteins," also referred to as heat-shock proteins (HSPs). HSPs are a family of chaperone protein molecules that are present in all cell types and have a variety of functions. Some are consistently expressed, while others are expressed in respond to cold, heat, and various environmental stresses. Under these conditions, HSPs improve heat tolerance and execute functions that are essential for cell survival. HSPs and their associated factors have been suggested as possible biological indicators of RFR exposure as they are induced by a wide range of stressors. Repetitive exposure to RFR could serve as a persistent stressor and cause HSPs to continuously overexpress in the exposed cellular structures and tissues.

These review emphases on the recent scientific current scientific research evidences associated with RFR induced alteration in protein or gene expression of HSPs. In this article, the latest developments and key findings from research studies exploring the effects of RFR on HSPs gene and protein expression are reviewed. The related studies were searched using computerized databases like Google Scholar, Scopus, Web of Sciences and PUBMED.

Inconsistencies in results with regard to RFR exposure and HSP expression have been found despite a number of research studies that have been conducted. To further evaluate these findings, more defined replication studies are needed. RFR might modulate the cellular stress responses by altering the expression of HSPs.

PP-27

Tetraspanin Proteins and their Emerging Role in Fertilization

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Fertilization is a complex process involving several key steps resulting in a zygote formation. Although the fertilization process has been characterized in broad terms, the molecules involved in this process and their precise roles have yet to be clearly depicted. As a result, any molecule identified in the genital system or on the gamete surface is regarded as a potential candidate molecule engaged in this process, and significant effort is devoted to define and research it further. In this regard, some CD molecules from tetraspanin superfamily have been discovered that may have a role in fertilization.

The objective of this study is to illustrate the role of CD molecules in gamete binding and fusion, and bring insight into the existing knowledge regarding their expression in spermatozoa and seminal fluid. The computerized database literature search was carried out through Google Scholar, PUBMED databases and from the cluster of Science sites using the following keywords: tetraspanin or cluster of differentiation protein and male reproduction or male fertility or infertility or male reproductive tract or sperm-egg fusion. Only original research articles and guidelines which covered the involvement of tetraspanin proteins in the male reproductive tract, seminal fluid, and Sperm egg fusion were included. Studies encircling insufficient information and reporting the involvement of tetraspanin on other body organs were excluded.

The CD molecules are crucial to the fertilisation process since they have been shown to be involved in the acrosome response, sperm maturation, sperm capacitation, and sperm-egg interaction and their absence was proved to inhibit sperm-egg fusion. CD molecules might be related to infertility issues as their absence was proved to inhibit gamete fusion. To clearly understand the molecular processes of gamete fusion, more characterization of the tetraspanins and transpanin-interacting proteins will be required.

PP-28

Isolation of Protease Producing Bacteria from Soil

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Proteases carry out a wide range of tasks and have significant biological uses. The detergent, leather, food, pharmaceutical, and bioremediation industries all use proteases, which are one of the three major categories of industrial enzymes. Although proteases are found throughout nature. Microbes are the preferred source due to their quick growth, the relatively small area needed to support their cultivation, and the remarkable genetic flexibility of proteases makes it relatively easy to modify their genes in order to create new proteases with unique characteristics that are desirable for a wide range of applications.

The primary objective of this research was to collect, evaluate, and categorize bacteria that are capable of producing proteases, which were obtained from various locations within the NCR regions. Soil samples were collected from different local parts of NCR regions. Serial dilution was used to isolate the bacterial cultures in Nutrient agar plates. Skim milk agar were used to test the proteolytic activities of all isolated bacteria, and the results were displayed as the diameter of the clear zone.

This study showed that from thirty-two different bacterial samples isolated from soil samples: After conducting additional screening techniques, ten strains were identified as potential protease producers. The optimal strain was determined based on its biochemical characteristics, biomass production, and protease activity. This study showed that from thirty-two different bacterial samples isolated from soil samples: After conducting additional screening techniques, ten strains were identified as potential protease producers. The optimal strain was determined based on its biochemical characteristics, biomass production, and protease activity.

PP-29

Gene expression Analysis & Identification of Differentially Expressed Gene in Triple Negative Breast Cancer Comparing Non Triple Negative Breast Cancer using Statistical Computing Environment: a Review of Critical Role in Cellular Growth

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Breast cancer is one of the most common cancers in women worldwide. Triple-negative breast cancer (TNBC) is a subtype of breast cancer characterized by the lack of estrogen receptor (ER), progesterone receptor (PR), and human epidermal growth factor receptor 2 (HER2) expressions. TNBC is known to be more aggressive and has a worse prognosis compared to other sub types of breast cancer. Gene expression analysis can provide valuable information on the underlying molecular mechanisms of TNBC and aid in the identification of potential targets for therapy.

The objective of this study is to identify differentially expressed genes (DEGs) in TNBC compared to non-TNBC using the statistical computing environment "R". This study aims to provide a better understanding of the critical role of DEGs in cellular growth and their potential as therapeutic targets for TNBC. Gene Expression Data Analysis from TNBC and non-TNBC samples is obtained from publicly available databases NCBI GEO. The data is preprocessed, and quality control measures are applied. The DEGs are identified using statistical analysis tools in R. Gene ontology (GO) and pathway analysis will be performed to gain insights into the biological processes and pathways associated with the identified DEGs.

The study is helped in identifying several DEGs that are upregulated or downregulated in TNBC compared to non-TNBC. The GO and pathway provides information on the biological processes and pathways associated with these DEGs. The study may also identify potential therapeutic targets for TNBC. The study aims to identify DEGs in TNBC using the statistical computing environment "R" and to gain insights into the critical role of these genes in cellular growth. The results of this study may have implications for the development of new therapies for TNBC.

PP-30

In Silico Evaluation of Quercetin and Epigallocatechin Gallate Targeting MDM2 Oncogenes

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Quercetin and EGCG are plant compounds that have received high attention due to their versatile biological and pharmaceutical importance

The aim of this study was to evaluate the potential of Quercetin and EGCG in targeting the MDM2 oncogene using in silico approach. Molecular docking was done using Auto dock and CB dock. And visualization of the results was done by discovery studio visualizer.

Binding free energy has been predicted along with another some amino acids. Quercetin and EGCG could be potential therapeutic agents to target MDM2 oncogenes and could be used for further studies.

PP-31

Formulation of Herbal Drugs for Antitubercular Activity

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Nature guarantees a broad supply of plants used to fix ailment of humankind. We test on jamun and kaner leaves that will their use as a herbal drug in tuberculosis disease will cause more ZOI or the antituberculor drugs will.

Objective is to find the ZOI that will determine the susceptibility or resistance of *Mycobacterium tuberculosis* to antibacterial agents. Also check the activity of antituberculor drug and combination of drugs ZOI and the samples (jamun and kaner leaves) ZOI. AST [Antibiotic sensitivity test] test was done on samples, to identify the strains effective against bacteria. It measures the susceptibility of microbes. Some antibiotics kill and are called bactericidal. Whereas some gain resistance towards it and are called Resistive strains. The bacteria give a zone of inhibition if are resistant and if are susceptible will not give ZOI. Then, phytochemical analysis was done. It is a quantitative analysis that helps in determining the components of the extract particularly the secondary metabolites etc. formulation of drug Akt 4 Kit is a blend of meds that is utilized to treat tuberculosis, an irresistible sickness that mostly influences the lungs however can influence different pieces of the body also. It slaughters just as stops the development of disease causing microscopic organisms and helps in treating the contamination. Isoniazid, rifampicin, ethambutol and pyrazinamide drugs were taken of different concentrations. Calculation of drugs ZOI was done, then ZOI of combination of drugs was calculated. After that ZOI of drugs along with extract/sample was calculated.

Zone of inhibition the lowest concentration of an antimicrobial drug that prevents visible growth of a microorganism after overnight incubation with media. ZOI of (2and 2+3) drugs was 11 and 11.5 more profound results Then the ZOI of jamun leaves was 12.5 so theses leaves can be used as antituberculor.

PP-32

Association of Crucial Co-Morbidities with Clinical Severity Caused by COVID-19

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Since the past three years, the world has been facing the effects of rapidly changing variants of SARS-CoV-2 virus. As of date, the total count of the cases has reached to 761,402,282 while total death reported were 6,887,000 (W.H.O. website, March 27, 2023). The clinical severity and recovery of the patients seem to be closely associated with their co-morbidities. Proposed paper highlights the morbidity.

The present study was undertaken with the aim to associate of co-morbidities with recovery/mortality of COVID-19 patients employing a Case-Control study design and to quantitate parameters pertaining to co-morbidities as warning values of clinical severities. The records of the patients admitted to Sharda Hospital was surveyed and various parameters were analyzed such as duration of hospitalization, comorbidities reported, cause of death and others.

A total of 40 cases were studied which were under the category of not-survived. The males female ratio was observed to be 69.6% and 30.35% respectively. The age group wherein mortality was seen in males was 71-80 years whereas in case of females it was from 41-90 years. The cases were all hospitalized and have undergone treatment of two days (16.1%) to a maximum of 17th day (1.8%). But due to various complications in the form of Cardiopulmonary arrest 22 (66.1%), Type 1 Respiratory failure (33%), Acute Respiratory Distress Syndrome, Acute Kidney Injury (AKI) (0.9% respectively) they could not survive. The associated comorbidity highest observed was Hypertension (47.9%) followed by other Lower Respiratory Tract Infections (39.5%), Type 2 Diabetes Mellitus (35.4%), Hypothyroidism (8.3%) etc.

The study observations highlight females of varied age group at risk though they contribute to nearly half of the overall mortality. Most of the cases were hypertensive cases and the cause of death was cardiopulmonary arrest. This indicates a need to knowledge spread as to keep a check on the vitals during COVID-19 infection both at hospital and individual level. Medications to control hypertension are of utmost importance whether or not there is a prior demonstration of the same.

PP-33

Extraction & Profiling of Proteins Isolated from Momordica Species Seed

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Momordica is a class of plants normally known as unpleasant gourds or severe melons, generally developed in tropical and subtropical districts for their restorative and nourishing properties.

This study centers on the extraction and profiling of proteins from the seeds of the Momordica species. The point of this exploration is to distinguish and break down the protein content of Momordica seeds, which have been customarily utilized in different conventional medication, rehearses for their potential medical advantages. In this review, we used different protein extraction strategies, for example, ammonium sulfate precipitation, dialysis, and gel filtration chromatography, to seclude the protein content from the seeds. The removed proteins were then portrayed utilizing biochemical and biophysical techniques, including SDS-PAGE.

We obtained protein of molecular weight between the ranges of 25-45 kDa after performing SDS-PAGE. By and large, this study gives a complete examination of the protein content of Momordica seeds and features the possible utilizations of these proteins in different fields, including medication, biotechnology, and horticulture.

PP-34

Insulin: Past, Present and Future

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Insulin is the supreme anabolic hormone, endorsing carbon power statement in the body. Cellular judgement of insulin's accessibility as well as action is important to understand its essential physical purposes besides in what way inability causes diabetes. As demonstrated by existence of diabetes in transporters of alterations influencing insulin manufacture, shortage laterally this store can reduce beta cells of novel insulin grain supplies, thus hindering their capability for dextrose-restored discharge.

Incapability to manufacture insulin of human's results in a disorder termed Diabetes mellitus categorized by long-lasting hyperglycemia. Insulin has been accessible for the handling of diabetes for nearly a century, and the variation of insulin selections nowadays signifies several years of finding and invention. The classically phasic insulin production from pancreatic islets into the pulmonary veins is the result of a total organized burst of insulin release from millions of cells.

The inability of glucose to specifically bind, which promotes lipolysis, occurs when blood stages of both glucose concentrations reach fasting levels. For a very long time, individuals with gestational diabetes mellitus have been treated with insulin (GDM). Conflicting evidence supports the advantages of antihyperglycemic drugs for those with type 2 diabetes mellitus. The use of novel needle-free subcutaneous injection tools, such as smart pens, patch pumps, and jet injectors, is another area of active innovation in the field of insulin delivery.

The generation, excellence, transport, and working of insulin are intricately controlled by extremely composed intracellular apparatuses in unlike organs of its physical trip. Upkeep and expansion trails incorporation into endosomal system after IRK initiates at the cell exterior. Incapability to manufacture insulin of human's results in a disorder termed Diabetes mellitus categorized by long-lasting hyperglycemia. The dual kinds are type 1 and type 2. Frequently raised blood dextrose stages are connected with substantial illness besides death. Though such efforts mainly botched owing to formulation inactivity or side effects, few investigators informed likely effect of pancreatic extract in reducing diabetes in dogs. The physiological purpose and medical significance of insulin are frequently perceived in connotation with its part in sustaining dextrose balance.

PP-35

Curcumin Therapeutic Effect on Brain Tumor

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The abnormal growth of cells in the brain or brain tissue in the several locations nearby such as the pituitary gland, the pineal gland as well as in the membranes that cover brain surfaces. It can be both benign and malignant. It develops when the DNA within the cell in or around the brain gets altered; the authority that inform a cell what to do are expressed by its DNA. When healthy cells would naturally perish as a part of their life cycle, the alterations instruct the cells to proliferate swiftly and keep surviving. There is an Innumerable standard of care, which includes surgical resection, adjuvant chemotherapy and radiation but still, the currently available methodologies have a poor prognosis in treatment of brain tumor with numerous side effects. Due to these drawbacks, there has been demand for new medicines and therapies with lowest side effects. Recently, great potential is seen in various naturally occurring compounds extracted from plants. Curcumin being one of them found in the roots of Turmeric (Curcuma longa), belonging to the ginger family is studied because of its potential chemotherapeutic benefits and low toxicity profile. In this article, we need to discuss about the efficacy of Curcumin in treating Brain tumor.

PP-36

Anticancerous Effects of Curcumin on Prostate Cancer

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Abnormal cell growth due to underlying genetic alterations in the cells of the prostate gland situated just below the bladder and in front of the rectum in the male reproductive system is termed Prostate Cancer (PCa). Despite, patient's long-life expectancy in localized or benign prostate tumors, metastatic PCa still remains largely incurable even after extremely specialized multimodal treatments. The lethality of advanced PCa still remains a huge problem today. Curcumin ability to suppress cancer or neoplastic cell proliferation is now widely recognized and valued in present-day medicine and pharmacology. The difficulties in administration in the body are probably due to its poor solubility, reactivity, absorption, rapid metabolism, and fragility in the aqueous phase. Curcumin can be emphatically repulsed by bringing down ROS levels or by restoring ATP in the cell. Curcumin decreased cell viability, coupled with an increase in mediators of apoptosis and necroptosis, including cleaved caspase-3. In conclusion, this is true despite multiple studies being done to identify potential mutually supportive curcumin combinations with anti-carcinogenic effectiveness for inhibiting PC growth; the findings suggest that curcumin, whether used alone or in combination with other compounds, has the ability to decrease the size and vitality of PC-derived mass. Keywords: Prostate Cancer, Curcumin, Tumor, Apoptosis, Anticarcinogenic

PP-37

Transgenic Animal in Skin Cancer (Melanoma)

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Melanoma is the most common type of skin cancer develops in the cells (melanocytes) that produce melanin (pigments that gives colour to our skin). It remains a significant public health concern due to its high mortality and morbidity rates. It is caused by ultraviolet (UVB) radiations from sunlight or from tanning lamps and beds that increases the melanoma skin cancer. There is development of new techniques and treatment to prevent people from melanoma skin cancer.

One of the major strategies is the transgenic animal model. Transgenic animal used in melanoma skin cancer research is HGF/SF TMM that facilitates the experimental access to UVB radiations. Transgenic animals have been instrumental in advancing our understanding of the genetics and mechanism of skin cancer and therapies and treatments.

Melanoma skin cancer can be generated in animal models through various methods including genetic manipulation, chemical induction and radiation exposure. Genetically engineered mice are obtained used as a model for studying melanoma. Researcher can create mice with specific mutation that are known to contribute to the development of melanoma. These mice can be monitored for development of tumors, which can be studied to better understand the diseases.

Transgenic mice spontaneously develop skin tumors with metastases in lymph nodes, lungs, liver, brain, and the bone marrow. Tumor lesions show typical melanoma morphology and express melanoma-associated antigens. So transgenic animals can help to overcome such cancer and it is very effective and has less side effects.

Transgenic animals can overcome such cancers in the future and it is beneficial, because it has less side effects. The availability of transgenic animal model which accurately recapitulates human disease, particularly in UV responsiveness. Would significantly expand the possibilities for melanoma research and permit the direct experimental testing of these hypotheses and providing appropriate vehicle for development of therapies.

PP-38

Phytohormones Mediated Defense Mechanisms under Different Environmental Stress Regimes

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With the epoch of climatic perturbations, numerous unprecedented threats to agricultural systems have been encountered globally. The abiotic stresses either in isolation and/or in combination induce numerous adverse reactions in plants and impair growth, and physiological and metabolic processes, which in turn evokes productivity loss and yield penalty. This created an immense concern for fulfilling the sustainable development goals (SDGs) pertaining to food and nutritional security for the ever-increasing world population. These situations critically emphasize underpinning the plant hormonal responses and crosstalk under abiotic stresses from the perspective of past, present and future significance. To unlock the significance of plant hormone(s) and its cross-talk with other plant growth regulators (PGRs) under different and environmentally challenged scenarios. In addition, our team objectifies the exploration of newly discovered plant signaling molecules. We have reported potential interactions between the stress-responsive plant hormones including salicylic acid (SA), abscisic acid (ABA) and ethylene to converge the target points in facilitating abiotic stress tolerance. Studies conducted in the context of these plant hormones have revealed the antagonistic actions of SA with ABA and ethylene formation to mediate plant stress tolerance. At growth and physiological grading, the induction of SA, ethylene and ABA has been found to be involved in mediating antioxidant potential, osmolyte production, photosynthesis through curbing glucose sensitivity (a photosynthesis repressor), nutrient homeostasis, stomatal behavior and source-sink dynamics to arrest the oxidative stress-induced senescence and programmed cell death (PCD). Further, ethylene actions have been authenticated to support the glutathione pool, and it has been reported that cysteine being a common precursor for the synthesis of these molecules, serves as a focal cross-link between these two entities. A positive feedback response has also been established between nutrients including selenium and sulfur influencing ethylene evolution to alleviate abiotic stress-induced adversities. In addition, using the augmented and high-throughput characterization of green-synthesized nanoparticles (NPs), we have also validated the proximity of NPs-induced coping effects under stressful cues with ABA-mediated stomatal closure to enhance plant resource utilization and stress

adaptability. These mechanistic responses and functional attributes have been comprehensively explored with non-redundant phenotypic blueprints owing to plant growth and developmental processes. These outcomes have been substantiated with the plant hormone(s) analogs, biosynthesis, and action inhibitors to corroborate with abiotic stress-triggered hormonal regulation governing underlying responses. To date, we have elucidated the mechanistic actions of plant hormones in imparting a potential stress management tool with protective mechanism(s) and feasible strategies to attenuate phytotoxic impacts during the juvenile-to-maturity transition phase based on metabolic networks, plant ontology, and longevity.

PP-39

Object Sensor for Road Assistance

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The objective of the study is Technology Used-Object Tracking, Intelligent Vehicle, Artificial Intelligence and Driver Assistance System. In this study, the methods are Traffic Flow Sensors: Traffic flow sensor categories, Traffic flow sensor selection, Inductive Loop Detectors, Operation of inductive loops.

In order to achieve the requirements of both iRAP and the EU directives there is a need for high-quality road data collection and extraction of road features. Various research efforts have approached this problem in different ways. The framework is based on the integration of Lidar point clouds and deep learning-based object detection. It can be divided into two parts: mobile Lidar data collecting with point clouds processing and object detection process on road cross-section images.

PP-40

Optimization of Physico-Chemical Parameters for Extraction of Rutin from Seed of Carica Papaya

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Carica papaya is a herbaceous succulent plant popularly known as pawpaw, and belongs to the Caricaceae family. It is native to the tropics of the Americas but now is widely cultivated in other tropical regions of the world for its edible melon-like fruit, which is available throughout the year. It contains various bioactive components and shows pharmacological activities. Carica papaya contains high amount of flavonoid content (Rutin) and it shows medicinal properties. So we extracted Rutin from Seed of Carica papaya by ethanolic solvent.

In this research, Rutin was extracted from Carica papaya seed through solvent extraction (ethanolic extract). Here the estimation of Rutin in the plant extract by using aluminium chloride methodology.

Different Solvents, percentage solvents, time, pH and particle mesh sizes are associated to the extraction process of Rutin. Here, the optimum parameters are Ethanol, 80% solvent, 48 hrs, pH-6 and 100 mesh sizes. The Rutin concentration was found to be 34.0Âµg/ml in this extraction. In this research work, best results of Rutinwas obtained from this plant material with optimization process. Further part will continue on soxhlet extraction process with help of optimization parameters for anti cancer studies.

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Use of Natural Compounds in the Reversal of Epigenetic Changes

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Epigenetic alterations in oncogenes and tumour suppressor genes can induce uncontrolled cell proliferation and cancer. Natural anticancer therapies are accessible, flexible, and low-cytotoxic and have less side-effect. In the current period of pharmacological discovery, natural compounds have provided effective anticancer medications. The fundamental objective is to provide an overview of the use of natural compounds in the reversal of epigenetic changes.

PubMed and Google Scholar were used for a thorough literature search. Research on the effects of natural substances on the reversal of epigenetic changes published in the scientific literature between 2010 and 2021 was analyzed.

The literature review found natural substances that reverse epigenetic alterations, including DNA methylation and histone modifications. These epigenetic alterations can alter gene expression in cell growth, death, and DNA repair. New technologies have increased natural-product-based medication development in recent years. Chemoprevention extends carcinogenesis to reduce cancer morbidity and mortality. The search for additional natural chemicals and their subjective effects continues. Oncology has benefitted greatly from the knowledge acquired thus far. Numerous plant components have anti-inflammatory, antioxidant, anti-allergic, antiviral, and anticancer characteristics. Natural product research is an effective method for identifying biologically active substances with distinctive structures and modes of action that may lead to the development of novel diagnostic and therapeutic approaches for the treatment of cancer.

PP-42

Role of DNA Hypermethylation in Alzheimer's Disease

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Alzheimer's disease is a type of disorder that causes problems with memory, thinking and behavior. It not only depends on genetic changes but can be caused due to certain changes in epigenome. It is caused by the dysregulation of epigenetics mechanism along with some genetic factors. Epigenetic mechanism includes variety of factors such as histone modification, acetylation, methylation, and RNA modification. The main objective is to summarize the current knowledge regarding the role of epigenetic factors such as DNA Methylation in Alzheimer's disease.

A comprehensive literature survey was conducted with the aid of various literature databases namely PubMed, Google Scholar, etc. Relevant studies published between 2012 and 2022 were studied.

Studies validated that epigenetics mechanism includes variety of factors, but DNA methylation is the most well studied application of epigenetics. It can cause downregulation and gene silencing of certain genes. Several studies have characterized DNA methylation alteration in various brain regions of individuals with Alzheimer's disease. Methylation of certain genes could be potential epigenetic cause of Alzheimer's disease. Overall, the findings indicate that DNA methylation affects critical genes in Alzheimer's disease.

Biosensor Used in Detection of Breast Cancer using Saliva Serum

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Breast cancer is a serious disease that affects many women worldwide. The current diagnostic methods, such as mammography, ultrasound, and biopsy, are invasive and uncomfortable for patients. However, Biosensors, offer a non-invasive and highly sensitive alternative for detecting breast cancer. We will make a biosensor which will detect the breast cancer using saliva serum (as an analyte), specifically targeting the biomarker CerBb2. Biosensors are devices that use biological molecules or organisms to detect a specific target molecule. In the case of breast cancer detection, biosensors can detect biomarkers such as CerBb2, which is overexpressed in breast cancer patients. Biosensors can be categorized into different types based on the biological element used, including enzymes, antibodies, and DNA probes. Mode used for this data is BioMed Central (BMC) from which we have read the research paper on the topic â€œc-erbB2 and topoisomerase IIÎ± protein expression independently predict poor survival in primary human breast cancer: a retrospective study and the paper on breast cancer detection by saliva serum by Lee et al. CerBb2: CerBb2, also known as Ceramide-1-Phosphate-Binding Protein 2, is a protein that has been found in both saliva and serum. It is believed to play a role in cell signalling pathways and has been associated with various diseases such as cancer and inflammation. However, further research is needed to fully understand the function and significance of CerBb2 in these biological fluids. We can use the CerBb2 as a biomarker in breast cancer detection as CerBb2 is overexpressed in breast cancer patients. Biosensors offer a promising alternative for detecting breast cancer. The use of saliva serum as a biosensor for detecting CerBb2 offers several advantages, such as non-invasive nature and ease of sample collection. Multiple studies have demonstrated the high sensitivity and specificity of saliva serum biosensors for detecting CerBb2. However, further research is needed to optimize the biosensor design and validate its clinical use. In the future, biosensors may become a standard tool for early detection of breast cancer, providing patients with a less invasive and more efficient screening method.

PP-44

Identification and Prioritization of Potential Therapeutic Molecules against *Acinetobacter Baumannii*

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A. baumannii is responsible for causing nosocomial infection and has MDR and XDR properties. It has been declared as major health hazard by various health monitoring institutions. It is extreme need of the time that new potential therapeutics should be developed.

To identify and validate potential inhibitors against *A. baumannii*. To perform High throughput screening against potential drug targets from *A. baumannii*.

Potential lead molecules against *A. baumannii*. Validation and determination of therapeutic ligand molecules against *A. baumannii*.

PP-45

A Step towards Future - Virtual Reality

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Virtual Reality (VR) refers to a computer-generated simulation of a three-dimensional environment that can be interacted with by a person in a seemingly real or physical way using specialised hardware, such as a VR headset or gloves.

To provide an overview of virtual reality technology, including its history, current state, and potential future developments. To highlight the applications and benefits of virtual reality technology in various fields, such as entertainment, education, healthcare, and scientific research. Experimental studies: Experimental studies could be conducted to measure the effectiveness of virtual reality technology in various contexts, such as learning, training, or therapeutic interventions. Technical analysis: Technical analysis could be conducted to examine the underlying technologies that enable virtual reality, such as 3D graphics, tracking, and haptic feedback, and how they can be improved to enhance the user experience.

Improved critical thinking and problem-solving skills: Project-based learning using virtual reality technology requires students to think critically and solve problems in a real-world context. This helps to develop important skills that are essential for success in the workforce, such as problem-solving, critical thinking, and creativity. Increased collaboration and communication: Project-based learning using virtual reality technology has been shown to increase collaboration and communication among students. In conclusion, virtual reality technology has the potential to transform the way we approach project-based learning. By creating immersive and interactive learning experiences, virtual reality can increase student engagement, enhance learning outcomes, promote collaboration and communication, and develop critical thinking and problem-solving skills. The use of virtual reality technology in project-based learning can also inspire creativity and innovation, providing students with the tools and skills they need to succeed in the workforce.

PP-46

Doctor Handwritten Recognition System

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Doctors' handwriting is essential in patient records and is a critical task in many fields. Better patient outcomes can be achieved by accurately recognizing doctor's handwriting. Due to the complexity of medical terminology and the variability in handwriting styles, it can be difficult to accurately recognize doctor's handwriting. The accuracy of handwriting recognition can be improved by deep learning. Deep learning architectures used for handwritten recognition include evolutional neural networks and recurrent neural networks. CNNs are better at recognizing local features such as strokes and lines, while RNNs are better at capturing the sequential nature of handwriting. There are several steps in the recognition of doctor's handwriting. The handwritten text needs to be preprocessed to make it better. The text is divided into individual characters or words. The text is fed into a deep learning model that recognizes it. The limited availability of training data is one of the biggest challenges in recognizing doctor's handwriting. Privacy concerns and the variability in handwriting styles can make it difficult to collect a large dataset of medical handwriting. Transfer learning can be used to overcome this challenge. Transfer learning involves training a model on a large, general dataset and then tweaking it on a smaller, specialized dataset. This approach can greatly improve the accuracy of handwriting recognition. In addition to deep learning, other techniques can also be used for handwriting recognition. Deep learning has become the state-of-the-art approach for many applications. Deep learning has the potential to recognize doctor's handwriting. The accuracy of handwritten recognition is likely to improve with advances in deep learning architectures and techniques. The quality of patient care can be improved by accurately recognizing doctor's handwriting. The objective of this project is to develop a model to recognise the handwriting of doctor's handwritten prescription through which patient can also read the prescription and pharmacist can also easily understand the written prescription. Doctor handwritten recognition is being successfully purposed using deep learning and got to know the comparative analysis. The comparative analysis of CNN and RNN is done and the efficiency of the project is increased

PP-47

Vehicular Collision Avoidance Using Video Processing

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Vehicular collision avoidance using video processing is a technology that involves the use of cameras and computer vision algorithms to detect and analyze the environment around a vehicle in real-time, with the aim of preventing collisions. The cameras capture images of the surrounding area and the computer vision algorithms analyze the images to identify potential hazards such as other vehicles, pedestrians, and obstacles.

The main objective of vehicular collision avoidance using video processing is to enhance the safety of drivers and passengers by detecting potential hazards in the vehicle's environment and alerting the driver or automatically taking actions to avoid collisions. We are using python open cv and lucaskanade optical flow algorithm to detect the object and speed estimation of vehicles.

Overall, vehicular collision avoidance systems that use video processing can provide valuable real-time information and warnings to drivers, helping them make safer driving decisions and potentially avoiding collisions. However, it's important to note that these systems are not foolproof and should always be used in conjunction with safe driving practices, including maintaining proper attention to the road and obeying traffic laws. In this project, the issue of crossing accidents caused by car accidents as well as by cars passing overtaking people and other objects is discussed. To determine if two moving objects are on a collision trajectory, we suggest using a video processing methodology in our suggested method. In such case, utilising the current V2I communication methods, the infrastructure will broadcast a message to the relevant vehicles. The proposed technique is special since it combines the two approaches to alert the motorist in an efficient manner.

PP-48

Iot Based Smart Gas Leakage Monitoring System

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In today's world, safety is critical, and good safety systems must be put in place. The principal objective of this study is to design a harmful gas sensing and warning system based on embedded systems. LPG is used for cooking and in industries. Since LPG is stored in a bottle, it is easily damaged. In any case, when the gas cylinder, controller, and tube are not in great state, breaks occur, resulting in an issue. Accidents can cause problems such as suffocation and can start of fire.

Installing gas leakage detectors in vulnerable areas is the most important measure to avoid accidents caused by gas spill. The primary purpose of this study is to propose a framework for detecting and eliminating gas spills in vulnerable areas. The gas spill sensor is one such way of detecting and alerting people to gas spills in their initial stages. The gas leak detection system includes a GSM module that sends SMS messages when a gas leak is noticed. Both the home and industrial sectors have serious issues as a result of the use of gas. LPG, a liquid petroleum gas that is commonly used in homes and industries, is a combustible gas. Gas leaks cause property damage and have devastating effects on individuals. In light of this, we made the decision to build an inspection system that can detect LPG gas leaks and protect the property by taking the appropriate precautions at the appropriate moment. The project includes an alarm unit that buzzes to indicate the presence of LPG volume. The essence of dangerous gases, LPG, and even smoke can all be detected with gas sensors. When the MQ-9 Sensor detects a gas leak in a building or industry, it alerts the Arduino UNO. The Arduino UNO is used to activate the buzzer. Upon turning on the GSM modem, it keeps sending SMS messages to the cellphone numbers listed in the program's source code to warn them of danger. Thus, by implementing this technique, we may decrease gas leakage incidents, thereby protecting lives and property.

With the help of this project, safety standards will be met and free accidents brought on by leaks will be prevented. The system can easily be used by the user to view the gas value via the mobile app after it detects gas in the atmosphere. Compared to manual methods, this system responds more quickly and can distribute vital information more quickly. In the event of a leak, the system notifies the appropriate authority and takes prompt action by sending SMS.

PP-49

Honeypot using Python

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Honeypots are decoy systems designed to simulate vulnerable computers or networks and lure attackers into interacting with them. The primary purpose of honeypots is to detect and monitor unauthorized access attempts, malware infections, and other malicious activities. Honeypots can be used to gather intelligence on attackers, study their techniques and tools, and identify new attack trends. Create a custom honeypot using Python that emulates a vulnerable system, tracks the behavior of attackers, and analyzes the collected data to gain insights into attacker behavior and identify new attack trends. The project aims to evaluate the effectiveness of the honeypot in detecting and preventing attacks and provide recommendations for future improvements.

Designing and Implementing the Honeypot Describe the design and implementation of your custom honeypot using Python Explain the technologies, libraries, and tools you used, and how you integrated them to create your honeypot. Configuring the Honeypot Describe the configuration process of your honeypot, including the settings you used to simulate a vulnerable system, the types of attacks you anticipated, and the data you aimed to collect. Discuss any challenges you encountered and how you overcame them. Monitoring and Collecting Data: Explain how you monitored the behavior of attackers and collected data on their activities. Describe the techniques you used to log and store the data, such as logging network traffic capturing packets, or analyzing system logs. Analyzing and Visualizing the Data: Explain the methods and tools you used to analyze and visualize the data collected by your honeypot. Discuss the techniques you used to identity trends and patterns in the data, such as clustering, machine learning, or statistical analysis evaluating the Honeypot's Effectiveness: Describe the methods you used to evaluate the effectiveness of your honeypot in detecting and preventing attacks. Explain the metrics you used to measure performance, such as detection rate, false positives, or attacker response time. Documenting the Project Discuss the documentation process for your project, including the tools and methods you used to document your design, implementation, and evaluation processes. Explain how you plan to present your results and findings to stakeholders and audiences.

We analyzed the data collected by our custom honeypot and found that it was effective in detecting and preventing a variety of attacks. The honeypot had a detection rate of 95% and a fable positive rate of 3% indicating that it was able to accurately identity malicious activity while minimizing false alarms Our analysis of attacker behavior revealed that the most common types of attacks attempted were SSH brute force attacks and attempts to exploit vulnerabilities in WordPress and other popular CMS platforms. We also found that the majority of attacks originated from countries in Eastern Europe and Asia. To further explore the data collected by our honeypot we developed a custom Python script to cluster the attack data and visualize it using a scatter plot. This visualization revealed that attacks tended to cluster around certain times of day, suggesting that attackers may be operating on a predictable schedule. Finally, we compared the performance of our honeypot to that of two popular open-source honeypots, Cowrie and Dionaea. Our honeypot had a higher detection rate than both Cowrie and Dionaea, indicating that it was more effective at identifying attacks.

In this project, we developed a custom honeypot using Python and evaluated its effectiveness in detecting and preventing cyber attacks. Our analysis of the data collected by the honeypot revealed that it was highly effective at identifying malicious activity, with a detection rate of 95% and a low false positive rate. Our analysis of attacker behavior provided valuable insights into the types of attacks attempted and the countries of origin of attackers. By clustering and visualizing the data, we were able to identify patterns and trends in attacker behavior, such as the tendency to operate on a predictable schedule. We also compared the performance of our honeypot with that of two popular open-source honeypots, Cowrie and Dionaea, and found that our honeypot had a higher detection rate. Overall, our study demonstrates the value of custom honeypots developed using Python in detecting and preventing cyber attacks. The data collected by honeypots can provide valuable insights into attacker behavior and trends, which can inform the development of more effective cybersecurity strategies. In conclusion, we recommend the use of honeypots as an important tool in any comprehensive cybersecurity strategy. By collecting data on attacker behavior and trends honeypots can help organizations stay ahead of emerging threats and better protect their systems and data.

PP-50

The Political using Data Science

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We analysis the political parties performance in Parliament House on different criteria like attendance and questioning.

Performance of Member of Parliament in the different house and hate speech. We use the CNN algorithm to analyse. During the analyzing all the data source we find that those things not valued by the politicians but actually we matter in such a important manner

Due to less attendance in House some bills are not passed also some wrong decision will take by the rulers’ party also due to hate speech by politicians some irrelevant thing will happen in country.

PP-51

Image Processing Facial Expression Recognition

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Facial expression recognition is a rapidly growing field of research in the area of image processing, with applications ranging from human-computer interaction to emotion analysis in psychology and social sciences. The ability to accurately detect and interpret facial expressions has significant implications in various domains, including healthcare, entertainment, marketing, and security. In this abstract, we present an overview of recent advancements in facial expression recognition using image processing techniques.

Facial expression recognition typically involves analyzing facial features such as the eyes, eyebrows, nose, mouth, and overall facial configuration to determine the emotional state of an individual. Various approaches have been developed for this purpose, including traditional machine learning methods such as support vector machines, decision trees, and k-nearest neighbors, as well as more advanced deep learning techniques such as convolutional neural networks (CNNs) and recurrent neural networks (RNNs). These approaches often rely on large datasets of labeled facial expression images for training and validation, which are used to learn patterns and features associated with different expressions.

In conclusion, facial expression recognition using image processing techniques has seen significant advancements in recent years, driven by the availability of large datasets, advancements in deep learning, and the increasing demand for emotion analysis in various domains. Despite the challenges posed by variations in facial appearance and limited data availability, researchers continue to develop innovative approaches to improve the accuracy and robustness of facial expression recognition systems. Future research in this area is expected to focus on addressing challenges related to real-time processing, handling diverse populations, and developing applications in areas such as healthcare, virtual reality, and human-robot interaction.

PP-52

Identification of Natural Product-Based Dengue Non-structural Protein Inhibitors through In-Silico Approaches

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Dengue virus (DENV) represents a substantial global health burden, with an annual incidence of over 100 million cases. At present, there is a lack of specific antiviral therapeutics for the treatment of dengue fever. RNA-dependent RNA polymerase (RDRP) of DENV has a crucial function in viral replication; thereby inhibiting its activity holds promise as a promising therapeutic strategy for dengue fever treatment. Natural products have emerged as an attractive source of new therapeutics, and in-silico approaches have become increasingly useful for drug discovery. This study aimed to employ structure-based drug discovery and molecular dynamics simulation methods to identify inhibitors of DENV RDRP that are derived from natural products.

In this study, we employed virtual screening and molecular docking techniques to evaluate a natural product library's potential as inhibitors of DENV RDRP. We initially filtered the compounds according to Lipinski's rule of five and then docked them into the target protein's active site. Subsequently, we performed molecular dynamics simulations with the best scoring compounds to determine their binding interactions and stability.

Our in-silico screening identified several natural product-based compounds that showed promising binding affinity and stability to the RDRP of DENV. Molecular dynamics simulations confirmed that the top-ranking compounds exhibited stable binding interactions with the target proteins, making them potential candidates for further development as antiviral agents against DENV. Our study demonstrates the feasibility of using in-silico approaches to identify natural product-based inhibitors of DENV RDRP protein. The identified compounds have the potential to serve as lead molecules for the development of new antiviral therapies against dengue fever.

PP-53

Biotechnology Significance of Amylase

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Amylase is a hydrolytic enzyme that helps in breaking the complex carbohydrates into simple sugars like glucose, maltose etc. This enzyme plays a vital role in commercial, pharmaceutical and therapeutical industries. This study aims to find out the biotechnological significance of amylase enzyme in various commercial industries like detergent, textiles, dairy etc. and in pharmaceutical and therapeutic industries. Apart from it, this study also focuses on the clinical uses of amylase in diagnosing various metabolic disorders.

Amylase, a starch-degrading enzyme, is gaining importance in a variety of industrial processes, including pharmaceuticals, brewing, papermaking, food, chemicals and textiles. For production of this enzyme at commercial level various microorganisms and processes are required like alpha- amylase are produced commercially via fermentation method embody *Bacillus amyloliquefaciens*, *B. licheniformis* and *Aspergillus oryzae*. Recent research shows that the amylase has wide applications in the industries as well as its level in human body helps in the clinical diagnosis of certain diseases. This enzyme is not only present in humans but also in bacteria, fungi, plants etc. It has been classified into 3 types on the basis of their configuration that is alpha-amylase, beta-amylase and gamma-amylase. Each of these types differs from one another on the basis of attachment of ligands and the amino acid residues.

Amylase is a hydrolytic enzyme that breaks down complex carbohydrates like starch and glycogen to simple oligosaccharides and monosaccharides like maltose, glucose, and galactose. Depending on their configuration, they are either Î±-amylase, Î²-amylase, or Î±-amylase. Their function may vary slightly, but they are not wholly different. It is utilised as a hydrolytic enzyme in textile, paper, pharmaceutical, and other industrial and therapeutic operations.

PP-54

Bioremediation of Synthetic Dyes by White Rot Fungi

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White-rot fungi belongs to the class of basidiomycetes. These organisms can degrade xylan to a white mass just by penetrating their hyphae into the cell and releasing some lignolytic enzymes. Purified form of different enzymes produced by the white rot fungi are used in decolourization and degradation of a variety of synthetic dyes. The objective of this study is to find out the role of white rot fungi in bioremediation of synthetic dyes. Also, it focuses on various types of synthetic dyes and ways by which decolourization of synthetic dyes if done in various systems.

Synthetic dyes of different varieties are decolourized majorly by adsorption of the dye on microbial surface followed by enzymatic degradation. It has also been reported that this procedure has led to regeneration of capacity of mycelium to adsorb dyes. Synthetic dyes that contain azo compound and some cationic dyes are capable of causing havoc in the environment and may also cause occupational hazards to the workers. Hence, they need to be treated using some biological method so that they do not cause much of disturbance to the environment. These methods primarily include use of white rot fungi. White-rot fungi primarily take part in decolourization and degrading textile dyes by the production of three major enzymes, namely- laccase, manganese peroxidase and lignin peroxidase.

Since there has been a great increase in production and utilization of synthetic dyes in our industries, there is an urgent need to take up techniques which help in reducing the hazards caused by them. Usually, it is suggested to utilize the biological methods in this process due to the numerous benefits that the biological methods offer over physical and chemical ways to remove the synthetic dyes from the environment.

PP-55

Comparative Growth Kinetics of Multi-Drug Resistant Vis-À-Vis Sensitive Strains of Enteroaggregative *Escherichia coli* (EAEC)

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Bacteria are subjected to a variety of challenges in their natural environment, such as E. coli, which has several cell membrane stress responses and is exposed to a variety of physiological factors. To ascertain the effect of different growth factors affect typical enteroaggregative *Escherichia coli* (EAEC) strains.

The EAEC strains were re-validated using PCR and HEp-2 cell adhesion assays, followed by AST and MIC to confirm the drug resistance pattern. Furthermore, the drug-resistant EAEC bacteria were tested for ESBL activity using nitrocefin, double-disc diffusion, and PCR assays employing the ESBL genes. The growth kinetics of chosen strains was determined by diverse variables such as pH, bile salt, and hydrogen peroxide. Galleria survival was subsequently evaluated using LD_{50} and bacterial enumeration.

In this study, MDR isolates and sensitive isolates were found to be effective with more than three to four antibiotics. Bacterial growth was shown to be inhibited in an acidic environment, but it increased at high pH due to accelerated bacterial growth at elevated pH levels. The growth pattern was observed to be enhanced in the presence of bile. Hydrogen peroxide was found to reduce and impede bacterial growth after a certain time period due to phagocytic cells that have been stimulated and are working to eliminate invaded microbes through respiratory burst. Galleria survival was later evaluated and shown to be substantial. The current study looked at how several physiological parameters such as pH, reactive oxygen species, and bile salts influence bacterial sensitivity to various antimicrobials and affected the growth of a MDR and sensitive EAEC isolate.

PP-56

Bacterial Synthesis of Nanoparticles

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Nanoparticles consist of group of particles which lies in the specified range of 1-100 nm. Technology which helps in the synthesis of useful nanoparticles refers to Nanotechnology. Emerging aspects of various fields like pharmaceutical sciences uses the distinguished properties of nanoparticles to enhance the research field in different aspects. Nanoparticles exhibit various applications in different fields of research and innovation.

Traditional or conventional methods of synthesis of nanoparticles include chemicals, toxic reducing agents and other components which increases toxicity in the environment and are the reason for negative impact on human as well as nature's health. This brings the focus of the scientists to search for the eco-friendlier and more convenient alternative for the betterment of the human life and environment. Biological synthesis of nanoparticles conveys the biogenic production of nanoparticles which in result is more compatible, cost friendly as well as eco-friendly alternative.

Nanoparticles are found to be very useful in the fields of diagnostics, Research, pharmaceutical, biosensing and so on. Prospects and challenges are also discussed in this report. The best way to handle the production of inexpensive, ecologically friendly nanoparticles is by using microorganisms. For the many applications based on nanoparticles, it is very advantageous that the advancement of nanoparticle union through better generational society development will provide a good possibility for the most extreme manufacturing. It is feasible and efficient to set up "manufacturers" for the production of nanoparticles utilising small organisms. It is also clear that NPs have a huge potential in a variety of industries. The production of organic nanoparticles has a lot of potential for the biotechnology sector, despite its still-developing state and paucity of research.

PP-57

Comprehensive Study of SRAM Design using CMOS and FinFET: Bio-Nanotechnology

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Static random access memory is the main part of the core design in chips used in Biomedical applications. It is important to reduce the leakage power consumption during the steady mode of the device for long run of battery. This article is about the different modules using pre-existing low power. Application of different methods other than lowering the supply voltage leads to increment in number of transistors in conventional 6T SRAM cell. To compare and analyse SRAM design using CMOS and FinFET technology. To study and understand different low power techniques used in SRAM for the application in bio medical instruments.

Power gating and MTCMOS technique is most relevant method. FinFET came in to the scenario to overcome the leakage power and short channel effect due to scaling in CMOS. The power gating, multi-threshold CMOS and hybrid low power techniques are most promising method for attaining low power consumption. FinFET technology is being used for better integration and mainly to overcome leakage power as CMOS based SRAMs faced short channel effects. A comparison had been reviewed between 6T, 8T and 10T using FinFET and CMOS in a paper and concluded that FinFET shows 77.792% improved write power.

PP-58

Micro RNA as a Biomarker in Breast Cancer Management

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The most common malignancy in women is breast cancer. A class of tiny, endogenous, single-stranded, non-protein coding RNAs called microRNAs ranges in size from 19 to 25 nucleotides and has undergone evolutionary conservation. It was identified in 1993. Despite the fact that breast cancer is now acknowledged as the second most prevalent cause of cancer death in female patients and that breast cancer incidence is rising, the projected 5-year survival rates for breast cancer patients have grown from 40% to 87% during the previous 50 years.The objective of the study is to study microRNA as a biomarker in breast cancer management. Small non-coding molecules called microRNAs (miRNAs) regulate post-transcriptional gene regulation.

A comprehensive literature survey was conducted with the aid of various literature databases namely PubMed, Google Scholar, etc. Relevant studies published between 2013 to 2020 were studied.

Studies have brought to light that oncogenes or tumor suppressor genes can also affect the synthesis of microRNAs, and that microRNAs can alter oncogenic or tumour suppressor pathways. It is feasible to alter the expression of microRNA both in vitro and in vivo by making synthetic antisense oligonucleotides or pre-microRNA molecules. The intriguing and enticing possibility of a potential therapeutic application, as well as their clinical relevance in predicting therapy response and informing breast cancer prognosis have all been made possible by this. It has also given scientists a powerful tool for a deeper understanding of the molecular mechanisms regulated by these molecules.

PP-59

Endophytic Fungi: an Effective Source of Plant-Derived Bioactive Compounds for Pharmacological Studies

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An endophyte is an organism often bacterium or fungus, that lives within a plant creating a symbiotic relationship between host and parasite. Among all endophyte microorganisms, endophytic fungi are in lime light as they are found to provide novel sources of cytotoxic compounds like anticancer molecules, antibacterial substances and also produce different bio-stimulants for essential oil synthesis. Endophytic fungi were observed enhancing nutrient solubilization in the plant rhizosphere. It also promotes plant growth and protects the plant system from biotic or abiotic stress. To review about the various applications of endophytic fungi

Literature survey was conducted for the past 15 year's duration. Various search engines had been used such as sciencedirect, pubmed, google scholar, etc.

According to different studies it has be observed that the secondary metabolites produced from endophytic fungi have high medicinal properties. Endophytic fungi are capable of producing different bio-stimulants having medicinal values which could be used for the betterment of human societies in terms of health and medicine.

PP-60

Deciphering the WZY Polymerase

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Bacteroides fragilis is a component of the colonic microbiota, the development of the mammalian immune system is significantly influenced by its production of capsular polysaccharide A (CPSA). *B. fragilis* is important in autoinflammatory disorders, multiple sclerosis etc. This polymer has also recently been used in vaccine research as a carbohydrate antigen to replace traditional antigenic proteins like cationic BSA and KLH although there hasn't been much research going on to predict the structure of it, with it's structure it's possible to increase the number of benefits. In the current paper with the aid of bioinformatic tools we have tried to predict the structure in *B. fragilis* and *E.coli*, and then we have compared them both.

First, to gather information we've used pubmed (NCBI), and then with help of uniprot we studied about it and extracted the sequence for the same. With protparam we were able to know its characteristics, using other tools like TOPCONS, smart, clustal omega, PDB we were able to predict it's location and perform phylogenetic analysis. Then we predicted there structure on phyreÂ² and swissmodeller and compared the final result.

Structures from both phyreÂ² and swissmodeller were obtained successfully. The structure from phyreÂ² has 22 transmembrane helices and from swissmodeller has 12 helices. The phyreÂ² shows results which is somewhat similar to another organism, *Cupriavidusmetallidurans*. With aid of bioinformatics in research, scientists have given endless possibilities for treatment of several diseases. *Cupriavidusmetallidurans* is gram negative bacteria which can survive heavy metal stress and by the results we've got, we can say that the O-antigen ligase is also resistant to several forms of stress because of which it is able to adapt in the colonic microbiota thus it will make it possible for many immunomodulatory theories to come true.

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Production and Applications of Bacterial Cellulose

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Bacterial cellulose (BC) biosynthesis is a complex process that involves the formation of 1, 4-β-glucan chains inside the cell. Enzymes work together to link these sugar molecules, forming long chains. These chains then congregate and crystallize into fibrils, which are thin structures. The fibrils are extruded outside the cell and self-assemble into larger structures. BC biosynthesis is tightly regulated and requires various enzymes, catalytic complexes, and regulatory proteins to work together in a coordinated manner to produce BC. The objective of this work is to expand novel bacterial cellulose nanomaterials with groundbreaking novel features and to enlighten its production and therapeutic applications.

BC is a bioactive substance with desirable properties such as high H_2O preoccupation, crystalline structure, high tensile strength, and biodegradability. BC Factors such as pH of the media, temperature and time of incubation, and sugar concentration in the carbon source influence the production of BC. It is a flexible bio-polymer with unique properties such as anti-bacterial and anti-biofilm qualities. It is highly pure, crystalline, absorbent, porous, and has high tensile strength. It is also biocompatible and biodegradable, making it suitable for various applications such as wound coverings, dental grafts, and ointments. Unlike plant cellulose, BC does not have any negative effects or dangerously high levels. Despite its low production, BC bio-composites have shown promising anti-biofilm efficiency, offering a new therapeutic approach for wounds and diseases caused by biofilms.

PP-62

Face Recognition Attendance System

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A student's life depends on their participation in class. The major goal is to increase involvement because it improves students' learning outcomes. The manual procedure of calling names from the rolls or distributing attendance papers takes time and may be subject to fraud. One of the significant developments in computer vision was the research of human face recognition, which has many uses, such as the attendance system. The automatic facial recognition attendance system suggested in this study will perform noticeably better than the one that is currently in use. The system will be integrated with our main database, which contains information about every student including their name, image, roll number, and attendance time. There are three steps to the application: Photos will be taken first. The primary database will also hold the most recent pictures. Finally, it will automatically mark all linked photographs on a spreadsheet as "absent"for the other students who were not present for the lecture. Three user groups-teachers, students, and staff can access the online application. The face-recognition (Python Dependency) is used torecognize faces and Dlib dependency is used to extract physical features of a face. SVM classifier (linear model of Machine Learning) is used to differentiate between the measurements of a given person. When students are standing in an imaging-friendly position, the experimental test shows a high accuracy of student classifier. Also, the distance between the camera and the standing student has an impact on how accurately faces are recognized.

Quantum Cryptography – A Modern Approach

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In our daily life we are getting very much dependent on internet or virtual reality. They are nothing butan illusion of a Cyberspace. It has effect on our every aspect of life, like education, sports, health etc. We are usingthe term Cryptography which is the science of using mathematics to encrypt and decrypt data. We had used variousEncryption standards in back days namely, DES, AES, RSA, Elliptical AES etc. But nowadays we are using Quantum Cryptography for this. It is nothing but use of Physics (mainly Quantum Physics) for encrypting the data. In thisresearch paper we will mainly focus on the new approaches that come in the path of Quantum Cryptography. We will also view some interaction of Quantum Cryptography in future Internet services. Quantum computing is yet to be explored but still the explored part has the capabilities to counter the "alien"hacking protocols if tested over any System. Older System were using protocols like RSA, AES, DES even some ofthem are more capable than our need, but the use of QC will not only secure the systems but there are major chances that eavesdropper got caught while eavesdropping. Also, QC is a pathway to secure communication. This paper includes the review of older state of Quantum Cryptography which will give us information about QKD algorithms and its protocol and we will also overview on its risk and security features. We will also provide a glimpse of current various works going in various Educational Institutions.

PP-64

AI and Big Data

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By enabling businesses to make better decisions and gain a competitive advantage, the availability and volume of data in the modern world have changed the rules of the game. Yet, the sheer volume of data has made it challenging to manually review and draw wise conclusions. The analysis and interpretation of massive amounts of data are made possible by the application of machine learning and advanced algorithms in big data analytics. We examine how artificial intelligence advances data processing and analysis and how big data impacts commercial decision-making processes. We begin by defining big data and examining its history. We emphasize that the term "big data" was only coined after enormous amounts of data had already been gathered and stored, making it difficult to manage and evaluate. We explore the problems that big data presents, such as the requirement for advanced tools and methods to manage the volume, diversity, and velocity of data. To make sure the data is correct, consistent, and pertinent, we talk about how crucial data preparation and cleansing are. We also look at the difficulty of protecting data security and privacy considering some of the data's sensitivity. The use of artificial intelligence in processing and studying massive data is the subject of our next section. We stress that artificial intelligence (AI) enables businesses to make better choices by analyzing and processing enormous quantities of information much more quickly and accurately than people. We discuss the many AI techniques used in big data analytics, including machine learning, deep learning, and natural language processing. We also go over the necessary setup and technical know-how for incorporating AI into big data analytics. The potential for mobile gadgets in big dataset analytics is the topic of our final discussion.

PP-65

Colorizing Grayscale Images with Deep Learning: A CNN-GAN Ensemble Approach

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Image colorization is a challenging computer vision task, but It has numerous significant uses in numerous fields,, such as medical and scientific imaging, virtual and augmented reality, and accessibility for people with color blindness. The colorization process adds value to images by making them more aesthetically pleasing, informative, and emotionally engaging. The use of machine learning techniques has recently gained popularity in automating the colorization process. In order to create realistic and visually attractive color images from grayscale ones, this study's primary goal is to present a unique method for image colorization using convolutional neural networks (CNN) and generative adversarial networks (GAN). The study also intends to compare the suggested strategy to cutting-edge approaches in terms of both human and machine metrics.

The proposed method consists of training a CNN to learn the mapping between grayscale and color images. A GAN is then employed to refine the output of the CNN and generate visually realistic color images. An Ensemble model is suggested, which combines the outputs of multiple CNN-GAN pairs to further improve the colorization quality. The method is evaluated on the CIFAR-10 dataset, which contains 60,000 32x32 pixel images.

The outcomes show that the suggested strategy outperforms cutting-edge methods in terms of visual quality, as evaluated by both human and machine metrics such as PSNR and SSIM. The Ensemble model shows further improvements in colorization accuracy. The study showcases the potential of deep learning techniques in enhancing the challenging task of image colorization. The proposed method offers promising results in image colorization, demonstrating the effectiveness of using CNNs and GANS together. The study highlights the importance of incorporating multiple models for improved performance. Future studies could explore more complex models and larger datasets to further enhance the quality of the colorization process.

PP-66

Fully Flexible Slot Based Timetable

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This paper presents a useful scheduling method capable of properly handling both strong and weak restrictions. With this adaptable slot-based time table, students can select their schedule in accordance with their convenience. When designing fully adjustable slot-based timetables for each student, instructors' accessibility and physical resource capabilities (such as classrooms, laboratories, and computer rooms), the availability of slots, and the rules that apply to various classes, semesters, teachers, and subject levels are all taken into account. Students generally struggle with their timetables since they are required to adhere tothe ones that the administration has established. Timetables are not always well received bystudents. Therefore, this completely variable slot-based timetable will give students the freedom to select their schedule in accordance with their preferences for faculty and convenience. In institutions, students often struggle with their schedules because many of them are day students. As a result, they desire a schedule that will be set in accordance with their timing. Additionally, thereare students that desire to only work with a certain academic member. Additionally, some people desire to choose their course based on the irpreferences. The answer to these issues is a fully flexible timetable basedon slots. The fully flexible slot-based scheduling system gives students total freedom to design their courses whatever they choose. It satisfies the desires and requirements of the entire student body. With this approach, a student can create his or her own schedule, including the specific courses and lecturers they want to take during that semester. This much fun was never had learning. It is a helpful system that is made to accommodate all different types of students with different learning requirements, regardless of whether a student wants to finish their coursework early or pursue courses from other branches to achieve a Minor/Honors degree.

PP-67

Smart Alert System for Fishermen on Marine Borders

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Recent days, we come across the major news of fishermen crossing the marine borders unintentionally and they end up getting charged by the guards. The fishermen's way of life forces them to unwittingly violate national borders, where they put themselves in danger of being murdered or taken prisoner. The fundamental cause of this issue is the difficulty in identifying the marine boundaries between nations. This paper presents a method for having a pre-warned system with microcontroller and by tracking the actual location using the gps controller for ensuring their safety and can avoid unnecessary imprisonment. The system involves having a LED and alarm system near the restricted area and even have signals send to the nearest coastal forces. To obtain precise latitude and longitude data, the microcontroller unit employs GPS. In order to determine the current position, the controller unit compares the latitudes and longitudinal data with the given value. Here, a ground-breaking marine border warning system using boats is demonstrated. It effectively monitors fisherman and alerts if they approach another country's border in danger. The new technology ZigBee used which ensures better signal connectivity. The planned border alert system warns fishermen in order to safeguard fisherman and promote goodwill among coastal nations. The alarm system notifies the fishermen with an audio and visual signal if they are dangerously close to the IMBL method. If the fisherman ignored notifications and continued to cast, the smart vessel should automatically turn around and relay the information.

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Computer Aided Drug Design for Cystic Fibrosis Transmembrane Conductance Regulator Protein

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Cystic Fibrosis (CF) is a congenital disease that has varying effects on the body. One of the most successful drugs for CF is Ivacaftor which is a potentiator of channels responsible for the disease. Due to numerous side effects and ever felt the requirement of newer drugs so as to combat diseases in multifarious ways, intervention of modern algorithms like that of docking and drug designing can be done for discovering novel molecules, present in varying databases, with similar structure and also binding ability like that of Ivacaftor. The comparison of 2D and 3D structural similarity of various molecules with that of Ivacaftor has been done with SIMCOMP, swiss similarity and chemmine tool. The results have been further substantiated by simulating docking or binding interactions carried out using iGemDock docking software. Many molecules showed high binding energy comparable to that of Ivacaftor with CFTR protein, at active site residues. Therefore the strategy can be applied for any other drug and any other disease provided wet lab experimentations confirm the validity of in-silico experimentation.

Computational Studies of Styrene Maleic Anhydride as a Key Molecule against Different Target Proteins of Prostate Cancer

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Prostate cancer is one of the 5 leading cancers in the world and foremost cause of high mortality rate observed in more than 48 countries across the globe. Development of effective therapeutics to treat Prostate cancer is the need of the hour. Androgen receptors have been recognized as promiscuous target for therapeutic development against prostate cancer. Studies show that the androgen receptor (AR) is crucial to the development and progression of prostate cancer, therefore blocking the AR with an antagonist or using a combination of AR antagonists and androgen blockade therapy may be effective treatments. Apart from AR, STEAP2 protein is also a key target to develop drugs against Prostate cancer. The six transmembrane antigen of the prostate 2 (STEAP2), also known as the six transmembrane protein of the prostate 1 (STAMP1), belongs to the metalloreductase family. Prostate cancer development is significantly influenced by STEAP2, as shown by in vitro and in vivo investigations. Both the plasma membrane and the Golgi complex of prostate cells contain STEAP2 and this molecule promotes the development of prostate cancer, regulates cell growth and differentiation, and suppresses programmed cell death. Knocking STEAP2 out of prostate cancer cells has been proven to slow down their oncogenesis and disease development by decreasing their invasiveness, increasing their apoptosis, and decreasing their migration. Scientific studies to find potent lead molecules against prostate cancer have revealed that MTT assay conducted on prostate cancer cell line, PC3 is giving promising results of Styrene maleic anhydride (SMA) compound for inhibiting these cells. Based on these studies, we have investigated the potential mechanism of inhibition of Prostate cancer by SMA. Molecular docking studies were conducted to estimate binding affinity of Styrene maleic anhydride with Androgen receptor and STEAP2 followed by comparison with known drugs against these targets which included celecoxib and nimesulide with AR and Triptorelin and Leuprolide with STEAP2. Binding affinity was obtained in the range of -7.5 Kcal/mol to -9.2 Kcal/mol for SMA against the target proteins, AR and STEAP2. LD50 of SMA was estimated to be 1190 mg per kg and it was estimated to be belonging to Class 4 of Toxic compounds as per the results obtained from Protox server. Further, SMA does not cause carcinogenicity, mutagenicity and cytotoxicity as shown by computational analysis. We propose SMA as a potential lead molecule against Prostate cancer based on our scientific investigations using computational biology approach.

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Utilization of *Ficus auriculata* for the Making of Pickle and Its Physicochemical Analysis

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Our study aimed to fill a gap in the literature by documenting the traditional recipe of pickle made from *Ficusauriculata* (Timla), a non-conventional fruit that is often underutilized. The nutraceutical and pharmaceutical properties of the *Ficus* genus make it a valuable fruit, but it is only available for a limited period, therefore it is necessary to make value-added products from this plant. In the current study, the physicochemical properties of the fresh fruit, edible mustard oil, stuffing material, and prepared pickle were analyzed.

The fresh raw fruits were pickled in salt, vinegar, sugar, and a Mixture (salt, oil, spices, and vinegar). The sensory attributes and titratable acidity of the pickle were evaluated during storage intervals of 15 days, the sample made with mixed method ranked the highest by the sensory panel. Changes in pH and acidity of the pickle were observed during storage. The moisture content of the pickle was observed highest (60%)in the mixed sample and lowest(23%) in the vinegar-preserved sample on the other hand the fat content was only observed (17.5%) in mix pickled sample. The ash content for all the preserved samples was observed at 10%, except for the mixed sample, which had ahigher ash percentage of 30%. The overall finding of our study provides an approach for individuals who have access to this fruit to utilize the fruit and generate revenue from it while highlighting its potential as an ingredient in traditional pickle preparation. The study aims to promote the use of underutilized fruits and contributes to the sustainable use of natural resources for livelihood security.

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Genes Involved In Breast Cancer

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Before focusing on the genetic and nongenetic components involved in the tendency of breast cancer in humans, the goal of this review was to define simple cancer genome, cancer genetics, and cancer epigenetics. Up to 25% of hereditary breast cancer cases are brought on by one of the few known rare but highly penetrant genes (BRCA1, BRCA2, PTEN, TP53, CDH1, and STK11), which carries a lifetime risk of the disease. A few extra cases are brought on by rare, moderate-penetrance gene mutations (such those in the genes CHEK2, BRIP1, ATM, and PALB2), each of which entails a two-fold increase in risk. Location of BRCA2 was chromosome 13. People with either a BRCA1 or BRCA2 mutation are more susceptible to breast and other malignancies.

We have read articles from Google Scholar, ncbi, and PubMed with titles like "Genes of Breast Cancer: "Overview of the Genetic Basis toward Early Detection of Breast Cancer," and "Genetics of Breast Cancer.

Many risk factors that predispose to the disease have been found, according to epidemiologic studies on breast cancer. In contrast to the other 90% of breast cancer cases, only about some percent of all breast cancer cases are due to nongenetic causes. Mammography, clinical breast examination (CBE), and breast - examination are the three clinical assessments that are taken into consideration for early screening of breast cancer. CRISPR is the new technology to treat breast cancer. Mastectomy and lumpectomy can also be done to treat the breast cancer at early stages.

Exploring the Biodegradation Potential of Crude SOR Enzyme from *Anoxybacillus* sp. for Azo Dye Removal: A Sustainable Approach for Industrial Wastewater Treatment

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Urbanization, globalization, and industrialization have led to the accumulation of environmental pollutants such as metals, organic chemicals, and dyes. The textile industry is one of the major contributors to environmental contamination due to its release of dye-containing wastewater, which contains toxic chemicals like azo and reactive dyes. Several microorganisms, including bacteria, fungi, algae, and yeasts, have been found to effectively degrade industrial dyes. However, the efficiency of microbial decolorization largely depends on the adaptability and activity of the chosen bacteria. This study aims to investigate the potential of crude SOR enzyme from Anoxybacillus strain in biodegradation of azo dyes at higher temperatures, which could provide a new approach in the treatment of wastewaters contaminated with different levels of azo dyes (RB5, Methyl orange, and Congo red).

In vitro decolorization of three structurally different azo dyes was monitored by the extracellular crude enzymes to determine its decolorization ability. The effect of crude SOR enzyme isolated from Anoxybacillus sp. on a wide range of pH (4-8) and temperatures (20-60Â°C) was investigated, and the residual concentrations of selected dyes were measured using a UV-Vis Spectrophotometer.

The results demonstrated that the crude SOR enzyme from Anoxybacillus strain exhibited a rapid decolorization of azo dyes, indicating its potential for industrial applications. The enzymatic reaction system showed a wide temperature and pH range, and the crude enzyme retained its high decolorization ability even at high temperatures. This study provides a basis for the production and application of SORs on a larger scale using a low-cost substrate, improved crude enzymatic capabilities and dye-decolorization efficiency make it an environment-friendly and effective bacterial isolate for industrial use.

PP-73

Vaccine Developments for AIDS

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Acquired Immunodeficiency Syndrome (AIDS) has been a concern paramount for global researchers. The syndrome caused by the infective Human Immunodeficiency Virus (HIV), kills the helper T- cells of the Adaptive Immune System, thereby degrading the body immunity unprecedented genetic variability of the virus and its ability to create a lifelong infection post-haste has made the infection fatal. Not a single patient has recovered from the infection on his own. These complex facts create numerous hurdles for scientists when it comes to developing an ideal vaccine for the infection. Albeit the traditional methods for vaccine development have culminated in the licensure of many current vaccines, they have failed to produce an ideal effective candidate. The only way, however, to combat the HIV epidemic is with an HIV vaccine. Organizations, although trying, are closer than ever to the goals. After more than a decade of process efforts, new HIV vaccine candidates based on the concept of stimulating B-cells of the immune system, that generate broadly neutralizing Antibodies (bnAb), are currently under trial. A few of the T-cell-based immunogens are also in development and under trial.

PP-74

Multi-threaded End to End Encrypted Cryptography

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Multithreaded end-to-end encrypted cryptography-based real-time chat refers to a type of chat application that provides a high level of security and privacy for users. In this type of chat application, messages are encrypted and decrypted on the sender and recipient's devices using advanced encryption algorithms. Multithreading refers to the ability of the application to handle multiple chat sessions simultaneously, allowing users to have real-time conversations with several people at once. This feature is particularly useful for group chats and enables the application to deliver a seamless experience to users. The main objectives of Multithreaded End to End Encrypted Cryptography-Based Real-Time Chat are: Security: The primary objective of this type of chat application is to provide a high level of security for users' messages. End-to-end encryption ensures that messages are protected from unauthorized access and only visible to the sender and intended recipient. Privacy: Another objective of this type of chat application is to protect users' privacy. By using end-to-end encryption, the application ensures that messages cannot be intercepted or read by anyone other than the sender and recipient.

User a initiates a chat with User B. User A generates a unique key that will be used to encrypt and decrypt the messages exchanged between them. User A encrypts the key using User B's public key, and sends it to User B. User B decrypts the key using their private key and stores it locally. User B generates their unique key, encrypts it using User A's public key, and sends it to User A. As an AI language model, I don't have access to information about specific projects or experiments unless it has been published publicly. However, I can provide some general information about the topic of multithreaded end-to-end encrypted cryptography-based real-time chat. Multithreading refers to a technique in computer programming where different parts of a program can execute concurrently, allowing for better utilization of resources and potentially faster execution. End-to-end encryption refers to a cryptographic communication protocol that ensures that only the sender and intended recipient can read the contents of a message. Real-time chat refers to a communication method where messages are sent and received immediately, creating a conversation in real-time. Multithreading refers to a technique in computer programming where different parts of a program can execute concurrently, allowing for better utilization of resources and potentially faster execution. End-to-end encryption refers to a cryptographic communication protocol that ensures that only the sender and intended recipient can read the contents of a message.

Comparative Response of C3 Plant, Wheat and C4 Plant, Maize to Water Stress

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The C4 plants are evolved 40 million of years ago in response to low co2 conc. in the atmosphere. The c4 plants evolved in earth temp was warm. Therefore, the c4 plants are often resistant to environmental stresses, high light, high temp, drought, and salt. However, they are contradicting to reports of stress tolerance behaviour of c3 and c4 plants. To probe further, the wheat, c3 plant and a maize, c4 plant were treated with water stress by applying either 50mM Polyethylene Glycol 6000 (PEG 6000) or withholding water from the stress plants. In response to water stress induce by withholding water on the 10th of stress treatment wheat loss around 89% chlorophyll whereas maize loss 35%. The osmotic stress caused by PEG treatment the PS II – DEPENDENT electron transport rate (ETR), calculated from fluorescence quantum yield of PS II (psi PS II*0.84*0.5*PAR value) declined in both wheat and maize. However, the percent decline of ETR in response to osmotic stress was lower in maize than wheat. These clearly demonstrate that in contrasts to several reports and in conformity with others, the c4 are comparatively more tolerant to water stress. Therefore, the c4 plants should be used for improvement and for climate resilient agriculture.

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A Review on Recent Advancements on Vaccine Development for COVID 19

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In recent years, mRNA vaccines have emerged as a promising tool in preventing infectious diseases, with significant advancements in the development of COVID-19 vaccines. mRNA vaccines have several advantages over traditional vaccines, including a shorter development cycle, ease of industrialization, a simple production process, flexibility to respond to new variants, and the capacity to induce a better immune response. To produce stable mRNA vaccines that can evade the body's immune system, scientists have employed various techniques, such as synthetic structure-modified RNAs, optimizing 5' cap structures, 3' poly (A) tails, and UTR sequences, and utilizing advanced formulation techniques such as lipid nanoparticles. The success of mRNA vaccines, particularly in the development of COVID-19 vaccines, has led to the rapid growth of the entire mRNA vaccine industry. The receptor binding domain (RBD) of the spike glycoprotein serves as the primary coding region for mRNA vaccines, and two novel mRNA vaccines against SARS-CoV-2, mRNA-1273 and BNT162b2, have been approved for clinical use worldwide and have demonstrated high efficacy in preventing SARS-CoV-2 infection in Phase III clinical trials. Due to the emergence of different viral variants, vaccine companies have shifted their focus to developing next-generation mRNA vaccine candidates, such as dimeric mRNA vaccines encoding both Delta and Omicron strains of RBD, which have shown increased antigen expression and induced higher neutralizing antibody titers compared to mRNA vaccines encoding only Alpha or Omicron. The speed of vaccine development for COVID-19 has increased substantially due to the availability of new and improved vaccine technologies, substantial investments, international collaborations between scientists, and faster regulatory review, demonstrating the essential role of vaccination in today's world and revolutionizing the vaccine industry.

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Crime Rate Analysis

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Crime is a pervasive problem in many societies worldwide, and understanding its patterns and trends is crucial for developing effective prevention strategies. In this project, we aim to analyze crime rates in a particular area over a period of time to identify patterns and trends in criminal activity. Our analysis will include various crime types such as dowry, rape, assault, kidnapping etc.

The objective of a crime rate analysis on women crime is to investigate and understand the patterns, trends, and reasons connected to women's participation in criminal activity. This kind of study seeks to evaluate the degree and character of women's engagement in crime as well as pinpoint potential contributing variables

We will gather data from Kaggle, including statistics on various sorts of crimes committed against women through year in various states and district, to built a comprehensive database of crime incidents in the area of interest. The data will be cleaned and processed to remove any errors or inconsistencies, and then analyzed using statistical techniques to identify patterns and trends in criminal activity over time

The results of our analysis will be presented in a detailed report that includes visualizations and statistical analysis. The report will provide insights into crime patterns and trends in the area, including which types of crimes are most prevalent, where crimes occur most frequently, and which demographic and socioeconomic factors may be associated with higher crime rates

The findings of this project will be useful for law enforcement agencies, policymakers, and community organizations to develop effective strategies for preventing and reducing crime in the area. Additionally, this project may provide insights into broader societal issues related to crime and how they can be addressed through targeted interventions.

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Biomimicry

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The idea of mimicking the structure and pattern of nature is known as biomimicry. Since the beginning of time, architects have been imitating the patterns of nature to bring up new innovations for humans. It has a lot of expertise in resolving issues pertaining to the environment and its inhabitants. Scientists are conducting research in this area to understand the design and unearth novel ideas in animals, environment, etc. The next generation of smart sensors will be built on a revolutionary opal-like material that was found in the sensors that were created using the pattern of peacock and butterfly wings.Due to the color-changing, flexible photonic crystals' versatility and sensitivity to chemical and physical stimuli, wearable medical devices can use these sensors Colloid crystals with angle-dependent structural colour.Sensor-made gadgets that react to specific stimuli one at a time and that react to multiple stimuli are expensive and not affordable for everyone. For example, previous cardiac pacemakers did not have any features other than oscillation. According to Moore's law, the features and efficiency of modern pacemakers have improved, making them more expensive, and the usage of sensors inside the body creates biofouling. Its use over time leads them to degrade.

Nanoscale structures found in peacock and butterfly feathers reflect and absorb light in various ways to produce colour. Brilliant iridescent colours are produced using this technique for light manipulation, which the creatures rely on for thermoregulation, and signalling to possible mates.Biomimicry has caused architects, designers, and engineers to solve problems and create new innovations in the field of engineering, such as turbins made from inspiration for whale fins, the bullet train problem of sonic sound and its increased efficiency due to inspiration from the beak of the bird, and so on. As a result, natural elements play a role in the majority of architect-created objects.

PP-79

Student Performance Analysis

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Educational institutions use the potent analytical techniques of data mining and maymore efficiently manage resources, staff, and proactively to monitor student performance. Themanagement structure may make its policies and programmes stronger in an effort to improvethe standard of the educational system. Several early academics made use of data mining are capable to improve student academics performance in education institutions.

We need Student data consisting of details. Also, we need the details of the respective courses. By this, we can get to a result aboutthat University and will be able to analyze it. First, we need to collect data from the Kaggle. Thatdataset will be not accurate to analyze, so we need to first clean and pre-process the data tocome to the final visualization. After cleaning it, we need to apply the proper algorithm sothat we can generate an outcome. By doing this, we'll be able to analyze the curve and the required changes occurring during the analysis.

The paper aims to predict different things related to Student data. The paper achieves the following objectives:

- Create a dataset consisting of different fields like
- Building prediction models using sklearn
- Comparing algorithms which gives maximum accuracy

The model employing the SVM classification algorithm for predicting the academic accomplishment of student enrolle in the bachelor's of computer applications and other programmes. The developed model was tested using data sets of students.

PP-80

Computation for Cancer

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Biocomputation is the use of biologically generated components in computational processes.In the area of "biocomputation," computational techniques are used to investigate biological systems and create novel cancer therapies. Integrative computational biology is used to find small groups of genes, proteins, or microRNAs that can be used to predict outcomes, enhance diagnosis, or determine how a patient will respond to treatment.

To better comprehend the biology of cancer and create new treatments, CRISPR, a gene-editing tool, is being used to manipulate and assess hundreds or thousands of genes at once. To increase the effectiveness of treatment, nanotechnology is also being investigated.

Additionally, biomarker testing is a method to look for genes, proteins, and other substances that may shed light on cancer and influence how some cancer treatments function. Scientists are using potent algorithms to better understand how cancers form and the best treatments to combat them. The objective is to create personalized therapies that are less harmful and more efficient than conventional chemotherapy.

PP-81

miRNAs and Stem Cells Targeted Therapies for Colorectal Cancer

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Among all cancers, colorectal cancer (CRC) is the third most common. Despite the introduction of chemotherapeutic methods, the WHO estimates that 2 million cases were diagnosed in 2020 and that 1 million people died from the disease. Finding quick, affordable ways to cure this malignancy can benefit people with advanced stages of cancer because one of the main problems of current therapy is that chemotherapy and other treatments frequently fail. Longer life expectancy for CRC patients may be achieved with the use of targeted medicines in conventional chemotherapy, which can improve chemosensitivity and reduce the quantity of potential tumour cells.

Colorectal cancer stem cells signalling pathways contain particular indicators that are exclusive to targeted therapy. They control these cells ability to regenerate and retain their pluripotency. Some miRNAs can be employed as prognostic indicators having a significant clinical role in targeted therapy. One of the miRNAs can precisely target the mRNAs of various cancer types, making it possible to employ them to target a variety of CRC-causing oncogenes.

The immunogenic miRNA limits exponential growth in cell quantity, their relocation, and induces necroptosis in the cancer cells, according to evidence from the animal models used.

PP-82

E-Authentication Methods for Document Verification

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Electronic authentication, also known as e-authentication, refers to the process of verifyingtheidentityofapersonorentitythroughelectronicmeans.Astheuseofonlineservices and transactions continue to grow, e-authentication has become increasingly important for ensuring the security of sensitive information. This process is essential in various industries, including finance, legal, and government, where the accuracy and integrity of documents are critical. In recent years, with the increase in digitalization and the ease of creating counterfeit documents, the need for robust document authentication measures has become more pressing. We start by outlining the key challenges of document verification, such as detecting fraudulent documents and ensuring authenticity.We then provide an overview of the various techniques used in document verification, including watermarking, digital signatures, forgery detection through image processing, and QR code. Finally, we highlight the emerging trends in document verification, such as the use of blockchain technology and the increasing importance of privacy- preserving techniques. It also discusses the challenges and limitations such as data privacy, security, and usability concerns associated with each method and provide examples of their successful implementation in real-world scenarios.

Our paper provides a comprehensive overview of e-authentication methods for document verification and serves as a valuable resource for researchers and practitioners in this field.

PP-83

Role of Naringenin in Alzheimer's Disease Treatment

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One of the common neurological conditions of the central nervous, Alzheimer's disease (AD) is characterized by increased beta-amyloid. A deposition and a resulting loss in learning and memory. In the current investigation, a rat model of Alzheimer's disease was used to assess the therapeutic effects of naringenin on learning and memory enhancement. Naringenin is a natural flavanoid possessing neuroprotective activities. A growing body of evidence has been the subject of particular attention to the variety of therapeutic targets as well as to the complex signalling pathways of the naringein, which suggest its potential therapeutic applications in several NDs. Here we describe the neuroprotective effects of naringenine, along with its pharmacological targets, signalling pathways, molecular mechanisms and clinical perspective. Focusing on Treating Neurodegenerative Disorder using a Flavonoid. Survey on Phylogenetic analysis involving 4 proteins

Here we will pay attention towards variety of therapeutic targets as well as complex signalling pathways of the naringenin. Another method is Phylogenetic Analysis: To understand the evolutionary relationships between distinct organisms, phylogenetic analysis aims to highlight those relationships.

Naringenin is a multi-target flavonoid found in natural products, we have identified therapeutic targets and signaling pathways with neuroprotective benefits. Despite thorough investigation, no successful treatment for NDs has been examined. Finding innovative multi-target therapies is becoming more important as a result of the complicated pathophysiological mechanisms of neurodegeneration and the paucity of effective and safe treatments for NDs.

PP-84

Neurodegeneration as a Secondary Effect of Leishmaniasis: A New through put towards Incidence of Alzheimer's Disease

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Leishmaniasis is a neglected sub-tropical disease which is incident all throughout the world and is becoming a major concern due to its occurrence as a co-infection with AIDS. There are mainly three forms of the disease namely visceral, cutaneous and mucocutaneous. Recent studies have shown leishmaniasis can be associated with other disorders as *Leishmania* parasite tilts the balance of host immune system. In this context, one characteristic observation in recent times has been induction of neuronal death and degeneration. The leishmanial parasite has been seen to modulate and suppress Th1 immune response causing imbalance of host immune response. Studies have shown that dysregulation of Th1 immune response is a major reason of neuronal lysis. As, Alzheimer's Disease (AD) is a major concern now, study of the former lined with parasitic disease is a necessity. Our study aims to correlate the promoting factors of AD and leishmanial infection as an approach to understand the co-incidence of neural degeneration, AD and Leishmaniasis.To study the correlation of leishmaniasis and neurodegeneration and underlying immune pathways that can initiate and substantiate the neural damage.

Herein we present a consolidated report on cross-connection between leishmaniasis and neurodegeneration and correlated changes in host immune system that might be responsible for these effects. As deduced from several published studies it can be concluded that leishmanial parasite can promote the onset of neuronal death and neurodegeneration. Downregulation of host immune response can cause damage to brain and also promote development of AD.

PP-85

Evaluation of the Medicinal Potential of Myricaesculenta's Phytoconstituents

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The popular medicinal herb Myrica esculenta, often called "Box Myrtle," "Bayberry," and "Kaphal," is primarily found in the Himalayas and all over the world in both subtropical areas.. Its berries are edible and are eaten locally as the state fruit of Uttarakhand in northern India. Its Genus Myrica is made up of little trees and fragrant shrubs from the Myricaceae family. It is widely used as folk remedy to cure a variety of infections, including those that cause asthma, coughing, chronic bronchitis, ulcers, inflammation, anaemia, fever, diarrhoea, and diseases of the nose and throat. This medicinal herb is highly regarded in the ayurvedic pharmacopoeia because of its multifaceted pharmacological and therapeutic properties. The goal of this study is to investigate this plant's phytogenetic capabilities in order to treat some severe, persistent respiratory inflammations.

Organoleptic analysis, macroscopy, microscopy, leaf constant, fluorescence analysis, and preliminary phytochemical screening were the methods used for pharmacognosticalcharacterisation.

Macroscopic studies have revealed that leaves have an acute apex, are tiny, spirally arranged dark green in colour, and astringent in flavour. On each surface, mesophyll cells underwent differentiation to form palisade cells in a single layer. In the centre of the rib, there are layers of spongy parenchyma, trichomes, and a bowl-shaped vascular bundle with xylem and phloem tissues. Alkaloids, sugars, flavonoids, glycosides, phenolic compounds, and tannins were discovered. Microscopy, fluorescence properties, and physical parameter analysis of the leaf constants produced useful information that can be used to set standards for the plant. Phytochemical studies of different part of plant like stem bark and leaf revealed the presence of various bioactive phytoconstituents such as phenolic compounds, tannins & phenolic acids, flavonoids, myricetin and beta-sitosterol. The research investigates various phytoconstituents and their pharmacological properties like antidiabetic, antimicrobial, antioxidant, antiallergic, analgesic, antihypertensive, antiulcer, and anti-inflammatory to be used as therapeutics.

PP-86

BIOCOMPUTING-The Future of Innovation

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The science over the years has been putting immense efforts to make cells into computer. It is logical enough since there are number of similarities between computers and living cells, as both store information in memory and work according to certain set of rules and so forth. Biocomputing is defined as the process of building biological computers i.e., computers which use biological materials, mimic biological organisms. Bio computing helps in facial recognition, stock market prediction, aerospace, finding evolution to current day species, customize disease prevention, drug development, etc.

Artificial neural network, phylogenetic analysis, personalisedmedicine, growmac, autodoc, BLAST, net turn P, net surf P, etc.

While advances in machine learning, high performance computing enables more applications of computational biology beyond laboratory environment. Lastly, advanced algorithms and biological modelling software are creating novel therapies for hard to treat diseases such as cancer.

PP-87

Use of Natural Compounds in the Reversal of Epigenetic Changes

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The study of epigenetics focuses on DNA or histone modifications that do not include modifications to the fundamental DNA sequence. Epigenetic alterations in oncogenes and tumour suppressor genes can induce uncontrolled cell proliferation and cancer. Natural anticancer therapies are accessible, flexible, and low-cytotoxic and have less side-effect. In the current period of pharmacological discovery, natural compounds have provided effective anticancer medications. The fundamental objective is to provide a overview on use of natural compounds in the reversal of epigenetic changes.

PubMed and Google Scholar were used for a thorough literature search Research on the effects of natural substances on reversal of epigenetic changes published in the scientific literature between 2010 and 2021 was analysed.

The literature review found natural substances that reverse epigenetic alterations, including DNA methylation and histone modifications. These epigenetic alterations can alter gene expression in cell growth, death, and DNA repair. New technologies have increased natural product-based medication development in recent years Chemoprevention extends carcinogenesis to reduce cancer morbidity and mortality. The search for additional natural chemicals and their subjective effects continues. Oncology has benefitted greatly from the knowledge acquired thus far. Numerous plant components have anti-inflammatory, antioxidant, anti-allergic, antiviral, and anticancer characteristics. Natural product research is an effective method for identifying biologically active substances with distinctive structures and modes of action that may lead to their development of novel diagnostic and therapeutic approaches for the treatment of cancer.

PP-88

Arsenic Salt's Effect on Plants and Potential Remediation via Co-Planting with Pteridophyte

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The quality of crops and agricultural productivity is essential for meeting the food demands of the growing population. Heavy metal pollution in the environment is caused by natural sources such as weathering, erosion, volcanic activity, and industrial and mining activities. Plant remediation is a low-cost, sustainable, and effective approach to remediation, but its effectiveness is limited depending on the concentration, type of contaminant, plant species, and environmental conditions. In this work, we aimed to explore the viability of employing ferns to Phyto-remediate soil polluted with arsenic. This was done by co-planting our plant samples with *Nephrolepisexaltata*known for their capability to absorb and utilize heavy metal such as Arsenic, in the same soil contaminated with arsenic. The plant samples selected for this purpose were *Rosa indica.* Determine the effectiveness of *Nephrolepisexaltata*in removing arsenic from contaminated soils; assess the ability of *Nephrolepisexaltata*to reduce arsenic uptake in *Rosa indica*, and; evaluate the potential of *Nephrolepisexaltata*to mitigate the effects of arsenic from the plants.

Develop control of *Rosa indica*; plant *Rosa indica* in arsenic-contaminated soil with & without *Nephrolepisexaltata*; and observe physiological changes due to effects of heavy metal poisoning.

The results showed that co-planting with ferns can effectively reduce the aftereffects of arsenic in contaminated soil. The presence of ferns in the contaminated soil significantly reduced the arsenic poisoning in the *Rosa indica* samples. Non-co-planted samples with arsenic showed reduced growth, chlorophyll turned grey brown and the plant dried out. Co-planting with ferns seems to be a successful strategy to lessen the negative effects of soil contamination with arsenic on plant growth and productivity. Although this strategy may solve the issue, additional study is needed to determine whether this approach is feasible for application with other plant species.

PP-89

Promising Potential of Naturally Occurring Ingredients in Food Preservation

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Food preservation is a domain with distinct traditional and modern methods to extend the shelf-life of food products. The main reason being the ease in availability of food products at any time throughout the year and to avoid the wastage of food, considering all the global issues. Traditionally, many preservatives, additives and other chemicals are used to preserve the food products along with some techniques. However, in commercial landscape chemical preservatives are chiefly used raising doubts about food safety. Under this scenario, natural ingredients that can help in food preservation without producing any toxic effects unhesitantly gain scientific and consumer preference. To review and summarize the advances in field of natural preservatives comprising of natural secondary metabolites, natural extracts and essential oils.

Different databases such as PubMed, Elsevier and Google Scholar were used to retrieve relevant literature using different key words like, Role of natural extracts in food preservation, Role of natural secondary metabolites in food preservation, Role of essential oils in food preservation. Records for past ten years (2023-2013) were included in present work.

Various studies that fulfilled the criteria of our review were mentioned and summarized. Natural extracts or natural essential oils or naturally occurring secondary metabolites hold tremendous potential in field of food preservation as these excel at shelf-life extension of many perishable food products. Some of the natural ingredients can either replace or complement already commercially used chemical preservatives.

PP-90

Acupuncture Induced Analgesia on Parkinson's Disease

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Neurological disorders like Parkinson's are brought on by the depletion of neurons in the brain's dopamine-producing regions like substantia nigra. We know there in no complete cure of neurological disorders like Parkinson's disease only symptoms can be relieved via medications and complementary therapies. Here, we are aiming to understand the potential of Acupuncture. The use of acupuncture more frequently has had excellent therapeutic results for some disorders. Endogenous opioid peptides are crucial to the effects of acupuncture and aid in producing analgesia. The EOP system, the most researched intrinsic pain-relieving system, is activated by acupuncture by modifying the synthesis and release of EOP. For analgesic actions, EOP binds to the relevant receptors. EOP causes analgesia by acting as neurotransmitters and neuromodulators at the three major types of receptors known as mu, delta, and kappa. This review aims to understand the acupuncture mechanism, acupuncture analgesia on PD, understanding EOP system of body, study of various cell signaling pathways associated with PD symptoms as well as a comparative study between various pharmacological and non-pharmacological approaches for PD treatment and confirming which is a better approach and has least number of side effects.

The extensive literature studies have shown that Acupuncture relieve both motor and non-motor symptoms of PD and has least number of side effects when compared to some pharmacological approaches of PD like levodopa, MAO-B inhibitors, COMT etc.It can be concluded that Acupuncture induces pain relief and therapeutic effects. When the needle is inserted, it causes a micro-injury, increasing blood flow and energy flow, promoting healing, and causing pain relief. Acupuncture stimulates the central nervous system. Acupuncture reduces pain by modulating endogenous opioid, serotonin, and norepinephrine levels, primarily through inhibition of visceral nociceptors, inflammatory cytokines, and CNS activation.

PP-91

Competitive Inhibition of Catechol from *Andrographis Paniculata*in the Complex of ERK2 in Lung Metastasis

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Lung cancer is the most common cancer worldwide, affecting 18% of cancer patients. However there are already 15 drugs on the market, but their side effects are severe, causing serious damage to other tissue systems, such as white blood cells. To combat these severe this study aims, the reported target ERK2 (Extracellular signal-regulated kinase) has been chosen as a therapeutic target for this disease. However, the complex of ERK2 with catechol has been used in this study to find a competitive inhibitor from *Andrographis paniculata*, which has been used for millennia to treat diseases such as cancer, diabetes, high blood pressure, ulcer, leprosy, bronchitis, skin conditions, flatulence, colic, influenza, dysentery, dyspepsia, and malaria on the continents of Asia, America, and Africa. As a result, four compounds > - 6.9 kcal/mol binding energy were identified in this study: 5-hydroxy-7,8,2',5'-tetramethoxyflavone, Andrographolide, 14-Deoxy-11,12-didehydroandrographolide & β-Sitosterol. The molecular analysis and ligand orientation were studied with the help of the computational approach. The binding and intermolecular energy shows that the compounds can be studied further in vivo to develop drugs against lung metastasis. Andrographis paniculata may play an important role in curing lung metastasis by alleviating drug side effects and serious damage to other tissue systems.

PP-92

Current Scenario of Lung Cancer

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Cancer starts when cells mutate and grow out of control. It is the proliferation of cell division in lungs. It is the 3rd most common cancer with more than 3 million cases registered. It is the frequent causes of cancer deaths in men and 2nd most common in women. The various cause of cancer are (i) Smoking is the major causes of lung cancer ,80% of deaths are because of smoking, (ii) Exposure to radon, air pollution, second-hand smoke are other factors and (iii) Genetic factor can also be the causes of lung cancer. Symptoms vary from excessive cough to chest pain or discomfort, appetite loss, weight loss, fatigue, and tiredness. Lung cancer can be of two types:

(i) Non-small cell lung cancer (nsclc) - It is the prominent type of lung cancer that is named after how cancer cells look under a microscope. The various examples are carcinoma and adenocarcinoma.

(ii) Small cell lung cancer (sclc) – it increases rapidly and is difficult to cure. It is less common than NSCLC, also known as oat cell cancer.

To identify various screening, methodology, and diagnostic methods for the treatment of lung cancer.

If condition get worse than screening is recommended Diagnoses is done by physical exam, blood test, chest x-ray. If suspected then a CT scan, biopsy followed by a PET scan. Treatment includes radiation method to cure the tumour, drug therapy, surgery, immunotherapy and chemotherapy.

Lung cancer is responsible for more deaths than other tumours combined. Delayed diagnosis can result in worsening of lung cancer. The above research will lead to a better understanding of the disease.

PP-93

Optimization of Pre-Processing Strategy for *Pennisetum purpureum*Schumach: A Potential Bioenergy Crop for Bioethanol Production

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A promising bioenergy crop for the generation of bioethanol is *Pennisetum purpureum*, generally known as Napier grass. It is preferred due to its high cellulose content, low concentration of lignin, high biomass productivity, ease of cultivation and relatively high herbage mass per year and per area. Napier grass is a perennial grass. In India, Napier grass is cultivated in high amount in the states of Uttar Pradesh, Uttarakhand, Bihar, Gujarat, Madhya Pradesh, Haryana, Punjab, Andhra Pradesh etc. Due to its promising characteristics, Napier grass has been extensively utilized by various pretreatment, saccharification, and fermentation procedures for ethanol generation.

Different Scientific investigations have showed that the dilute acid pretreatment method had the highest sugar yield (57.6%) and ethanol yield (22.6 g/L) as compared to alkaline hydrolysis and simultaneous saccharification. The current study done in our work shows the efficient pretreatment strategies which result in higher production of cellulose and enhanced delignification from Pennisetum purpureum. Different combinations of pretreatment methods, involving variable concentrations of acid, alkali and enzymatic units and varying time of treatment have been investigated to enhance the efficiency of obtaining cellulose from Napier grass. Pretreatment with varying concentrations of Sulfuric acid and Sodium hydroxide followed by cellulase treatment have given promising results. To ascertain the effects of the various pretreatments, raw and pretreated biomass were analyzed using Fourier transform infrared spectroscopy and then subjected to SEM examination.

Cellulose, Hemicellulose and Lignin content of raw and pretreated biomass were compared to assess the efficacy of pretreatment. Further, Dinitro salicylic acid test was conducted to assess the sugar content after various pretreatments. Optimized pretreatment reported in this work will open the avenue for higher ethanol production utilizing the bioenergy crop, Pennisetum purpureum.

PP-94

Spectrum of other Respiratory Viruses during Post COVID-19 Phase

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The effect of SARS-CoV-2 virus has led to worldwide devastating effect over the past three years.If the statistics till date is reviewed, then an estimate of 44,707,525 cases and 530,841 deaths have occurred in India as per World Health Organization reports (January 2020 till March 2023). If the overall impact of Respiratory viral diseases is analyzed, then nearly one or the other viral infection are reported throughout the year, which also accounts to the amount of antibodies being generated in our body against each of these in coming pathogens. Now as we are in the post COVID pandemic phase and as much comorbidity was associated with this respiratory infection, it is very necessary to evaluate the trend in the occurrence of other respiratory viruses.

The present study is aimed to understand the occurrence of respiratory viruses emerging during post SARS-CoV-2 pandemic phases and to evaluate mixed burden of closely related viruses. The patients referring to Jaypee Hospital U.P. and Sharda Hospital, U.P. were taken for the study. A total of 85 patients were taken for the study. Around 13 respiratory viruses were identified during this period i.e. Adenovirus (29.54%), Type A Influenza virus (18.18%), Rhinovirus (13.63%), H3N2 (13.63%), Human Respiratory Syncytial Virus (5.3%), Human Boca Virus (3.78%), Enterovirus (3.78%), Human Metapneumo virus (3.78%), pdm H1N1 Inf virus (2.27%), Parainfluenza Type 3 virus (2.27%), Type C Influenza virus (1.51%), Human Peracho virus (1.51%) and Type B Influenza virus (0.75%). These viruses contributed to single (56.47%), dual (34.11%) and triple (8.23%) form of infection and one patient (1.17%) was reported to have 4 type of viral strain. Type A

Influenza virus and H3N2 appeared to be mostly associated in dual infections followed by Adenovirus and Rhinovirus.The occurrence of multiple respiratory infections during post COVID-19 period appears to be important and highlights crucial need to wholly investigate patients with dual, triple and more infections at one point of time to understand innate and adaptive immune response of patient in the event of mixed infections.

PP-95

Capsaicin Reverses Promoter Hypermethylation of CADM1 and SOCS1 in Cervical Cancer Cell Line

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One of the most prevalent malignant tumours in the world, cervical cancer poses a major threat to the health of women. Cervical cancer can be detected in 10- 15% of women worldwide at some point in their lifespan. Capsaicin can be used to reverse the inhibition of tumor-suppressor gene production caused by hypermethylation, which can be seen as changes in the methylation-specific and unmethylation-specific bands in MS-PCR, respectively.

Methylation Specific PCR.The current study demonstrates the demethylation of the CADM1 and SOCS1 genes after 72 hours, which increased further after 6 days of treatment with 20 M capsaicin, making capsaicin a potent option for demethylating the CADM1 and SOCS1 genes and possibly reactivating the downregulated gene.Capsaicin was found to be a strong phytochemical in in vitro experiments that could reverse the methylation of the CADM1 and SOCS1 genes in cervical cancer cell lines. To achieve greater results, it can also be taken in a synergistic combination therapy with several other substances.

PP-96

Advancement of Computational Biology Approach Human Welfare

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Bioinformatics and computational biotechnology are two closely related fields that utilise computer science, mathematics, statistics, and information technology to analyse and interpret biological data. These two fields are critical for advancing our understanding of living systems and their interactions, as well as for developing new methods and tools for drug discovery, disease diagnosis, and personalised medicine. Bioinformatics involves the development of algorithms and software tools to analyse and simplify biological data, such as DNA and protein sequences, gene expression data, and protein structures. This field combines elements of computer science, mathematics, and biology to facilitate the analysis and explanation of complex biological data sets. Computational biotechnology, on the other hand, is focused more on the development of computational tools and techniques for the design and optimisation of biological systems, such as metabolic pathways, gene regulatory networks, and synthetic biological circuits. This field relies on computational models and simulations to predict the behaviour of biological systems and to design novel biological constructs with desired properties. Together, bioinformatics and computational biotechnology are transforming the way we study and understand living systems, and are helping to unlock the potential of biotechnology to address some of the world's most pressing challenges in healthcare, agriculture, and the environment.To understand the fundamentals of computational biotechnology to provide a better pathway for data analysis and assist in human welfare. Bioinformatics and computational biotechnology have been transformative, revolutionising many aspects of biology, biotechnology, and medicine. Key Words: Data analysis, prediction and modelling, Database development, Machine and deep learning, Translational research, collaborative research

PP-97

Antimicrobial Activity of Traditional Medicinal Plant *Ferulaasafoetida*

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Pathogenic microorganisms have been a danger to the human race since their genesis, being a major cause of human mortality and morbidity. Until the discovery of the first true antibiotic penicillin in 1928 and sulfa drugs in the 1930s, besides the toxic arsenic. Since, incidences of antimicrobial resistance amongst pathogenic microbes and unresponsiveness of existing antibiotics is increasing at an alarming rate; it becomes important to discover new more efficacious and safer antimicrobial compounds. Till date, an exceptional number of plant secondary metabolites are known to have diverse biological activities which include antifungal, antibacterial, and anticancer activities. Keeping this tremendous potential of plant extracts in mind, the aim of our present study is to investigate antimicrobial activity and nature of plant secondary metabolites present in traditional Indian medicinal plant Ferulaasafoetida.To determine the antimicrobial properties of various Ferulaasafoetida fractions and evaluate the nature of plant secondary metabolites present in these fractions.The methodology of our work includes preparation of plant fractions by percolation method using two solvents hexane and ethanol, followed by analysis of plant secondary metabolites present in these fractions and evaluation of their antimicrobial potential using disc diffusion assay and calculation of MIC values.In our investigation, we observed potent inhibitory microbicidal activity of F. asafoetida and detected the presence of flavonoids and steroids in the test fractions which might be contributing to the observed antimicrobial activity.*F. asafoetida* solvent fractions exhibited antibacterial properties that can be correlated to the presence of plant secondary plant metabolites including flavonoids and steroids were present in large quantities in the fractions. Future studies aimed in identifying the possible health benefits of *F. asafoetida* and developing novel pharmaceutical compounds from this plant should use the study's findings.

PP-98

Risk factors of Polycystic Ovary Syndrome as a Promoting cause towards Alzheimer's Disease : an Insight towards Incidence in Neurodegeneration

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With the advances in field of biotechnology, there has been a significant progress in understanding of molecular mechanism(s) associated with a disease. The more we have understood the molecular mechanisms of different diseases the more we have come to know that two or diseases might be interlinked and may be spreading in human body through common mechanisms. These interlinking mechanisms may be presented as common risk factors that can be used to restrict the development of certain diseases. In this context, Polycystic Ovary Syndrome (PCOS) is a female reproductive tract disorder characterised by hyperandrogenism and fluctuations in the hormonal levels. PCOS is marked by endocrinal dysregulation which may cause neurodegeneration in the host. Neurodegeneration in Alzheimerâ€™s disease (AD) is associated with cytokine-mediated inflammation, vascular destruction and unregulated lipid and carbohydrate metabolism. Recent studies have noted that downregulation of hormonal factors induced because of PCOS can prove to be risk factor and promoter of neurodegenerative disorders like AD.To study the risk factors of PCOS and connect them to the incidence of AD by upregulation of its promoting factors.The incidence of AD can be directly linked to the incidence of PCOS by the analysis of the common risk factors including hyperandrogenism. Fluctuation of the overall chemical coordination system of the body is seen to impart a stress situation over the brain and neuronal linings thereby promoting neurodegeneration.A conclusion can be drawn out that due to changing lifestyles of people, incidence of multiple diseases has drawn out attention. PCOS has been prevailing in the world since decades but its association with neurodegeneration has given a new insight to medical sciences. However, the exact reason for the incidence of neurodegeneration because of PCOS remains vague due to lack of studies.

PP-99

Cell Transplantation as a Future Therapy for Cardiovascular Diseases

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Cardiovascular disease (CVD) is the leading cause of death in the developed as well as in the developing world. The annual mortality of CVD is expected to reach 23.6 million by 2030 (Alissa and Ferns, 2011). CVD is a group of diseases that includes Coronary Heart Disease, Cerebrovascular Disease, Rheumatic Heart Disease, Deep Vein Thrombosis and Pulmonary Embolism. Cardiovascular Disease (CVD) is one of the major problems worldwide. These days it is getting more common among youngsters and it remains significant public health concern morbidity, mortality rate. Approximately 85% of strokes are caused by inadequate blood flow to the brain, i.e. ischemic stroke.The use of clever biomaterials and biometrics to serve as scaffolds on which to seed and grow desirable cells. Scaffolds can be made from animal small intestine, biopolymers, collagen, and bioactive glass. These substances can be produced in specialized shapes and are being tested for a variety of clinical uses, such as the formation of artificial blood vessels and pulmonary valves. These substances present a substantial array of advantages for cell transplantation.The concept of cell transplantation provides a unique opportunity to address the pathophysiology of cardiovascular disease. Whether cell transplantation will become an alternative to organ transplantation is not resolved. However, the research is producing novel, imaginative concepts, and the indications are that a variety of other uses will emerge from this technology. In concert with other modern technologies, cell transplantation presents some exciting possibilities for disease therapy and research.This can help to identify new targets for the development of novel therapies for the Cardiovascular Disease (CVD).

PP-100

Riboflavin (Vitamin B2) Fortification of Probiotic Soymilk Through In-Situ Fermentation to Prevent Riboflavin Deficiency using Response Surface Methodology by Riboflavin-Producing Strains Lactiplantibacillus Plantarum MTCC 25432, MTCC 25433 and Traditional Starter Culture Lactobacillus Acidophilus NCDC 2902

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The consumption of probiotic-containing beverages and fermented foods delivers health benefits to the host and has now become a growing trend worldwide (Verbeke, 2005). Previously, several food products have been formed to deliver probiotics, and these products are specifically of dairy origin because of their direct association with lactic fermentation (Ghosh et al., 2019). But delivery of probiotics through dairy-based foods has the disadvantage of not being suitable for lactose intolerant individuals (Randheera et al., 2017). Among some of the non-dairy sources, soy-milk has been considered a suitable medium for the development of probiotic containing fermented functional foods (Bhushan et al. 2017). The objective of the study is as follows:- 1.. The first aim of this study was to develop riboflavin-enriched fermented soymilk in combination with two riboflavin-producing probiotic strains of Lactiplantibacillus plantarum MTCC 25432, MTCC 25433, and a traditional starter culture of Lactobacillus acidophilus NCDC 2902. 2. Analysis of the technological and functional properties of the developed products. The methodology of the study is as follows: 1. The RSM was used to assess the impact of six independent factors, including X1 (temperature), X2 (pH), X3 (time), X4 (inoculation concentration of Lactobacillus plantarum MTCC 25432), X5 (inoculation concentration of Lactobacillus plantarum MTCC 25433), and X6 (inoculation concentration of Lactobacillus acidophilus NCIM 2902), on two response variables, R1 and R2, (probiotic count and riboflavin content) respectively. 2. Techno-functional characterization of fermented soy milk.The result showed that, in comparison to non-fermented soymilk, the fermented soymilk made with the combination of L. plantarum MTCC 25432, MTCC 25433, and NCDC 2902 had considerably higher hardness and cohesiveness ($p<0.05$). Similarly, the combination of the strains two L. plantarum (MTCC 25432 and MTCC 25433) and a Lactobacillus acidophilus NCDC

2902 also produced greater G0 (2.1Ã—102 Pa), G" (1.49Ã— 102 Pa), and G* (4.9Ã— 102 Pa) values, indicating that the gel formed was stiffer and had a solid nature. The riboflavin content of the fermented soymilk prepared using riboflavin-producing strains; L. plantarum MTCC 25432, MTCC 25433 combined with starter culture NCDC 2902 was significantly higher (480 Âµg/L) than the non-fermented soymilk. The final product had a higher probiotic count (9 log cfu/mL), which is also necessary for probiotic-containing functional foods to exert host health benefits.The statistical experimental design gives a pragmatic method for implementing physical parameter optimization into practice.The results of verification experiments indicated that optimum parameters led to a noticeable improvement in riboflavin production as well as probiotic viability from a combination of probiotic cultures.However, the main focus of our study is a large deformation experiment of fermented soymilk that explains, the optimum conditions from a techno-functional standpoint, and how the texture and nutritional quality of fermented soymilk differs as a result of proteolysis and production of riboflavin by LAB fermentation.

PP-101

Development and Characterization of Whey Protein Drink Using Encapsulated Lactobacillus Rhamnosus Probiotic Powder

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Probiotics are live microorganisms that, when consumed in adequate numbers provide health benefits to the consumer (FAO/WHO, 2002). Their beneficial effects include alleviation of lactose intolerance, control of diarrhea, cholesterol regulation, immune modulation, etc. (Mishra et al., 2015). In recent years, there has been a significant global rise in demand for and consumption of probiotic beverages (Min et al., 2018). However, the stability of probiotic products is often compromised during industrial processing strategies. Therefore, probiotic encapsulation technology is an alternate and growing area of research to stabilize probiotic microorganisms in products, acidification (post-fermentation), pH, preservatives, and processing/storage temperatures. The objective of the study is as follows: 1. Development and characterization of a whey protein drink using encapsulated Lactobacillus rhamnosus probiotic powder in different matrices 2. Sensory evaluation of developed whey protein drinks in different flavours.

In this study, the probiotic L. rhamnosus strain was encapsulated in five different matrices using the spray drying technique and assessed for bacterial viability. Microencapsulation is defined as a process in which tiny droplets of active substances are coated with a minuscule capsule. The colour, flavour, body texture, and general acceptability of the whey protein drink made for this study were assessed by using a 9-point hedonic scale: 9 = like extremely, 8 = like very much, 7 = like moderately, 6 = like slightly, 5 = neither like nor dislike, 4 = dislike slightly, 3 = dislike moderately, 2 = dislike very much, and 1 = dislike extremely.Amongst all the tested wall matrices, skim milk powder was found to impart the highest viability. Furthermore, the encapsulated bacteria were used to formulate a whey protein-based probiotic and characterized for various physico-chemical, sensory, and probiotic attributes.

The overall sensory score of the probiotic drink was 7.35, which indicates that it was well liked by the trained sensory panelists. The overall sensory score on a nine-point hedonic scale including texture, color, flavor, and overall acceptability was a significantly different to the commercial whey protein drinks and control samples in seven distinct flavors.The overall sensory score on a nine-point hedonic scale, including texture, color, flavor, and overall acceptability, was a significantly different to the commercial whey protein drinks and control samples in seven distinct flavors.

PP-102

Evaluation of Acute Oral Toxicity of Ipomoea Turpethum extract Loaded Polymeric Nanoparticles in Wistar Rats

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Ipomoea turpethum is a perennial herb (Convolvulaceae family) known for its medical uses since ages. The combination of novel drug delivery technique with the potential drugs is considered as the most promising tool for the treatment of diseases. Nanoparticles has been used as a drug delivery vehicle due to its ability of increasing the retention time, permeability, stability, and target specificity. In our study, we have employed N-isopropylacrylamide, N- vinyl pyrrolidone, and acrylic acid (NIPAAM-VPAA) copolymeric nanoparticles for delivering I. turpethum root extract.Present study was carried out to evaluate the safety of I. turpethum root extract loaded NIPAAM-VP-AA polymeric nanoparticles (NVA-IT) in Wistar rats. The study is divided into three parts: 1) Synthesis and characterization of NIPAAM-VP-AA polymeric nanoparticles, 2) Identification of different compounds present in the ethanolic root extract of Ipomoea turpethum plant, and finally 3) Acute oral toxicity study of I. turpethum root extract loaded nanoparticles in female Wistar rats. Acute oral toxicity study was conducted in accordance with OECD guidelines 423 for testing of chemicals. Different doses of NVA-IT i.e., 5mg/kg, 50mg/kg, 300mg/kg, and 2000mg/kg were administered to female Wistar rats in stepwise manner using oral gavage. The toxicity signs were thoroughly observed for next 14 days. In the end of the study, the blood and vital organs were harvested for hematological, biochemical, and histopathological study.In this study, we have successfully synthesized polymeric nanoparticles using NIPAAM, vinyl pyrrolidone and acrylic acid as monomers, and loaded them with ethanolic root extract of Ipomoea turpethum. Using GC-MS analysis, we have identified 42 volatile compounds in the root extract. No mortality or pathological anomalies were observed in rats post NVA-IT oral dose administration even at the highest dose which exemplify that lethal dose would be more than 2000mg/kg body weight (GSH category 5). Behavioural changes, biochemical parameters, and histopathology of vital organs were also normal after NVA-IT administration.This study demonstrated that NVA-IT nanoparticle is non-toxic and can be considered for therapeutic use for the treatment of different diseases such as inflammation, CNS diseases, Cancer etc.

PP-103

Preparation of Riboflavin Enriched Yogurt using Microencapsulated Riboflavin Producing Probiotic Strain of Lactiplantibacillus Plantarum MTCC 25432 with Standard Starter Cultures of Yogurt

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Microencapsulation is an optimistic method for delivery of live microbial cells through different food products. Prebiotics such as â€œinulin and maltodextrin (MD)â€ can use as an encapsulating material to produce synbiotics. In addition, the high glass transition temperature (Tg) of both inulin and maltodextrin minimize the stickiness when using as an encapsulating material throughout the spray-drying technique. microencapsulation of probiotic strain Lactobacillus plantarum MTCC 25432 using spray dryer incorporation of encapsulated strain into yogurt with standard starter culture [Streptococcus thermophilus NCDC 295 and L. delbrueckii subsp. bulgaricus NCDC 293] to enhance riboflavin content. Mixture of activated culture with different encapsulating material dried with laboratory-scale spray dryer (18 SMST, India). To provide the uniform temperature throughout the operation the spry dryer was started before 20-30 minutes at constant inlet and outlet temperatures 120 Â± 2 ËšC and 65 Â± 2 ËšC respectively. The activated culture with different encapsulating material (feed solution) was kept with magnetic agitation at room temperature and the feed pump (peristaltic pump) connected with feed solution at feed rate 6 mL min-1. The airflow rate and air pressure were constantly set at 30 m3 and 0.275 Mpa respectively. The spry dried microcapsules collected from the bottom of the dryer chamber and kept in laminate and low-density polyethylene film pouches at 4 ËšC and 25 ËšC for further analysis. 1gm (w/w) encapsulated powder (1.2 Ã— 108 CFU/g) with riboflavin producing producing strain (Lactiplantibacillus plantarum MTCC 25432 was inoculated in lukewarm (~ 42C) full cream cow milk containing 2 % (v/v) yogurt cultures (Streptococcus thermophilus NCDC 295 and L. delbrueckii subsp. bulgaricus NCDC 293; each of 1.3 Ã— 107 CFU/mL in PBS, pH 7.3) and incubated at 42 C for up to 20 h. The yogurt obtained by the addition of the starter culture (2 %, v/v) served as a control. The efficiency of encapsulation can be increase in combination with MD and Inulin to encapsulating the probiotic strains of Lactobacillus plantarum. The microencapsulation accomplished with the combinations of wall material such as MD+Inulin (1:1). Additionally, the

microcapsules with maltodextrin reduced the storage viability, stability and tolerance of encapsulated cells in the simulated gastrointestinal environment. The FTIR and TGA analysis performed to determine the presence of encapsulating wall material and thermal behavior of the material respectively. The overall comparison of this study, the microcapsules with MD+Inulin of 1:1 core-to-wall ratio has more efficiency than the other used encapsulating material.In conclusion, the use of encapsulated riboflavin-producing L. plantarum MTCC 25432 along with standard yogurt cultures could be the best approach to enhancing riboflavin content in yogurt (2.19 mg/L) and fulfilling the daily riboflavin requirement in humans.

PP-104

Investigation and Characterization of Multi Species, Drug-resistant, Biofilm Forming Food-borne Pathogens and Safe Intervention Strategies

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Microbial food contamination is a global food safety and public health concern. Unsafe food causes 600 million foodborne diseases and 420,000 deaths worldwide. According to the Centre for Disease Control and Prevention (CDC), biofilms are responsible for approximately 65 percent of all microbial illnesses. Biofilms are microbial consortia embedded inside a self-produced matrix that adheres to solid surfaces or forms on the liquid-air interface and imparts antimicrobial resistance and protection against adverse conditions. Most natural biofilms are produced by more than two different kinds of microorganisms, show higher resistance toward antimicrobials and disinfectants, and produce toxins harmful to human health.This study characterized the multispecies biofilm forming ability of AMR (Antimicrobial resistance) foodborne isolates Escherichia coli EMC17 and Salmonella typhimurium SMC25.Biofilm forming potential of single and multi-species food-borne pathogens was evaluated using Crystal Violet assay and Fluorescence microscopy. Antimicrobial susceptibility of both strains was evaluated using MIC antibiotic strips. For the efficient microbial intervention, a plant-based derivative (Quercetin) and class I preservatives (Malic acid/ Citric acid) were used against these AMR foodborne pathogens by Checker-Board assay (Synergy Test). E. coli EMC17 and S. typhimurium SMC25 shows resistant against 5 antibiotics. Crystal violet assay and Fluorescence microscopy confirms that these strains form more potent films in mix-species form than single species biofilms.Thus, the result shows that, a plant-based derivative (Quercetin) in combination with class I preservatives (Malic acid/ Citric acid) can be used as a potent alternative of antibiotics against these pathogens and a better approach against these pathogens unlike antibiotics in terms of food safety and human health.

PP-105

Review: Development of Composites from Commodity Plastics and Biomass through Pyrolysis and their Use for Corrosion Protection of Metals

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Due to the relatively sluggish pace of technical advancement, solid waste management is one of the most significant global concerns facing humanity today. With the development of odours and byproducts that are harmful to the environment and have an influence on human health, the practise of landfills is unsustainable and expensive in terms of environmental costs.To study the thermal co-processing of plastic waste and biomass using thermogravimetry analysis (TGA) at different heating rate. To study the non-isothermal kinetics and to compare activation energy of thermal degradation of solid waste plastics with that reported in the literature. To evaluate the thermodynamics parameters and synergism of co-processing of plastics with biomass. The commodity plastic materials procured from various sources were vacuum dried at 70oC in vacuum desiccators. Thermal analysis of samples is carried out using a Perkin-Elmer STA-6000 simultaneous TG-DTA-DSC thermo-gravimetric analyzer under non-isothermal conditions.The development of co-pyrolysis of waste plastic and solid biomasses into synergistic fuels and value-added products as it can provide synergistic solution for waste management, climate change and environmental protection.This review's main focus is on the advancement of this method of waste disposal and energy production.

PP-106

Screening of Phytocompounds from Traditional Medicinal Plants towards their Anti-Cancerous Property using Molecular Docking

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The World Health Organization has confirmed that cervical cancer is the fourth most common cancer in women. Cervical cancer is majorly caused by HPV. HPV stands for Human Papillomavirus. HPV is the most common viral infection in the reproductive tract in sexually active females and males. As per recent researches, DNA (cytosine-5)-methyltransferase 1 (DNMT1) has answered to be a reason for cervical malignant growth.The aim of the present study is screening of phytocompounds from traditional medicinal plants towards their anti-cancerous property using molecular docking. In this study literature survey of traditional medicinal plants with anti-cancerous property, Molecular docking of major phytocompounds from selected medicinal plants with cancerous target protein and Drug-likeness and toxicity prediction of phytocompounds showing binding energy stronger than control drugs.: About 32 phytocompounds were taken from different plants used to treat cervical cancer. Their sdf structures were obtained from PubChem database. The structure of protein molecule which is a cervical cancer causing protein was downloaded from Protein Data Bank (PDB) with X-ray diffraction resolution of 2.62Ã…. Docking was done with the help of Autodock vina and Discovery Studio. The phytocompounds were screened according to their binding affinity with the receptor as compared to the binding affinity of a FDA approved drug for cervical cancer (Taxol).In this research only one phytocompound followed Lipinski’s rule named Ursolic acid. Ursolic acid follows Lipinski’s rule with higher binding affinity with 4wxx. And hence it can be used for treating cervical cancer.

PP-107

Synthesis of Copper Graphene Quantum Dots in Combination with Leaves of Azadirachtaindica and Evaluation of Its Antibacterial Activity on MDR Bacteria

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The development of antibiotic-resistant bacteria creates a great health care problem worldwide. As per a CDC report, more than 700,000 deaths worldwide occur due to infection caused by MDR pathogens. The most common causative gram-negative bacteria E. coli developed MDR (Jean et al., 2016).Most effective antibiotics like Fosfomycin, amikacin, oxacillin, etc. used to treat gram-negative pathogens are failed to prevent infections(Bader et al., 2017).To study the antibacterial activity of copper graphene-quantum dots and their combination with Azadirachtaindica against MDR bacteria.This study employed synthesis of copper-graphene quantum dots (Cu-GQDs) in combination with leaves of Azadirachtaindica by hydrothermal method. The size, shape, morphology of resultant Cu-GQDs were investigated by UV-Visible spectroscopy, SEM, TEM, XRD. Crude extract were assessed to determine the phytochemicals i.e., presence of flavonoids, alkaloids, phenols, saponins and tannins.The antimicrobial activity of synthesized Cu-GQDs was evaluated by Agar well diffusion assay. Methicillin Resistant Staphylococcus aureus, E.coli from SGT Hospital. Streptomycin and Vancomycin were used as a standard. Muller- Hinton agar (MHA) and Sabouraud Dextrose agar (SDA) were used seeding the plates. The synthesized Cu-GQDs at different concentrations were added into the plates. The zone of inhibition and MIC were measured.The UV- Visible absorption spectra show peak at 257nm and 312nm. In TEM analysis, the average size diameter of Cu-GQDs was found to be â‰ˆ11nm. The crystal structure of synthesized Cu-GQDs was determined by using XRD and showed its peak at 22.5Ö¯ .The present study suggests that the synthesized Cu-GQDs in combination with leaves of Azadirachtaindica showed prominent antibacterial activity.

PP-108

Environmental Biotechnology: Harnessing Nature's Power for Sustainable Development

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Environmental pollution is a significant challenge on a worldwide scale, and traditional pollution management approaches are often expensive and unsustainable. By using the inherent capacities of microbes and plants to digest pollutants and support environmental sustainability, environmental biotechnology provides a long-term solution to ecological contamination.This study aims to give readers an overview of recent developments in environmental biotechnology and how they may be used to promote sustainable development. The review emphasizes the potential advantages of these technologies in lowering pollution, minimizing climate change, and boosting the circular economy. It concentrates on bioremediation, phytoremediation, biofuels, and bioplastics.

A thorough literature survey was done to identify necessary research and breakthroughs in environmental biotechnology. The review focused on peer-reviewed works over the last few years, including books, journals, and online resources. Among the search phrases used were environmental biotechnology, bioremediation, biofuels, and bioplastics.

The review emphasizes how environmental biotechnology can tackle some of the most important ecological problems the world is now experiencing. While biofuels and bioplastics provide environmentally friendly substitutes for fossil fuels and conventional polymers, bioremediation and phytoremediation are efficient and sustainable ways of eliminating contaminants from polluted places.By decreasing pollution, mitigating climate change, and promoting the circular economy, environmental biotechnology offers enormous potential to support sustainable development. Additional study is necessary to completely comprehend the mechanics underpinning these technologies and their potential effects on the environment and human health. The assessment lays the groundwork for further investigation and advancement in environmental biotechnology.

PP-109

Cross Border Decentralized Educational and Transactional System

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Cross border Education is a field in which different universities, colleges, industries and several government share their courses, certificates, project and credits sharing present in this platform. In the current technology era Blockchain becomes the most growing and secure technologies at that time.In the current online educational system there are lots of third parties platform of providing different courses but they does not provides the censorship of our data and the credit does not transfer securely for the network but in our platform we instantly share Transaction from globally from one country to different country into it. They change the environment of trust in it and provide the fast sharing of our data into the blockchain nodes. In this multiple universities will add into a particular educational blockchain public network and student will created our won node and join the chain of the university and access the courses and data into it. As the blockchain is immutable in nature once you share or access the courses and enrolled and completion of any courses stored into the blockchain and no one changes the data into it.

Blockchain is fully secure network and no one can hack the blockchain because they follow the four layer of abstraction in the backend of it. In this we connected our Application with the Wallet and User interface created into it. Consensus Protocol: In consensus protocol, in our project we use proof of stake on the Ethereum blockchain stored into in it. Distributed ledger: Stored the hash value generated by the IPFS and stored in the immutable ledger and this is also transparent in nature. IPFS stands for interplanetary file system they converted our image data into the form of hash that stored into the blockchain this will take less gas fees as compared to the images stored into the blockchain.

This model is Fully Secure and transparent model for accessing the courses and transfers the Data into it. Fastly and Securly Money transfer into a one click instance that takes a very less amount of Gas Price. All The certificates, Reports and marksheet is generated on the MetaMask wallet in the form of NFT and no one can copy or transfer to the other user. This will contain the Power BI report at the end that end user will easily anaysis the Growth of learning and marks of the courses in it.By the help of above these functionality our model is able to handled the data into the blockchain ledger and by the help we can transfer our credits, Academic details and result of our courses into it.

PP-110

AI based Emotion Recognition in Real Time with Application to Human-Computer Interactions

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Facial expression is a key to human emotions.The recognition system is growing with its vast inventions and applications in various areas in real life like human psychology, human computer interactions, mental health of a person and many more. Real time expressions were recognised by extracting the facial features by designing various feature extraction algorithms but with the advancement of artificial intelligence and machine learning techniques information technology has now become more intelligent. Now with CNN, computers can understand real emotions more accurately.There are some difficulties in facial expression recognition with pose change, illumination change but the accuracy in real time should be more as compared with the still images.To improve the accuracy in real time expression recognition is done with machine learning technique to eliminate the difficulties with pose change and illumination change by training the images with different angles using CNN and classifying them into 7 classes.

The system has been implemented on python platform with FER2013 dataset and real time faces. The dataset contains more than 35000 images.The training and validation will be done on dataset and further validation will be done on real time faces. Face detection will be done by Viola Jones algorithm. The detected face will be trained with CNN and the classification will be done on SVM classifier to classify the facial expressions in 7 different classes with emotions happy, sad, fear, neutral, disgust.

The experiment gives 75% recognition accuracy with the proposed algorithm with the data set and 80% accuracy with real time images.The obtained results shows that CNN is very effective in facial expression on huge public datasets and also in real time to achieve improvement in the existing results. CNN can be widely used to eliminate the difficulties in expression classification in real time to allow human computer interactions in the wild.

PP-111

The Promising Aspect of Naturally Occurring Plant Secondary Metabolites in Combating Multi-drug Resistance

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For a few decades over the world anti-microbials have been the sole source to battle against distinctive sort of diseases caused by microbes. The incidence of microbial infections has increased dramatically in past decades and drug-resistant microorganisms have emerged that are able to resist the attack of antimicrobial drugs. This has resulted in ineffective treatment that causes infections to persist and spread further. However, certain microorganisms have developed drug resistance to more than one drugs resulting in multi-drug resistance (MDR). The rapid emergence of such strains has complicated the status of various immunocompromised diseases such as HIV infection, diabetes, organ transplant patients and severe burn patients makes the body an easy target for hospital-acquired infectious diseases, which contributes to the further spread of MDR. Treatment costs are also increased by MDR, as pathogens have become resistant to commercially available drugs, necessitating the use of more expensive therapies. MDR strains are harder to treat, patients harboring MDR strains require organization of more progressed anti-microbials which lead to very noteworthy side-effects. Since of all these actualities, MDR is presently recognized as an open wellbeing issue that requires quick consideration for advancement of modern drugs that can proficiently combat these flexible organisms. Plant secondary metabolites hold a promising potential in this respect. Plant based drugs already dominate pharma market and humankind has always primarily relied on plants for medicinal uses. In this setting, we display the current situation of MDR, its effects on worldwide wellbeing, and potential of naturally occurring plant metabolites in this battle.

PP-112

Exploration of Microbicidal Activity of Cinnamomum Fractions

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For generations, people in India have employed the medicinal herb Cinnamomum for its healing powers. It has been demonstrated in prior research that Cinnamomum is rich in number of bioactive chemicals (secondary metabolites) that impart Cinnamon its traditional medicinal properties. Keeping in mind the medicinal potential of Cinnamon, this study aims to look into the antimicrobial properties of various Cinnamomum fractions.To determine the antimicrobial properties of various Cinnamomum fractions and evaluate the nature of plant secondary metabolites present in these fractions.

Various fractions of Cinnamon extract were prepared through percolation extraction method and antimicrobial activity was studied through disc diffusion assay and MIC values were determined. The plant secondary metabolites were estimated through qualitative analytical methods and as well as gas chromatography-mass spectrometry.

Hexane and ethanolic Cinnamon fractions We identified the types of secondary plant metabolites found in the cinnamon fractions and found flavonoids, steroids, and tannins in our test fractions.The solvent fractions of Cinnamomum possessed antimicrobial properties. The fractions had abundant presence of plant secondary metabolites such as flavonoids, tannins, and steroids. These secondary metabolites may contribute to Cinnamon's antimicrobial efficacy and may have positive health effects. The findings of this study are important for future research targeted at discovering Cinnamon's potential health advantages and creating novel medicinal compounds from this plant.

PP-113

Mycotoxin-Induced Neurotoxicity in the Learning and Memory Formation Region of Wistar Rats

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Fusarium species such as Fusarium moniliforme, *F. oxysporum, F. subglutinans, F. solani, F. proliferatum* etc. produces fusaric acid (FA) a food borne mycotoxin and picolinic acid derivative and commonly known as 5-butylpicolinic acid. The secondary metabolites which is toxic in nature widely contaminates the worldâ€™s major staple diets like maize, tomato, fruits, spices, corn and other essential diet. It has the ability to alter brain and pineal transmitters. FA is a potent divalent metal chelator; the human immune system is complex and can be susceptible to this. The study was undertaken to investigate the toxic effect on Wistar male ratâ€™s liver and brain are carried out.The main objective of this project is to do a detailed study on the effects of FA which leads to the neurotoxic effects and the neurodegenerative changes in the brain of rats. Where we have taken Wistar male rats as an animal model.This study reviews a mechanism of neurotoxicity and neurodegenerative disorder when FA is induced to the experimental animal where our region of interest is hippocampus, which is analyzed.

First line of toxicity test was on liver through histopathology study where there was increasing number of pyknotic nuclei in liver sections. Followed by morphological study of hippocampus. There was increasing pyknotic bodies that shows the toxic effect on brain which resulted in the cellular damage due to oxidative stress. Our work concluded with the biochemical analysis i.e. antioxidant assay. Upon the increasing dosage the accumulation of reactive oxygen species (ROS) increased, it leads to the oxidative damage of tissue and cells causing varieties of diseases. Thereby affecting the autonomic nervous system by causing significant alterations in catecholamine metabolism. This study summarizes the liver histopathology, morphological characterization of the hippocampus and the knowledge about activities, regulations, properties and biological effect of peroxidase (POD) and superoxide dismutase (SOD) in understanding the mechanism and adverse effect on exposure of FA at the region of hippocampus.

PP-114

Transgenic Animal in Lung Cancer Research

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Lung cancer is a major global health issue, responsible for a significant proportion of cancer-related deaths worldwide. Despite advances in diagnosis and treatment, the mortality rate of lung cancer remains high. The need for innovative and effective strategies for the prevention, diagnosis, and treatment of lung cancer is evident.The use of transgenic animal models for lung cancer research can help identify new targets for the development of novel therapies for lung cancer. Therefore, the present study aims to develop a transgenic mouse model for lung cancer to study the molecular mechanisms underlying lung cancer development and progression. Lung cancer is one of the most common types of cancer worldwide, and it remains a significant public health concern morbidity, mortality rates.

There is need for the development of the new strategies for transplant, prevention and treatment of lung cancer. Transgenic animal models have come out valuable tools for studying the molecular mechanism of lung cancer development and progression. Transgenic animal models are animals that have been genetically modified to carry specific genes. One of the most commonly used transgenic animal models for lung cancer research is the mouse model. Why Mice? Mice are selected because they share a great similarity with human in terms of lung anatomy, physiology, and genetics.

Transgenic animal models have emerged as valuable tools for studying the molecular mechanisms of cancer development and progression. These models involve the genetic modification of animals to carry specific genes, which can be used to study the role of these genes in the development and progression of cancer. Mice are often used as transgenic animal models for lung cancer research due to their similarity with humans in terms of lung anatomy, physiology, and genetics. The development of lung cancer in mice can be induced through inhalation of carcinogens, genetic modifications, or the injection of cancer cells. The most commonly used method for inducing lung cancer in mice involves the genetic modification of lung epithelial cells using a viral vector to introduce a specific gene.This can help to identify new targets for the development of novel therapies for lung cancer.

PP-115

Role of Epigenetic Mutations of Apoptotic Genes in Acute Lymphoblastic Leukemia

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Acute lymphoblastic leukemias are the most common cancer diagnosed in children, representing approximately 25% of ALL among children younger than 15 years. Multiple mutations are known to play important role in the diagnosis and prognosis of ALL. Recent research stresses on the role of modifiable epigenetic mutations in the pathogenesis of ALL.The objective was to summarize the recent research being carried out in the field of epigenetic modifications of apoptotic genes in ALL.

A comprehensive literature review was conducted using PubMed and Google Scholar databases. Relevant studies published between 2000 and 2021 were studied.It was noted that several epigenetic modifications of apoptotic genes like DAPK,APAF1,ASPP etc occur in the initiation and progression of ALL. These modifications involve DNA methylation, histone modifications, and non-coding RNAs. Modifiable factors may lead to promoter hypermethylation leading to the initiation of leukemia by affecting cell proliferation, apoptosis, and DNA repair, depending on which group of genes has been affected.

It can be concluded although genetic mutations are involved in the diagnosis and prognosis of Acute lymphoblastic leukemias epigenetic modifications play an important role in the pathogenesis of ALL. These are modifiable changes that become important in cancer detection and management at early stages. However, further studies are needed to understand the role of epigenetics in leukemia biology.

PP-116

NDK/NME Proteins: a Hostpathogen Interface Perspective towards Therapeutics

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No effective vaccine is available for any parasitic disease. The treatment for these is exclusively dependent on chemotherapy, which is always threatened by the development of drug resistance in parasites. This guarantees the identification of new drug targets. Here, we discuss pathogen nucleoside diphosphate kinases (NDKs) that alter host intracellular and extracellular environments as novel drug targets to simultaneously address multiple pathogens. NDKs, which have different functions, are highly conserved between prokaryotes and eukaryotes (mammalian NDKs are called NMEs [non-metastatic enzymes]). However, NDK and NME have been separately analysed for their structure and function in the past. The role of pathogen NDK in the modulation of inflammation, phagocytosis, apoptosis and ROS generation in the host is known. Conversely, its combined contribution in the host-pathogen interaction has not yet been studied. Through sequence and domain analysis, we found that NDKs can be classified into two groups. One group included NME 1â€“4 and several NDKs of selected essential protozoan parasites and the bacterium Mycobacterium tuberculosis. The second group included NME7 and other NDKs of these parasites, which presents a challenge in the development of drugs that specifically target pathogen NDKs without affecting NME7. However, common drugs targeting the NDKs of group 2 pathogens can be designed because group 2 NME7 is only expressed in ciliated host cells. Thus, this study for the first time comparatively analyses the structures and functions of human NMEs and pathogenic NDKs and predicts the possibilities of NDKs as drug targets. Additionally, pathogenic NDKs have now been provided with a nomenclature consistent with the NME of humans.

PP-117

Utilization of Plant Extracts and Phytochemicals: A Sustainable Approach to Reduce Food Spoilage

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Food spoilage acts as a crucial problem affecting public health, environment, and the economy in the conditions where the population is on a high rise accompanied with degradation of natural resources. Spoilage of food can arise at each of the food production stage from harvesting till it reaches to the consumer. Degradation of the food is largely dependent upon the existence of the moisture and the food pathogens. Some of the pathogens that cause this around the globe involve various sub species of Xanthomonas which includes Xanthomonas compestries, Xanthomonas oryzae, Xanthomonas phaseoli and various fungal species which involves Botrytis cinerea, Fusarium oxysporum were frequently linked to food spoilage. Conventional techniques such as the use of synthetic additives which are being followed by the industries for food preservation are not only expensive, but they also have potential adverse side effects. Therefore there is a demand to explore an eco-friendly alternative way by which we can inhibit the food pathogens and prevent food wastage

The current study focuses on the potential of plant extracts and phytochemicals as an alternative to reduce the growth of the pathogens.Medicinal plants have been used traditionally for the treatment of various ailments. Plant extracts consist of various phytoconstituents which can be explored further for their antimicrobial potential against different pathogens which are responsible for spoilage of food

The growth of pathogens that cause foodborne infections was found to be effectively reduced by a number of plant extracts and phytochemicals in vitro systems.Plant extracts needs to be further investigated as it can serve as an opportunity to reduce food wastage, improve shelf life and nutritional quality of food.

PP-118

Visceral Leishmaniasis-HIV Co-infection: Current Challenges and Advances in Treatment

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One of the deadliest types of leishmaniasis is known to be visceral leishmaniasis (VL), also known as kala azar. At least two Leishmania species are responsible for the occurrence of human VL. VL is an immune-suppressive disease in which the Leishmania parasites home inside host macrophages and severely downmodulate cell mediated immunity (CMI). Infection with the Human Immunodeficiency Virus (HIV) has a similar impact on the body where virus infiltrates essential immune system cells such helper CD4 + T cells, macrophages, etc. HIV infection lowers the body CD4 + cell count, which lowers CMI and increases the risk of contracting other illnesses or infections. VL-HIV coinfection together presents a much bigger challenge which further impedes the therapeutic efforts that are necessary to curtail both the infections. The increasing incidences of co-infection also pose a serious danger to South-East Asia efforts to eradicate VL. Particularly, in Bihar, India, VL-HIV coinfection patients are common, and migrant workers account for the majority of infected cases. Miltefosine and liposomal amphotericin B (L- AmB) are currently available as options for treating HIV-VL coinfection. L-AmB is costly, and there is a risk of drug resistance against Miltefosine which is also teratogenic. Thus, more modern medications or vaccinations are needed to fight this dangerous co-infection. In this context, we examine the current state of HIV-VL co-infection, the treatment choices available, and advances in the field of drug discovery to combat HIV-VL co-infection.

Isolation of Plant Growth Promoting Rhizobacteria Inoculants for Biofertilizer

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Enzymes have a wide range of industrial uses, including in the textile, bioenergy, food, beverage, animal feed, laundry, pulp and paper, and food sector. Comparing enzyme use to chemical catalyst use, industrial manufacturing can be more economical and efficient. In order to produce industrial quantities of protein, fungi utilised. This study is aimed to isolate and characterize various species of Plant Growth Promoting Rhizospheric Bacteria from Brinjal rhizospheric soil to enhance the productivity.

The Rhizospheric soil samples were collected from agricultural field of Brinjal. For the identification of bacteria, Gram straining, PGP factors estimation and Biochemical methods were done.Estimation of production of plant growth promoting growth factor: Phosphate solubilization by Qualitative method. Phosphate solubilization by Quantitative method. Quantitative estimation of indole acetic acid (IAA) by Spectrophotometer analysis. Detection of ammonia production.The populations of PGPR differ according to the part of the plant not to the soil. The higher PGPR populations were found in rhizosphere soil. Isolated bacteria were screened for plant growth promoting rhizobacterial (PGPR) activity. Out of twenty five isolates fifteen bacterial strains were selected on the basis of their activities like IAA production, N_2-fixation activity and phosphate solubilizing activity, ammonia (NH_3) production, hydrogen cyanide production. Fifteen isolates were selected for characterization by their morphological, biochemical, PGPR and physiological characteristics. Morphological characterization was done. Biochemical tests which were performed include Grama stain, carbohydrate fermentation test for glucose, sucrose, lactose, galactose, Nitrate reductase, NH3 production respectively. Therefore, we can use the isolated bacteria as inoculants for the development of Biofertilizers.

Brassinolide Promotes the Interaction between Chloroplasts and Mitochondria in Mesophyll Cell Protoplasts of Arabidopsis Thaliana during Optimization of Photosynthesis

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In plants, the cyanide-sensitive cytochrome oxidase (COX) pathway and the cyanide-resistant alternative oxidase (AOX) pathway of the mitochondrial electron transport chain (mETC) are known to play a significant role in optimizing photosynthesis. Besides, brassinolide (BL), an important form of brassinosteroid hormone is known to increase the efficiency of photosynthesis by enhancing the activity of redox-sensitive Calvin-Benson cycle (CBC) enzymes.The present study unveils the role of BL in augmenting the cross talk between chloroplasts and mETC to strengthen the efficiency of the photosynthesis.

Mesophyll cell protoplasts (MCP) of Arabidopsis thaliana were treated with BL in the absence or presence of mETC inhibitors under light and its impact on total respiration (TR) and its pathway capacities, photosynthetic carbon assimilation (PCA), PSII activity, redox ratios of pyridine nucleotides, reactive oxygen species (ROS), pyruvate, malate, CBC enzymes and their transcript levels was assessed.The addition of optimal concentration of BL to MCP stimulated the (i) TR, (ii) PCA, and (iii) PSII activity along with an increase in the enzyme activity or transcript levels of CBC enzymes. Also, the addition of BL to MCP accelerated the capacity COX and AOX pathways concurrently with an increase in total cellular pyruvate and ROS levels. Besides, malate valve components (Malate, Chl-MDH, M-MDH) increased while cellular redox ratios of pyridine nucleotides were decreased in response to BL. However, BL could not keep up the activity of CBC enzymes and their transcript levels when mETC through COX or AOX pathway is restricted by antimycin A (AA) or salicylhydroxamic acid (SHAM), respectively. Further, adding BL to MCP under restricted electron flow through mETC showed aggravation in total cellular ROS, pyruvate, malate, and redox ratio of pyridine nucleotides with a concomitant increase in transcripts associated with malate valve and antioxidant systems.BL enhances the PCA by coordinating in cross talk of chloroplasts and mitochondria to regulate the cellular redox ratio or ROS through the involvement of COX and AOX pathways along with the malate valve and antioxidant systems.

PP-121

Microorganisms Causing a Toxic Action towards Female Reproductive Tract: Microbiota Mediated Cervical Carcinoma

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The incidence of cervical cancer unlike other cancers have been noted due to action of Human Papilloma Virus (HPV), which is seen to be an etiological factor towards the incidence of cervical carcinoma (CC) besides other notable cofactors. The female reproductive tract is seen to have several bacterial colonies which notably play a pivotal role in maintaining homeostatic balance in the tract, thereby promoting a healthy reproductive environment. However, situations like secondary infections, fluctuation of hormonal levels, sexually transmitted diseases and improper hygiene practices have been seen to disrupt the normal balance of the microbial colonies residing in the reproductive tract causing dysbiosis of these bacterial colonies which may favour promotion of cancer. Recent studies have shown that modulations in the microbial environment of the vagina initiated by vaginal HPV infections and other related cofactors. This study aims to explain the related signalling pathways associated with the vaginal microbiota which cause upregulation of the HPV infections and cancerous lesions in the vaginal orifice. To study the cervical cancer incidence, role of HPV mediated signalling pathways promoting cancer, the following dysbiosis and potential of probiotics in alleviation of CC. The study through available literature shows that modulation of the properties of vaginal microbial colonies mediated via HPV or other notable cofactors have increased the risk of incidence of cervical carcinoma. The study enlists how cervical alternations are created by the HPV and thereby is a potential factor in promoting cervical carcinoma via vaginal microbial dysbiosis, promoting female infertility as well. The cervical cancer is seen to be major causes of death of females. The microbial dysbiosis mediated CC also reveals how improper lifestyle, irregular diet and bad hygiene can prove fatal for the human race.

PP-122

A Human Polycomb Response Elements exhibits Long-range Chromosmal Interactions

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Cellular Memory Modules participate in maintenance of the activated or silenced state of gene upon activation from transitory signals. We have identified a human PRE-PIK3C2B, a polycomb response element that interacts with both polycomb as well as trithorax members regulating transcriptional activation as well as silencing. Using 3C-Seq (Capturing Chromosomal Conformation-Sequencing), we identified long-range chromatin interactions associated with PRE-PIK3C2B. We identified intra- as well as inter-chromosomal interactions, a large proportion of which were found to be closely distributed around transcriptional start sites (TSS). A significant number of interactions associated with heterochromatic regions. Mapping the Chromatin interactions over the ENCODE ChIP-Seq data identified an overall enrichment of YY1, CTCF as well as histone modifications such as H3K4me3 and H3K27memarks in different cell lines. Almost 90% interactions were derived from either intronic or intergenic regions. Large proportion of intronic interactors was either unique sequences or LINE/SINE derived, In case of intergenic interactions, majority of the interaction were associated with LINE/SINE repeats. We further found that genes proximal to the interactor sequences were co-expressed, they showed reduced expression. To the best of our knowledge this is one of the early demonstrations of long-range interaction of PRE sequences in human genome.

PP-123

Wastewater Treatment and Power Generation by Microbial Fuel Cells

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Electricity demand is growing at the same time as the world's population and economy. Effective performance requires constant effort. We need to change the way we live because natural resources such as fossil fuels will soon run out. One change that is thought to have a lot of potential is the use of microbes to generate electricity. Microbial fuel cells **(**MFCs**)** can rapidly use a variety of organic or inorganic materials to produce electricity**.** The MFC consists of a flexible membrane (PEM) that separates the cathode from the anode on one side**.** As biocatalysts, microorganisms on the anode break down substrates, producing protons and electrons through cellular respiration**.** PEM transports protons, while electrons are transferred by an external electric current. The discovery of bacteria**-**within**-**bacteria **(**nanowires**)** such as *Shewanellaoneidensis* and *Geobactersulfurreducens* greatly increased efficiency and reduced costs**.** The recovery of silver and copper from wastewater has become an important part of MFC-based wastewater treatment in recent years, which also aims to remove impurities**.** MFCs can produce both electricity and hydrogen gas simultaneously. The process is called electro hydrogenation+. This method could open the door to revolutionary concepts of clean renewable energy sources.

PP-124

Nutraceutical Compounds for Alzheimer's Diseases

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Alzheimer's disease is a progressive neurodegenerative disorder characterized by cognitive decline, memory loss, and behavioral changes. There is currently no cure for the disease, and existing treatments offer only limited symptomatic relief. Nutraceutical compounds, derived from natural sources, have gained attention as a potential therapeutic option for Alzheimer's disease due to their ability to exert neuroprotective and anti-inflammatory effects.The objective of this review is to summarize the current evidence on the use of nutraceutical compounds in the treatment of Alzheimer's disease and to evaluate their efficacy and safety. A comprehensive literature search was conducted in PubMed, and Web of Science databases to identify relevant studies on the use of nutraceutical compounds for Alzheimer's disease.The search identified several nutraceutical compounds that have been investigated for their potential therapeutic effects in Alzheimer's disease, including omega-3 fatty acids, curcumin, resveratrol, and ginkgo biloba extract. Omega-3 fatty acids have been shown to improve cognitive function and reduce the risk of Alzheimer's disease, while curcumin has been found to have anti-inflammatory and antioxidant effects in the brain. Resveratrol has also been shown to have neuroprotective effects and improve cognitive function in animal models of Alzheimer's disease. However, the clinical evidence for the efficacy of these compounds in humans is limited and inconsistent.Nutraceutical compounds have shown promise as a potential therapeutic option for Alzheimer's disease, but further research is needed to establish their efficacy and safety. Future studies should focus on larger, well-designed clinical trials to determine the optimal dosages and duration of treatment for these compounds. In addition, the potential interactions between nutraceutical compounds and existing medications should be considered when evaluating their safety.

PP-125

Synthesis of Copper Graphene Quantum Dots in Combination with Leaves of Azadirachta Indica and Evaluation of Its Antibacterial Activity on MDR Bacteria

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This study employed synthesis of copper-graphene quantum dots (Cu-GQDs) in combination with leaves of Azadirachta indica by hydrothermal method. The size, shape, morphology of resultant Cu-GQDs were investigated by UV-Visible spectroscopy, SEM, TEM, XRD. Crude extract were assessed to determine the phytochemicals i.e., presence of flavonoids, alkaloids, phenols, saponins and tannins. The UV- Visible absorption spectra show peak at 257nm and 312nm. In Tem analysis, the average size diameter of Cu-GQDs was found to be ≈11nm. The crystal structure of synthesized Cu-GQDs was determined by using XRD and showed its peak at 22.5 °. The antimicrobial activity of synthesized Cu-GQDs was evaluated by Agar well diffusion assay. Methicillin Resistant *Staphylococcus aureus, E.coli* from SGT Hospital. Streptomycin and Vancomycin were used as a standard. Muller- Hinton agar (MHA) and Sabouraud Dextrose agar (SDA) were used seeding the plates. The synthesized Cu-GQDs at different concentrations were added into the plates. The zone of inhibition and MIC were measured. The present study suggests that the synthesized Cu-GQDs in combination with leaves of *Azadirachta indica* showed prominent antibacterial activity.

Digging Brassica Cuticleleads to Surprises

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Genetics and mutant analysis of cuticle biosynthesis isrelatively very well studied in plants but reports on cuticle proteins and their abundances are scanty. Therefore, leaf cuticle proteome was examined in four agronomically important Brassicaceae members namely, B. juncea, B. nigra, B. rapa, and R. sativus using gel-based (MALDI TOF/TOF) and quantitative shotgun proetomics (nLC MSMS) for understanding physiological relevance of cuticle proteins. nLC MSMS analysis identified 181 secretory proteins, majorly associated with catalytic activity (22%), defense related (16%), protein metabolism (16%), lipid metabolism (14%) and oxidoreductase activity. Validations of myrosinase and its associating protein, GDSL esterase/lipase ESM1 (involved in cuticle structuring and defense) in leaf cuticle hinted towards an extracellular "mustard oil bomb". Besides, four abundant classical secretory proteins including GDSL-esterase/lipase ESM1, β-glucanase (an antifreeze protein), peroxidase, and ascorbate peroxidase showed activity in cuticle extracts. Nanoliter osmometer-phase contrast microscopy analysis detected antifreeze activity due to non-protein components. Cutinsomes sphericalnano structures were synthesized from leaves of four species. Cutin being a resilient biopolymer has been employed for bioplastic formation. Comparison of B. juncea leaf and stem cutinsomes indicated stem cuticle to bea better candidate for bioplastics from agro-waste.This study besidesidentifying leaf cuticle proteins has also laid the foundation for exploring the extracellular glucosinolate-myrosinase system, PTM crosstalk, antifreeze activity as well as other stress adaptive strategies in Brassicaceae. The effort towardsexploring the translational potential of cutinsomes towards bioplastics formation is underway from Brassicaagro-waste, an underutilized Bioresources in India.

Phytochemicals Targeting Mitophagy in Alzheimer's Disease

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Alzheimer's sickness is the most widely recognized type of dementia, which influences in excess of 35 million individuals overall with expanding propensity. It is not accessible to 197ulfil treatments and counteraction. Starting from the principal portrayal of the lethal moderate neurodegenerative illness in 1907, nonetheless, significant discoveries on the sub-atomic systems have been accounted for. Current clinical preliminaries target different angles and standards of Promotion, like the age and total of amyloid-β(Aβ). Despite the fact that there are numerous phytochemicals which are valuable in Promotion however they are just useful in starting phase of Promotion. Likewise have extremely sluggish activity and are not exceptionally supportive. There are a few drug drugs utilized for Promotion in beginning stage, which are demonstrated extremely supportive yet there is continuous work for a fix more reasonable. Clinically it's not 100 percent exact and furthermore makes a great deal of side impacts.From various studies we have collected a list of Phytochemicals targeting mitophagy in Alzheimer's disease. These Phytochemical collected by using PubMed and PubChem, we are going to find the properties along with their interactions to the target proteins. For this study we usedPyRx, chimera, PDB, PubMed etc tools. The protected utilization of these substances as a possible treatment for Promotion, more examination of phytochemicals and their one of a kind sub-atomic targets is required. An exhaustive investigation of the writing currently accessible on phytochemicals used to treat Promotion patients was completed. Choice norms contained: Age 60 years; Promotion analysis as per Public Organization on Maturing Affiliation Alzheimer's (NIAAA) measures; and Fitting tests to evaluate clinical, mental, and practical status.The survey started with the exploration of phytochemicals starting mitophagy so the Promotion could be fix however we got to be aware through all the examination that phytochemicals are useful yet not the only one we want to track down an ever increasing number of particles and mixtures to obtain a few exact outcomes about Advertisement fix. By the assistance of drug sedates and actuated phytochemicals we will unquestionably get some were near the exploration. There are promising procedure for decrease of irritation and poisons yet the exploration is ongoing for treatment. Scientists Distinguish Protein That Adds to Tau Neurotoxicity in Alzheimer's Sickness.

PP-128

Biohydrogen Production through Microalgae using Wastewater

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In order to address the global energy and climate change challenges and promote environmental sustainability, hydrogen is a clean energy source. Making biohydrogen from microalgae is a viable way to create clean energy carriers without compromising the carbon neutrality and sustainability of bioenergy. Microalgae produce hydrogen through dark fermentation as opposed to other processes that rely on sunlight. Due to its capacity to make hydrogen from easily accessible resources like light and water, biophotolysis of water employing cyanobacteria, green algae, dark fermentation, photofermentation, and microbial electrolysis cell is also of interest. This paper examines hydrogen-producing enzymes with an emphasis on their production and localization in microalgae and highlights green microalgae and cyanobacteria as prospective hydrogen generators. Since, it is 10 to 100 times more active than [Ni-Fe]-hydrogenase and 1000 times more active than nitrogenase, [Fe-Fe]-hydrogenase is the most effective hydrogenase. The study also identifies elements that influence the effectiveness of energy conversion and the vulnerability of oxygenase, an enzyme that produces hydrogen. Recent years have seen considerable advancements in the synthesis of biohydrogen from microalgae, including the use of genetic engineering, microalgae-bacteria consortia, electrobiohydrogenation, and nanomaterials to increase enzymatic stability and hydrolysis efficiency. Biohydrogen is created from the biomass of marine macroalgae by sonication and the sonic decay of surfactants, both of which are energy-efficient decay processes. According to the study, sonication decay has a lower energy ratio than sonic surfactant decay. Using Microalgae for generating biohydrogen production and treating wastewater towards approaching sustainable development to create clean energy carriers without compromising carbon neutrality

PP-129

A Text Mining approach towards the Indentificationof Promising Anti-Cancerous Phytochemicals

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Cancer is a serious concern at present. A large number of patients die each year due to cancer illnesses in spite of several interventions available. Development of an effective and side effects lacking anticancer therapy is the trending research direction in healthcare pharmacy. Bioactive phytochemicals are preferential as they pretend differentially on cancer cells only, without altering normal cells. Carcinogenesis is a complex process and includes multiple signalling events. Phytochemicals exert antitumor effects via distinct mechanisms. They selectively kill rapidly dividing cells, target abnormally expressed molecular factors, remove oxidative stress, modulate cell growth factors, inhibit angiogenesis of cancerous tissue and induce apoptosis.Ashwagandha is an evergreen shrub that grows in India, the Middle East, and parts of Africa. It has a long history of use in traditional medicine. The herb is also known as Indian ginseng or winter cherry. Based on the literature, we identified Ashwagandha as a promising plant that contains chemicals that might help calm the brain, reduce swelling, lower blood pressure, and alter the immune system. Since ashwagandha is traditionally used as an adaptogen that is believed to help the body resist physical and mental stress.Once we identified the plant, we used the IMMPAT database to check physicochemical and ADMET properties. Together with the results of Lipinski's and ADMET properties, we identified three promising molecules from Ashwagandha for further investigation.

PP-130

Diet Monitoring Application for Patients

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Medical complications can greatly affect an individual's eating habits, causing them to avoid certain foods that contain nutrients that may be contributing to their condition. Although healthcare professionals can provide general advice on foods to avoid, the variety of packaged and unpackaged foods available in our daily lives can make it difficult to make informed decisions about what to avoid eating.To help people overcome this problem, we have developed an app that can predict the impact of specific nutrients in food on an individual's health based on their specific severity of the medical condition. Our app is designed to help people with various medical conditions to keep a close eye on their food intake and make informed decisions about their diet. The Patient specific app uses advanced algorithms to analyze the nutritional value of foods and identify nutrients or ingredients that may contribute to an individual's condition that can be harmful for IgE-mediated food triggers. This information is then presented in a clear and understandable format, allowing users to quickly and easily make informed decisions about their food choices.The app allows users to enter their disease profile and disease severity in the form of a scoring system. It then offers options to scan the food/package using the camera module or to enter the name of the food available in the application. Then there are certain algorithms going on in the background which identify the nutrients of the food and cross check it with the severity of the medical condition a person is having. The results are then displayed in the form of a simplified scoring system. From the scoring system people can easily identify the severity of the food item they are consuming.

The advantages of our application are numerous. First, it can help individuals manage their condition by avoiding foods that may trigger symptoms. It can create health awareness among the ill or allergic people allowing them to improve their life expectancy.Our app can save user time and money by providing them with the information they need to make informed food choices without having to visit a doctor or nutritionist for advice. Our app is also very easy to use. Users simply enter their medical conditions into the app, and the algorithms do the rest. The app will provide users with a list of foods to avoid along with nutritional information and suggestions for alternative foods that may provide the same information.

PP-131

Cyber Security

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Computer security, cybersecurity (cyber security), or information technology security (IT security) is the protection of computer systems and networks from attack by malicious actors that may result in unauthorized information disclosure, theft of, or damage to hardware, software, or data, as well as from the disruption or misdirection of the services they provide. The objective of cybersecurity is to protect electronic systems, networks, and sensitive information from unauthorized access, theft, damage, and other malicious activities. This involves implementing various technologies, processes, and best practices to prevent cyberattacks and data breaches, and to ensure the confidentiality, integrity, and availability of digital assets. It is provide a clear and actionable plan for improving the organization's cybersecurity posture and reducing risk exposure.This paper is basically trying to tell about the various cyber- attacks and the various security methods that can used to prevent our device from getting attacked.

PP-132

Repurposing FDA approved Drugs and Nanoparticle as Medicament against Drug Tolerance in *Mycobacterium Tuberculosis*

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The persistence of *Mycobacterium tuberculosis* (*M.tb*) against antibiotics underlines the requirement of multidrug chemotherapy in effective control of tuberculosis (TB). Biofilms formed by Mycobacteria harbor several non-tuberculous bacteria as well that may lead to secondary manifestations of TB. Biofilms matrix restricts penetrance of drugs that allow pathogenic microbial species within biofilms to develop dormant persister cells. These cells exhibit upto 1000 times higher minimum inhibitory concentration (MIC), confer drug tolerance, endow propensity to evade host immune system causing chronic infections and are a cause for recalcitrance of 80% of all hospital associated infections.The purpose of this study was to examine the efficacy of repurposed drug on drug tolerant *Mycobacterium tuberculosis*.We have explored new medicaments for disruption of biofilms using repurposed FDA drugs and nanoparticles. Drug sensitivity for repurposed drug has been tested on biofilm formation induced by *M.tb*. Our studies highlighted that *M.tb* cyclophilin protein, PpiB, plays a key role in biofilm formation.The *M.tb* target protein showed high degree of similarity in the active site of homologous protein in other biofilm forming pathogens, suggestive of being a novel target against biofilms based infection and pathogenesis. Molecular docking of target protein with FDA drugs and gallium nanoparticle (GaNP) showed high degree of interaction. Formulation of anti-TB drugs in combination with FDA approved drugs or their nanoformulation and GaNP reduced the minimum inhibitory concentration of anti-TB drugs by upto eight fold. These formulations exhibit drug synergism and are effective against biofilm formed by *M.tb* H_{37}Rv. Our studies suggest that targeting PpiB could be masterstroke required for tackling biofilms in a wide spectrum of microorganisms.Our results indicates that repurposed drug is effective on drug tolerant mycobacterium.

PP-133

Overexpression of Rv0567 plays a Role in Mycobacterium Stresses Survival and Cell Wall Modulation

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Mycobacterium tuberculosis (*M.tb*), the causal agent of tuberculosis, is a successful intracellular pathogen adept at withstanding a variety of stress conditions. Uncovering the molecular basis regulating this enhanced adaptation will promote better control for tuberculosis (TB). Despite a reductive evolution, *M.tb* genome still retains about 121 Methyltransferases suggesting that they might play an essential role in the pathogenesis of the bacterium. Understanding the biological function of these MTases will thus aid our comprehension of the fundamental ideas underlying mycobacterial metabolism and disease. The putative methyltransferase, Rv0567, is found only in obligate pathogenic mycobacterial species implying a probable role in the virulence and pathogenesis of tuberculosis. A recent study demonstrated that Rv0567 protein is present in culture filtrate of *M.tb* clinical isolates, indicating an immunologically important role of the protein.We aimed to explore the function of Rv0567 protein in *M. tb* virulence and pathogenesis as it may help advance our understanding of the metabolic pathways crucial for mycobacterial survival & speed up the identification of promising mycobacterial targets for TB diagnosis and prevention.To explore this potential, we created a recombinant *Mycobacterium smegmatis* strain constitutively expressing Rv0567 protein & studied the physiological changes & its ability to survive under different stress conditions. Initial characterization revealed that the expression of Rv0567 contributed to morphological as well as physiological changes in the recombinant. The recombinant displays

higher passive motility and stress tolerance, and a lower ability to form biofilm. Further, *in-vitro* findings demonstrate that *Ms*_Rv0567 survives longer inside host macrophages & treatment with Rv0567 protein also elevated the secretion of pro-inflammatory cytokines.Rv0567 can thus be observed to play in mycobacterial response to external stress and modulate its cell wall characteristics & is a prospective candidate for the development of innovative therapeutics.

PP-134

Structural and Functional Characterisation of Multifaceted *RvXXXX*, a Unique Histidinol Phosphate Aminotransferase, Aiding in Virulence of *Mycobacterium Tuberculosis*

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Mycobacterium tuberculosis (*M.tb*) is a highly successful pathogen sneakily proliferating for decades avoiding being targeted by the host immune system. Nitrogen metabolism is crucial for its survival in host cell. *M.tb* has evolved with well orchestrated strategies to switch between *de novo* synthesis and uptake of different amino acids from host cells to fulfill metabolic requirements during infection. Important class of essential amino acid biosynthetic enzymes includes pyridoxal phosphate dependent Histidinol-phosphate aminotransferase (HspAT) catalyzing seventh step of histidine pathway. This study demonstrated that *RvXXXX* is a novel HspAT of *M.tb*. The objective of the work is to study role of *RvXXXX* in *M.tb* infection. *RvXXXX* was cloned in pET28a and pSTKi vector and recombinant protein was purified and characterised. RAW264.7 cells were infected with Recombinant *M.smegmatis* expressing RvXXXX and its role in infection was studied. RvXXXX is a novel HspAT of *M.tb* with catalytic efficiency (k_{cat}/k_M) of $(0.72\pm0.02)*10^6 M^{-1}S^{-1}$. The Michaelis constant (k_M) was observed to be 0.6±0.05mM and k_{cat} was calculated as $(4.33\pm0.07)*10^2 S^{-1}$.RvXXXX facilitates recombinant *M.smegmatis* virulence and survival in RAW264.7 macrophages. Its expression was found to be 10 fold higher after 24hrs of infection in macrophages. RvXXXX is a secretory protein also present in cell wall extract. Recombinant RvXXXX protein exists as a properly folded globular monomeric protein of molecular weight 44KDa comprising approximately of 25% α-helix and 19% β-sheet and the melting temperature is around 65°C. RvXXXX is a specific TLR4 agonist facilitating host immunmodulation by suppressing secretion of proinflammatory cytokines. It further repressed expression of activation markers

MHC-I, CD80, and CD86 and production of Reactive Nitrogen Species all promoting M2 Macrophage polarisation. Intrinsic apoptotic pathway was inhibited avoiding recognition by host immune cells counterbalanced by enhanced necroptosis and pyroptosis promoting bacterial dissemination. It was also seen to promote pellicle formation.RvXXXX is an essential metabolic regulator that possesses multiple functions that dampen host defenses to increase virulence.

PP-135

Critical Infectious Pathogens and Healthcare in India

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One of the top 10 global health threats today is antimicrobial resistance (AMR), which has the potential to have a significant impact on the economy, society, food safety, and public health. The burden of infections acquired in the community and by healthcare providers is significantly increased by diseases brought on by bacteria that are resistant to antibiotics. At the global, national, and sub-national levels, concerted activities are needed to reduce the emergence and spread of AMR.According to the WHO, one of the top ten worldwide public health hazards to humanity in 2019 is AMR. Presently, 143 nations (representing 90% of the global population), including the 11 WHO Member States Region of South East Asia. The objective of the study is to identify the most important resistant bacteria at the national level in India for which there is an urgent need to develop novel drugs and treatments.In this study, we have used desk review of biomedical literature on key antibiotic-resistant bacteria in the Indian context; analysis of available data and information on bacterial drug resistance mechanisms and prepare a list of prioritised antibiotic-resistant bacteria and key resistance mechanisms.Based on the information obtained from a detailed literature survey, Escherichia coli was most commonly isolated (24.7%), followed by Klebsiella pneumoniae (18%), Acinetobacter baumannii (12.9%), Pseudomonas aeruginosa (12.1%), and Staphylococcus aureus (9.2%). This study concludes that Imipenem susceptibility of E. coli has dropped steadily from 86% in 2016 to 64% in 2021 and that of Klebsiella pneumoniae dropped steadily from 65% in 2016 to 45% in 2020 and was at 43% for the year 2021. Resistance to carbapenems in Acinetobacter baumannii was recorded as 87.5% in the year 2021. In Pseudomonas aeruginosa, more than 60% susceptibility was observed for various aminoglycosides and fluoroquinolones in 2021. AMR is a multifaceted, cross-sectoral problem that affects people, animals, food, and the environment. Wesuggest that research and development of novel antibiotics—particularly those effective against multidrug- and extensively drug-resistant Gram-negative bacteria is a high priority.

PP-136

Acinetobacter Baumannii : an Important Nosocomial Pathogen

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The property of antibiotic resistance developed by the ESKAPE pathogens is increasing worldwide which lead to increment of the mortality rate of the immuniocompromized patients. Hospital-acquired infection (HAI) has increased the property of multidrug resistance (MDR) by these opportunistic pathogens and a lack of novel antibiotics to treat the infection caused by them. According to a study conducted by Clinical Centre of University of Szeged Hungary, The occurrence of these ESKAPE pathogens increased within the decades of 2010-2020. According to them, the most challenging ESKAPE pathogen is Acinetobacter baumannii and their MDR (multidrug resistant) forms. They also predict that A. baumannii could be the next serious threat among ESKAPE pathogens by 2030 as these strains shows increase in sensitivity and virulence over the past decades and still growing.*A. baumannii* is a Gram-negative, aerobic, oxidase-negative, and non-motile opportunistic pathogen. They are usually isolated from the urine, saliva, secretions from the respiratory system, and open wounds in patients. Moreover, the bacterium is known to grow irrigation fluids and intravenous fluids. Acinetobacter comprises a number of species, but A. baumannii is the one with the highest clinical importance.The study's objective is to get comprehensive information onA. baumannii concerning various aspects related to infections, antibiotic resistance, biofilm-forming nature etc. In this study, we have used text mining approaches with the aid of the PubMed database to explore comprehensive information on A. baumannii.Based on the information obtained from a detailed literature survey, drug target proteins will be identified from various critical pathways and facilitate designing potent inhibitors against them. This study concludes that A. baumanniiresisted diverse classes of antibiotics. Moreover, they can develop biofilm on the surface of analytical and other medical strategies, which is one of its critical pathogenic aspects. Moreover, this pathogenic microorganism showed resistance against diverse classes of antibiotics, particularly *carbapenems*. Due to this bacterium's MDR (Multi-drug resistant), XDR (Extensive drug resistant) and biofilm-forming nature, this particular organism is considered a critical pathogen for further investigations on identifying target proteins and their inhibitors.

PP-137

siRNA of FGFR1 Targets for Gene Silencing and Expression in Heterogeneous Breast Cancer

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In the 21st century, cancer is the leading cause of death; thus, control measures and new treatments are the need of the hour. As per scientists, the FGFR system can be a new emerging therapeutic agent due to its alteration in FGFR signalling in all types of breast cancer. The objective of the study is as follows: 1. Find out the target gene, signalling pathways and their role in breast cancer using the KEGG database and GEPIA 2. Carry out a genomic analysis of the gene and its variants to design the gene silencing targets, construction of siRNA.

KEGG database provided the metabolic pathway of gene FGFR1 gene and identified the molecular targets in breast cancer. The pathway depicted that the variant amplifies the Amplified FGFR to PI3K signaling pathway and Amplified FGFR to RAS-ERK signaling pathway. Gene Sequences were taken from the NCBI. Analysis of the gene sequences by employing different software. Structural Analysis or the Sequence Manipulation Suite. SiRNA Genscript analysis was done and Target finder RNA FOLD server GEPIA server.

We analyzed the FGFR1 gene in cancer and normal gene persons i.e. expression profiling and interactive analyses by using GEPIA and results are mentioned below: GEPIA differential expression analysis components of the FGFR1 gene i.e. Profile, Boxplots, Stage plots, and correlation were done. The results of the GEPIA gave the idea that FGFR1 gene silencing can help to treat breast cancer patients and constructed siRNA which can be employed as gene-silencing agent. KEGG metabolic pathway predicted that FGFR1 Gene alters the pathway of fibroblast growth factor functioning as oncogenes and confers resistance to endocrine therapies The secondary structure of the siRNA by using RNAFOLD described the minimum free energy prediction. We identified the target gene FGFR1 and variants role in the amplification of the Amplified FGFR to PI3K along with the FGFR to RAS-ERK signaling pathway.

PP-138

Computational Analysis of Alcohol Oxidase from *Aspergillus Terreus* MTCC6324: Insights into 3D Structure, Active Site and Substrate Specificity through Alpha Fold and Molecular Docking

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Alcohol oxidase (AOx) is a valuable enzyme that has potential applications in biosensors, bioremediation, and biofuel cells. Aspergillus terreus MTCC6324 is a prospective AOx source. However, the absence of crystal structure and mechanism through which AOx may oxidize several different kinds of alcohols make comprehensive characterization difficult. Furthermore, the in-silico investigations, such as molecular docking and dynamics simulation, are effective techniques for predicting AOx substrate specificity and interaction patterns. This research focus to use Alphafold, which combines deep neural networks and Monte Carlo simulation techniques, to predict the 3D structure of alcohol oxidase (AOx) from Aspergillus terreus MTCC6324. Current research also aims to predict the active site and co-factor binding region of AOx through the application of blind molecular docking utilizing AutoDock Vina on Ubuntu. Furthermore, molecular docking and dynamics modelling will be employed to assess the functional affinity of AOx towards alcohol substrates. The AlphaFold v2.1.0 and PROCHECK tool were used to predict and validate the three-dimensional structure of the Alcohol oxidase (AOx) enzyme from Aspergillus terreus MTCC 6324. The research also included BLASTp-based sequential and comparative analysis, Clustal Omega-based multiple sequence alignment, and identification of conserved motifs. Virtual screening of several AOx substrates was done, and molecular docking was done in Ubuntu 20.04.5 LTS using AutoDock Vina 1.2. The Ramachandran plot analysis revealed that 87.6% of residues were placed in the most favoured region. The research examined the active sites for co-factor FAD and several alcohol substrates, and results indicated that cinnamyl alcohol demonstrated the highest binding affinity (-7.2 kcal/mol) in molecular docking analysis. The prediction of the 3D structure and active site of AOx and the identification of cinnamyl alcohol as a high-affinity substrate, have important novel implications for the biotechnological applications of this enzyme. These findings pave the way for future research aimed at developing efficient biocatalytic systems for various industrial applications.

PP-139

Quercetin as Potential Inhibitors of Glypican-1: Phytoconstituent Targeting Alzheimer's Disease

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Glypican-1 is a protein responsible for causing Alzheimer's disease. Glypican-1 acts as a catalyst to speed up the process of prion protein PRPN(C) to PRNP (Sc) conversion by binding to both forms of PRPN, directing them to lipid rafts, and promoting their interaction. It inhibits FGF-mediated signalling by sequestering FGF2 in lipid rafts, where it can't bind to receptors (FGFRs) and hence, glypican-1 functions as a potential therapeutic target and plays a role in the initiation and development of neurodegeneration and cancer. The objective of the study was to develop a lead molecule from the plant *Bauhinia variegata* to treat Alzheimer's disease.

Virtual screening of phytochemicals from the *Bauhinia variegata* was performed followed by analysis through Lipinski rule of five. The parent library's compounds were initially eliminated based on their physicochemical characteristics. Then, by using a variety of computational methods, virtual screening of compounds, docking, Pan Assay Interference Compounds filter, ADMET, Prediction of Activity Spectra for Substances analysis, and molecular dynamics (MD) simulation were carried out consecutively to eliminate obstacles that would make it difficult to identify prospective glypican-1 inhibitors.

Quercetin may work as a good inhibitor for treating Alzheimer's disease, according to *in silico* research, and future *in vitro* and *in vivo* analysis may confirm its effectiveness. Conclusions: We propose that the Quercetin-elucidated compounds be used further in the drug development process for *in vitro* and *in vivo* research and may function as medicines in the medical sector to treat Alzheimer's disease.

PP-140

Therapeutic Repurposing of FDA approved Drugs against *Leishmania* Parasite: An *In Vitro* Study

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Leishmaniasis is a tropical disease that is represented in three clinical forms: cutaneous, mucocutaneous, and visceral. The most severe of the three is Visceral Leishmaniasis (VL), which can turn fatal in the absence of any treatment. The currently available antileishmanial chemotherapeutics include drawbacks, such as toxicity, high cost, and drawn-out administration. Thus, new, potent, and reasonably priced medications are therefore urgently required to treat this condition.To screen commercially available drugs and find out if they can be repurposed for leishmaniasis using *in silico* tools and *in vitro* studies.

In silico analysis was done with commercially available drugs against critical drug targets of *Leishmania* parasites followed estimation of cytotoxicity, anti-promastigote and anti-amastigote activity.Two potential drug candidates revealed through *in silico* analysis were tested *in vitro.* Both the drug candidates (Compound 1 and Compound 2) exhibited remarkable antileishmanial activity with IC_{50} 1.49 & 0.74 µM. Safety profile against mammalian macrophages (THP-1) was evaluated and drugs exhibited a good safety profile. Finally, both the compounds significant anti-amastigote activity comparable with standard commercially available drugs Amphotericin B and Miltefosine.Our study suggests that compound 1 and compound 2 have potential for drug repurposing as anti-leishmanial agents. However, *in vivo* activity and the mechanism of action of these drugs needs to be further investigated to optimize their use as anti-leishmanial agents.

Impact and Complications of Crispr/Cas9 in Various Diseases

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CRISPR/CAS9 allows scientists studying medicine to modify certain DNA sequences to specific regions of the genome. This started when a peculiar, repeated DNA sequence, CRISPR, was found in the E.coli genome during an investigation of genes involved in phosphate metabolism in 1987, later turned out to be the bacterial immune system. Professors Jennifer Doudna and Emmanuelle Charpentier discovered that Cas 9 is a dual RNA guided protein. The Cas 9 enzyme is directed to its target viral RNA using the stored viral DNA segments that have been transcribed into RNA molecules called crRNA. To study the impact and complications of this technique in treatment of various diseases. This technique can be used in treatment of Cancer, by coupling CRISPRs to cas9 protein which cleaves DNA at specific sites; eliminates oncogene providing lasting cancer treatment by altering their expression and preventing formation of tumors. This can also be applied in Blindness and HIV-1.The complications of CRISPR/CAS9 are off target mutations, substantial chromosomal conformational changes caused by cas9 nuclease's off target activity which disrupts normal gene function. While CRISPR/CAS9 is an innovative therapeutic technique it still has its fair share of complications to it.Research papers from Pubmed were identified, key components and their functioning of the technique were studied, Conclusions and complications were made from previous clinical trials. Future prospects were reasoned.CRISPR/Cas9 offers advantages due to its straightforward vector generation and targeting effectiveness by introducing gene codes to rectify damaged genes, it can mend some genetic illnesses. The bacterium type II CRISPR-Cas9 technique has been employed for RNA-guided engineered nucleases due to its ease of portability. RISPR/CAS9 will have an impact on cancer biology in future.

PP-142

Millets; Emerging Super-food

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An expanding population results in constant demand for food. The inequality in accessibility of soil, land and water resources can be directly impacted by climate change which can have negative impact on our agriculture systems and crop productivity particularly on main grains like rice, wheat, and maize. Generally, these crops need more water for production in comparison to millets. Although, millets can be grown under unfavorable climatic conditions because they are C4 plant as they are tolerant to crop diseases, pests, resistant to drought, can be maintained with little effort, and can adjust to climatic shocks. They could also be a beneficial substitute for commonly traded grains when any sudden shocks impact the food grain market. Millets are a kind of cereal that belongs to family poaceae. Millets are produced all over the world and India is one of the top 5 nations in the world for millet exports. Market demand for gluten-free foods is increasing rapidly since consumers are more conscious of their heath. It is essential to enhance consumer awareness about the benefits of eating gluten-free food having essential micro and macro nutrients such as vitamins, minerals, dietary fiber and phenolic compounds as antioxidants. Moreover, millets are rich source of iron, methionine, thiamine, riboflavin isoleucine, leucine, and phenylalanine. These have low glycemic index and helps in improving insulin sensitivity and useful for diabetics. Because of increasing incidence of celiac diseases, millets have become a staple in our diets. This has a favorable impact on human health. In this review millets are discussed for their potential in combating hidden hunger in which people does not get nutrient for their growth "thereby suffers from malnutrition".

PP-143

Breast Cancer Detection using Data Science

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Breast cancer is the primary reason for deaths from cancer in women. The likelihood of successful treatment and survival is greatly increased by early identification. Breast cancer has been found and diagnosed using a variety of medical imaging techniques over the years, including mammography, ultrasound, and magnetic resonance imaging (MRI).Traditional methods of finding breast cancer do have certain drawbacks. These issues may be resolved by enhancing the efficacy and accuracy of breast cancer diagnosis using current technology advancement.The goal of applying data science to detect breast cancer is to increase the precision and effectiveness of breast cancer detection and diagnosis. Traditional methods of finding breast cancer, like mammography and ultrasound, have drawbacks like high incidence of false-positive results and inconsistent interpretation.In order to learn how to recognize patterns and anomalies that may be indicative of breast cancer, these algorithms can be trained on large datasets of medical mages, such as mammograms. NLP procedures can be utilized .Natural language handling (NLP) procedures can be utilized to separate data from clinical records, like patient chronicles and analytic reports, to recognize risk variables. Another Ensemble Modelling used in order to reduce errors and increase accuracy in the detection of breast cancer, The use of artificial intelligence (AI) to identify dangerous breast tumor has shown promising results in the detection of breast cancer, according to various studies. Here are a few example of outcomes from AI-based breast cancer detection:1)According to a research in Nature, a deep learning system could detect breast cancer in mammograms with an AUC (area under the curve) of 0.94, which was better than what human radiologists could do. The potential options for the identification and diagnosis of breast cancer are provided by data science techniques as machine learning, radiomics, natural language processing (NLP),and data visualization. These techniques have the potential to increase the precision and efficacy of breast cancer detection and have demonstrated high accuracy rates in identifying malignant breast lesions.

PP-144

Green Synthesis, Characterization and Antibacterial Potential of Zinc Oxide Nanoparticles Synthesized from Passiflora Incarnata L. Leaf Extract

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Antibiotic resistance is a public health issue since it might result in treatment failure. Despite being susceptible to a wide range of antibiotics, Listeria monocytogenes has developed resistance to several conventionally used antibiotics. Alternative therapeutics that can either complement or replace antibiotics is highly desired to resolve the issue of drug resistance. Thus, the search for antibacterial agents against such emerging drug-resistant bacteria is currently an area of research worldwide. In this regard, several green synthesized nanoparticles have been known to exhibit for their antibacterial properties and, therefore, may aid in alleviating the problem of bacterial resistance in Listeria monocytogenes. Therefore, the present study aimed at the evaluation of the antibacterial potential of Passiflora incarnata leaf extract mediated copper oxide nanoparticles (CuO-NPs) and zinc oxide nanoparticles (ZnO-NPs) against Listeria monocytogenes. To evaluate the antibacterial potential of P. incarnata leaf mediated CuO-NPs and ZnO-NPs against Listeria monoctogenes and to assess their in vitro side effects on normal mammalian cell lines.CuO-NPs and ZnO-NPs were synthesized by a green synthesis method from the aqueous leaf extracts of P. incarnata .The synthesis of both nanoparticles was confirmed using UV-Visible spectroscopy, Scanning Electron Microscopy (SEM), X-ray Diffraction (XRD), Fourier Transform Infrared Spectroscopy (FTIR), and Dynamic Light Scattering (DLS) techniques and the antibacterial activity was evaluated against Listeria monocytogenes using agar well diffusion method. Furthermore, the cytotoxic effect of the prepared CuO-NPs and ZnO-NPs was tested by MTT assay on HEK 293 cell line. Rod shaped CuO-NPs having 15.02 nm crystalline size and spherical shaped ZnO-NPs with an average crystalline size of 38.68 nm were prepared. The prepared CuO-NPs and ZnO-NPs have shown good antibacterial activity against Listeria monocytogenes 29±1.73mm and 14.67±0.58mm respectively. Both CuO-NPs and ZnO-NPs did not show cytotoxic effect on HEK 293 cell lines. Hence, from the present work, it could be concluded that Passiflora incarnata mediated CuO-NPs and ZnO-NPs can be used as potential antibacterial agent for treating Listeria monocytogenes-related infections. However, more research work is needed to figure out the mechanism of action of the synthesized nanoparticles against the target microbe.

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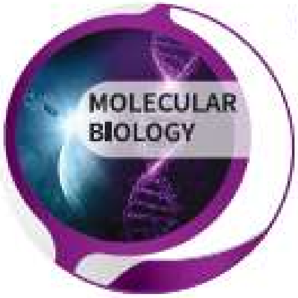

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Check List for Oocyte Donor

As per new ART (Regulation) Act 2021 & the surrogacy (Regulation)
Act 2021 through the office of the appropriate Authority
(Ministry of Health & Family Welfare)

- ☑ Egg Donor UHID No. & Face/ Ratina Screening
- ☑ Egg Donor Scaning Reports
- ☑ Stimulation Chart (Injection Name & Dose)
- ☑ Form 24B/M1 & Form 13
- ☑ Egg Donor Aadhar Card
- ☑ Egg Donor's Husband Aadhar Card
- ☑ Egg Donor Affidavit (From Notary)
- ☑ I P Affidavit (From Executive Magistrate)
- ☑ Video Consent of Donor
- ☑ Lab Report
- ☑ ECG, X-Ray
- ☑ Fitness Certificate of Donor by Doctor
- ☑ Psychologist Counselling Certificate of Donor by Doctor
- ☑ Egg Donor Health Insurance
  (which cover treatment from day 1 due to Egg Retrieval problem)
- ☑ Egg Retrieval Report From ART Clinic
- ☑ Submit Egg donor Report on monthly basis to Govt. Authority
- ☑ Keep Egg Donor Record in MRD Room for 18 Years
- ☑ Manage all Record Under super Vision of Grievance Cell

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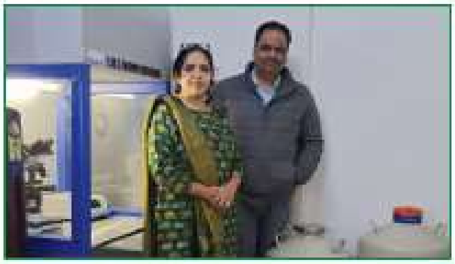
Sample of Egg Donor UHID Card


IAS Medicare Art Bank

Name:Pooja Sharma Mob:8860001023
Sex:F Age:26Y
DOB:02-03-1997 Blood Group: O+
UID:ADAWB95633 CLINIC ID:424
Add:HR, IN



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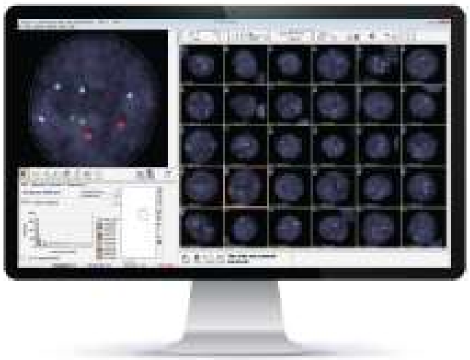
- **Review and approval of final statistics**



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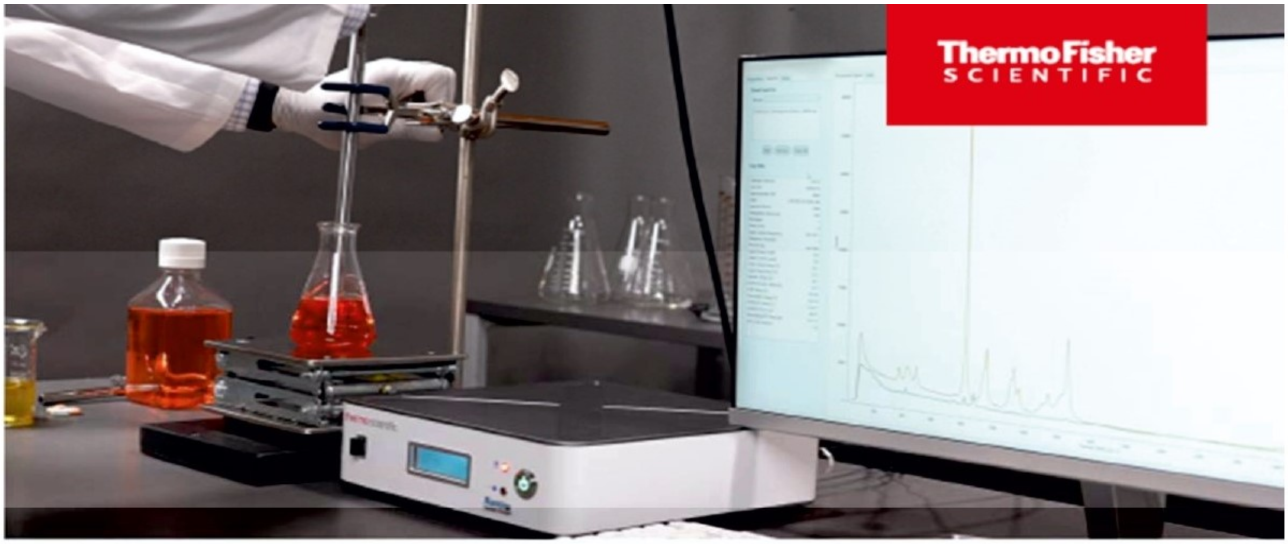

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