



OHC 2026

ONE HEALTH CONFERENCE - ANNUAL

Theme:

"One Health Approach:
Integrating Human, Animal & Environmental Health
for Sustainable Futures"

Date:
9 - 10 October 2026

Venue:
Conference Hall,
Guru Nanak Dev University

organized by:
One Health India Organization, New Delhi

In collaboration with
Guru Nanak Dev University, Amritsar

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Welcome to

One Health Conference 2026 - Annual

Organized by

One Health India Organization, New Delhi

In collaboration with

Guru Nanak Dev University, Amritsar

Scheduled on:

October 9 - 10, 2026

@

Conference Hall, Guru Nanak Dev University, Amritsar

A two-day conference consisting of a scientific program, comprehensive talks, special sessions, oral & poster presentations of peer-reviewed contributed papers and exciting and innovative research products which can be exhibited for further development in the field on One health.

For In Person Participants:

- Access (Entry) to all conference sessions, poster & exhibition area
- Conference kit including Nametag, Program & Abstract booklet
- 2 Coffee breaks and lunch for all the conference days
- Certificate accreditation from Organizing Committee

OHC 2026 Supporters



Message from the Vice-Chancellor, Guru Nanak Dev University, Amritsar



It is my great pleasure to offer my warmest greetings and best wishes for the One Health Annual Conference 2026, to be organized at Guru Nanak Dev University, Amritsar, from 9-10 October, 2026, in association with the One Health India Organization.

The year 2027 marks the 450th Foundation Anniversary of Amritsar, a historic and sacred city founded by Sri Guru Ram Das Ji. It is particularly heartening that this significant conference is being held in this culturally and spiritually renowned city. The life and teachings of Sri Guru Ram Das Ji embody the enduring values of compassion, selflessness, inclusiveness, service and collective welfare. The universal ethos of 'Seva' and 'Sarbat da Bhala' (welfare of all) resonates deeply with the philosophy of One Health, which recognizes the intrinsic interconnectedness of human, animal and environmental health.

The theme of the conference, Integrating Human, Animal & Environmental Health for Sustainable Futures, is indeed very apt and relevant. I am sure that this conference would contribute towards meaningful discussion, collaboration and innovation for a better future.

I wish the distinguished speakers, delegates, researchers, students and organizers all the very best for an intellectual event.

Prof. (Dr.) Karamjeet Singh
Vice-Chancellor
Guru Nanak Dev University,
Amritsar, Punjab

WELCOME MESSAGE FROM OHC 2026 ORGANIZING COMMITTEE

It gives us immense pleasure to welcome you to the City of Sri Guru Ram Das Ji to attend the One Health Annual Conference 2026, organized by the One Health India Organization (OHIO), a unit of BBIF, in collaboration with Guru Nanak Dev University, Amritsar, on 9th and 10th October 2026.

The theme of this year's conference, "One Health Approach: Integrating Human, Animal & Environmental Health for Sustainable Futures," reflects the growing need for collaborative and interdisciplinary approaches to address the complex health challenges of our time.

The conference brings together experts, researchers, clinicians, veterinarians, environmental scientists, public health professionals, policymakers, students, and industry representatives to exchange knowledge and explore innovative solutions in zoonotic diseases, infectious diseases, antimicrobial resistance, climate and environmental health, genomics, biobanking, diagnostics, vaccines, translational research, and public health.

We are particularly pleased to include the BBIFCC Cancer Awareness Walkathon, reinforcing our commitment to prevention, early detection, healthy living, and community engagement. We believe that meaningful and sustainable progress in health can only be achieved through collaboration across disciplines, sectors, and communities.

With the blessings, visionary guidance, and continued encouragement of Prof. Dr. Karamjeet Singh, Vice Chancellor, Guru Nanak Dev University, we are confident that this conference will provide a vibrant platform for scientific exchange and meaningful collaboration.

We hope it will inspire new partnerships, stimulate interdisciplinary dialogue, and foster innovative ideas that can be translated into meaningful action for a healthier, more resilient, and sustainable future. We extend our sincere gratitude to all distinguished speakers, chairs, delegates, volunteers, partners, and supporters for being part of this important initiative.

Together, let us advance One Health—connecting people, animals, and our environment for a healthier future.



Dr. Birendra Kumar Yadav
Convenor & Organizing Chair



Dr Suresh Singh Yadav
Co-Convenor & Co-Organizing Chair

WELCOME MESSAGE FROM BBIFCC EAST UP COORDINATOR



It gives me immense pleasure to welcome all distinguished guests, speakers, delegates, researchers, clinicians, veterinarians, environmental experts, policymakers, and students to the One Health Annual Conference 2026, organized by the One Health India Organization (OHIO), a unit of BBIF, in collaboration with Guru Nanak Dev University, Amritsar, on 9th and 10th October 2026.

The theme, “One Health Approach: Integrating Human, Animal & Environmental Health for Sustainable Futures,” reflects the urgent need for collaboration across disciplines to address emerging and re-emerging diseases, antimicrobial resistance, climate change, environmental challenges, and public health threats.

One Health reminds us that the well-being of humans, animals, and our environment is deeply interconnected. This conference provides an important platform for sharing knowledge, strengthening interdisciplinary partnerships, and translating scientific innovation into meaningful solutions for communities.

I am particularly pleased to see discussions encompassing zoonotic diseases, pandemic preparedness, AMR, climate and environmental health, genomics, biobanking, diagnostics, vaccines, translational research, and community health. The Cancer Awareness Walkathon, organized in collaboration with BBIF Cancer Care and Guru Nanak Dev University, further strengthens our commitment to prevention, early detection, awareness, and community participation.

I congratulate the organizers, scientific committee, speakers, volunteers, and partners for bringing together this important scientific gathering. I am confident that the conference will inspire meaningful collaborations and contribute to advancing the One Health movement in India and globally.

Let us work together towards a healthier, safer, and more sustainable future.

Warm regards,
Prof. (Dr.) K.K. Pandey
BBIF Cancer Care Coordinator (East U.P.)
Ex. Head, Department of Sangyahan
Faculty of Ayurveda, Institute of Medical Sciences, BHU, Varanasi



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Guru Nanak Dev University, Amritsar

Scientific Program

9th OCTOBER 2026 (Friday)

Theme: “Integrating Human, Animal & Environmental Health for Sustainable Futures”

DAY 1- 9 OCTOBER 2026, FRIDAY

THEME: One Health, Cancer, Infectious Diseases & Global Health

DAY 1- 9 OCTOBER 2026, FRIDAY THEME: One Health, Cancer, Infectious Diseases & Global Health		
8.30-09.30 A.M	Registration & Breakfast	
09:30-09:35 A.M	Welcome address, about the conference	Dr. Birendra Kr. Yadav (Convener and Organizing Chair) Dr. Suresh Singh Yadav (Co-convener and CO- Organizing Chair)
09:35-09:40 A.M	Lamp lightening	Dignitaries Present on the Dais
09:40-09:48 A.M	Inaugural Address	TBD
	Address by Guest of Honor	Prof. Dr. Vasudha Sambyal (Professor & Director GJCEI, GNDU, Amritsar)
09:48-09:55 A.M	Address by Patron	Prof. (Dr.) Harvinder Saini, Dean, Academic Affairs, GNDU, Amritsar
09:55-10:05 A.M	OHIO 2026 Award announcement	Dr. Birendra Kumar Yadav National Director, One Health India Organization, New Delhi
10:05-10:15 A.M	Vote of thanks and abstract book release	Prof. (Dr.) K.K. Pandey Ex. Sr. Prof. & HOD FoAy, IMS BHU, BBIFCC Fellow & Advisor
10:20–10:50  Tea & Networking Break		
Keynote Session		Chairpersons: Prof. (Dr.) Naresh Kumar Singh, Director of Research at the Bihar Animal Sciences

		University(BASU)
10:50–11:15 A.M	Cancer: A Globally Challenged Non-Communicable Disease and Perspectives of Holistic Approach of Treatment	Prof. (Dr.) K.K. Pandey Ex. Sr. Prof. & HOD FoAy, IMS BHU, BBIFCC Fellow & Advisor
SESSION I:	Cancer, Precision Medicine & Translational Health	Chairpersons: Dr. Kamlesh Guleria Prof. and HOD of Human Genetics, GNDU, Amritsar Dr. Prof. (Dr.) K.K. Pandey Ex. Sr. Prof. & HOD, FoAy, IMS BHU, BBIFCC Fellow & Advisor
11:15-11:35 A.M	Epigenetic Reprogramming in Cancer: A One Health Perspective for Precision Oncology and Translational Therapeutics	Dr. Umesh Kumar Professor & Assistant Director, University Centre for Research & Development, Chandigarh University
11:35-11:55 A.M	Long Non-Coding RNAs as Emerging and Reliable Molecular Signatures in Oral Squamous Cell Carcinoma	Dr. Shelly Sehgal Associate Professor, Centre for Molecular Biology, Central University of Jammu
SESSION 2:	One Health, Zoonoses & Infectious Diseases	Chairpersons: Dr. Gagandeep Kaur Gahlay Associate Professor and Head Department of Mol. Bio. & Biochem., GNDU, Amritsar Dr. Praveen Kumar Mehta Professor, Centre for Computational Biology and Bioinformatics, Central University of Himachal Pradesh, Dharamshala
12:00 A.M -12:20 P.M	Veterinary Science and One Health: Connecting the Dots across Species and Sectors	Dr. Simranpreet Kaur Professor, Centre for One Health, Guru Angad Dev Veterinary and Animal Sciences University, Ludhiana
12:20-12:40 P.M	Beyond the Patients: A One Health	Dr. Rajiv Kumar Assistant Professor

	Perspective on Visceral Leishmaniasis in India	Centre of Experimental Medicine & Surgery, Institute of Medical Sciences, Banaras Hindu University
12:40-13:00 P.M	Impact of Fungal Infections on Human Health	Dr. Manjot Kaur, Assistant Professor, School of Pharmacy, Khalsa University, Amritsar
13:00-14:20 P.M	Lunch, Poster Presentation & Exhibition	Poster Viewing • Poster Judging • Networking • Exhibition
SESSION 3:	Antimicrobial Resistance & Emerging Therapeutic Strategies	Chairperson: Dr. Vasudha Sambyal (Professor & Director GJCEI, GNDU, Amritsar) Dr. Ashok Kumar Yadav Professor, Department of Zoology, Central University of Jammu, Jammu, J&K
14:20-14:40 P.M	Phytochemicals as Multi-Target Strategies against Antimicrobial Resistance in the One Health Ecosystem	Dr. Sonia Kaushal Chemist, Department of Chemistry, Punjab Agricultural University, Ludhiana
14:40 –15:00 P.M	Targeting the MksB Condensin Complex: Exploiting Novel Structural Vulnerabilities to Block Mycobacterial Chromosome Condensation	Dr. Ravi Kumar Associate Professor, School of Biotechnology, Jawaharlal Nehru University, New Delhi
15:00-15:20 P.M	PVC-Plastics, a threat to Mental and Physical health: Is it changing the disease dynamics in India	Dr. Rita Singh Professor, Department of Zoology, University of Delhi, New Delhi
SESSION 4:	One Health Policy, Evidence & Global Health Challenges	Chairpersons: Dr. Rita Singh Professor, Department of Zoology, University of Delhi, New Delhi Dr. Sachin Kumar Assistant Professor, Department of Apparel and textile Technology,

		GNDU, Amritsar
15:30--15:50 P.M	Modernizing Biomedical Research and Regulatory Policies to Advance Human Health	Dr. Anjana Aggarwal Scientist & Research Policy Advisor, PETA India
15:50--16:10 P.M	Impact of Climate Variability on Disease Patterns and Population Health	Dr. Rashi Sharma Professor, Faculty of Ayurveda, IMS, BHU
16:10–16:20 P.M	Interactive Scientific Discussion & Audience Engagement	
16:20- 17:20	Young Scientists – Oral Presentations	Chairpersons: Dr. Rajiv Kumar Assistant Professor Centre of Experimental Medicine and Surgery, IMS, BHU Varanasi Dr. Akhilendra Kumar Maurya Assistant Professor, Department of Zoology, Institute of Science, Banaras Hindu University
19:30- 21:00 DINNER		
DAY 2 – 10 OCTOBER 2026, SATURDAY THEME: Environment, Sustainability, Emerging Technologies & Future of One Health		
6:15-07.30	BBIFCC CANCER AWARENESS WALKETHON <i>Promoting health awareness, healthy lifestyles and the One Health approach</i>	Organized by BBIF Cancer Care & Guru Nanak Dev University
8.30-09.30 Registration & Breakfast		

	Keynote Session	Chairpersons: Dr. Birendra K Yadav National Director, OHIO, New Delhi
9.30-10.00	Bridging Epidemiology, Molecular Pathology Artificial Intelligence and Biobanking: Building Foundation for Precision Medicine and Digital Health	Dr. Umesh Bhanot, MSKCC, New York, USA
SESSION 5:	Environment, Sustainability & One Health	Chairpersons: Dr. Jyoti Parkash Associate Professor, Department of Zoology, School of Basic Sciences, Central University of Punjab, Bathinda Dr. Rachna Hora Professor, Department of Molecular Biology and Biochemistry, GNDU, Amritsar
10:15–10:35 A.M	Identification, Characterization and Evaluation of Indigenous Potential Probiotic <i>Lactobacillus</i> Strains for Nutraceutical and Health Applications	Prof. Ashok Kumar Yadav Department of Zoology, Central University of Jammu, J&K
10:35–10:55 A.M	Bridging Waste Utilization and Health: Thermostable Levan Production, Structural Analysis, and Sustainable Bio-Film Fabrication for Food Packaging	Dr. Praveen Kumar Mehta Professor, Centre for Computational Biology and Bioinformatics, Central University of Himachal Pradesh, Dharamshala
10:55–11:15 A.M	Timing the Clock using photic and non-photoc cues to alleviate circadian disruption in mice	Dr. Dhananajay Kumar Associate Professor, Department of Zoology, Central University of Jammu, Jammu
SESSION 6	Molecular Biology, Neuroscience & Human Health	Chairpersons: Dr. Harish Changotra, Professor, Department of Molecular Biology and Biochemistry, GNDU, Amritsar

		Dr. Dhanananjay Kumar Associate Professor, Department of Zoology, Central University of Jammu, Jammu
11:15–11:35 A.M	KNDy/nNOS Neurons Interplay in GnRH Development and Regulation in the Adult Brain	Dr. Jyoti Parkash Associate Professor, Department of Zoology, School of Basic Sciences, Central University of Punjab, Bathinda
11:35–11:55 A.M	The SPRTN Protease and the Molecular Logic of DNA-Protein Crosslink Metabolism	Dr. Swagata Halder DPhil, Assistant Professor, Biological Systems Engineering, Plaksha University
11:55A.M–12:15P.M	From Histones to Ribosomes: Decoding Gene Expression from Chromatin to Cellular Function	Dr. Rohini Ravindran Nair Assistant Professor, Department of Medical Biotechnology, Gujarat Biotechnology University, Gandhinagar
12:15–12:35 P.M	Mapping the Regulatory Architecture of Ischemic Stroke	Dr. Arti Sharma Assistant Professor, Department of Computational Sciences, Central University of Punjab
SESSION 7	Phytochemicals, Ayurveda & Integrative Health	Chairpersons: Dr. Satwinder Jeet Kaur Professor, Department of Botanical and Environmental Sciences, GNDU, Amritsar Dr. Rohini Ravindran Nair Assistant Professor, Department of Medical Biotechnology, Gujarat Biotechnology University, Gandhinagar
12:35–12:55 P.M	Unlocking Phytochemical Potential: Gut Microbiota and ER Stress Pathways in Colorectal Cancer Prevention	Dr. Akhilendra Kumar Maurya Assistant Professor, Biochemistry & Molecular Biology Lab, Department of Zoology, Institute of Science, Banaras Hindu University
12:55–13:15 P.M	Antiproliferative Effect of Some Ayurvedic Drugs in the Management of Psoriasis: A Clinical and Experimental Study	Dr. O. P. Singh Professor & Former Head, Department of Kayachikitsa, FoA, IMS, BHU, Varanasi

13:15–14:15 LUNCH		
	Panel Discussion One Health at The Interface of Molecules, Microbiome, Medicine and Biobanking	Moderator: Dr. Naresh Kumar Singh, Director of Research at the Bihar Animal Sciences University (BASU) Panelists • Dr. K.K. Pandey • Dr. Birendra Kumar Yadav • Dr. Akhilendra Kumar Maurya • Dr. Rohini Ravindran Nair • Dr. Sonia Kaushal
14:15–15:00 P.M	★ VALEDICTORY FUNCTION & AWARDS ★	Oral and Poster Awards; reel competition award.
15:00	Vote of Thanks	

OHC 2026 Abstracts



Title: Cancer - A Globally Challenged Noncommunicable Disease and Perspectives of Holistic Approach of Treatment

Author: Prof. (Dr.) K.K. Pandey, Ex. Sr. Prof. & HOD, FoAy, IMS, BHU, BBIFCC Fellow & Advisor

Abstract: Non - Communicable diseases like Heart diseases, Diabetes, Cancers, and COPDs – globally affecting younger generation. The millions of productive individuals lost prematurely to NCDs are seriously undermining - social and economic development. About 5.8 million Indians die from heart and lung diseases, stroke, cancer and diabetes.

Surprisingly 1 in 4 Indians risks dying from an NCD before they reach the age of 70. Being a scholar of Ayurveda working in the field of holistic approach of treatment of cancer pain and palliative care since last 35 yrs, I will be talking on Cancer as a most challenging NCD and the perspectives of holistic approach of treatment.

While defining cancer the Indian language Sanskrit shares a common ancestor with Greek. Cancer is a hyper proliferative disorder which involves Transformation, Dysregulation of Apoptosis, Proliferation, Invasion, Angiogenesis and Metastasis. That behaves like a biological suicide and derecognizes identity with the organism.

The Govt. of India has launched a National Cancer control programme in 1975 and revised its strategies in 1984-85, stressing on primary prevention and early detection of cancer. Burden of cancer is increasing very fast, more than 9 out of 10 cancer people are + 45 yrs and 28% of all new cancer cases are older than 74 yrs. About 800,000 new cancers cases in India per year are only because of altered Life Style.

There are many challenges while treating cancer are as poor life style, unawareness, delayed diagnosis, improper and insufficient facilities, cost of treatment, ill effects of conventional treatments, poor immunity and multiple systemic disorders. Different physiology of people and the rate their bodies will metabolize drugs, blood supply to the tumor affecting the drug getting into the tumor and the fact that the tumor can continue to change.

The holistic approach of Ayurveda for treating such diseases there is mention of tridimensional approach of care -Daivavyapashrya chikitsa (spiritual therapy) Yuktivyapashrya chikitsa (drug, diet, life style) Satvavajaya chikitsa (psychotherapy).

The objectively planned drug therapy includes use of specific medicine, potent pain killers, symptoms relieving medicine for the improvement of metabolic activities, good dietary regimen and use of rasayana. Psychological therapy developing quality of mind for freedom from desires with the application of Yoga and meditation.

Perspectives of holistic approach of treatment includes techniques and therapeutics like Rasayana, Panchakarma, Yoga are being accepted to accomplish the goals of treatment to Strengthen immune system. detoxification system, responsive inflammatory system. optimal metabolic system to balance the regulatory system of patient.

Which ultimately enhances regenerative system and harmonizes the life force. Free radical scavenging or antioxidants, use of rasayanas (Promotive Therapy) longevity makes free from diseases

The noninvasive approach of treatment with the application of aroma therapy is a newer dimension in this regard .This rejuvenates the body systems , beneficial to health, elevates mood, provides cheerfulness & strength , improves vital functions, reduces induced disorders and thus there is relaxation of mind & body .

The antidepressant ,analgesia properties of many aromas helps in positive rehabilitation .Noninvasive approach of treatment includes herbal analgesics and Medhya(nootropics) drugs along with conventional cancer therapy has shown very promising results.

There is a need of an integration of allopathic & Ayurvedic sciences. Both the sciences have potentials as well as weaknesses. Effective fusion of both can offer good life, qualitative as well as quantitative, to the patient as an offensive and defensive strategy.

This combination of defence and offense strategy can provide the best results providing Symbio-health. Hence, if Ayurveda and Allopathic medical world work hand in hand many problems of health care can be solved. The matter in detailed be discussed and presented.



Title: Epigenetic Reprogramming in Cancer: A One Health Perspective for Precision Oncology and Translational Therapeutics

Author: Prof. (Dr.) Umesh Kumar, Professor & Assistant Director, University Centre for Research & Development, Chandigarh University

Abstract: Cancer is a complex and dynamic disease shaped by interactions between genetic alterations, epigenetic mechanisms, environmental exposures, lifestyle, nutrition, infectious agents, and the host microbiome. Epigenetic reprogramming—including DNA methylation, histone modifications, chromatin remodeling, non-coding RNAs, and epitranscriptomic regulation—acts as a critical molecular interface through which these interconnected factors influence tumor initiation, progression, metastasis, immune evasion, therapeutic resistance, and recurrence.

A One Health perspective provides an integrated framework for understanding these relationships by connecting human health with environmental and biological determinants, including diet, pollutants, occupational exposures, infectious organisms, microbial ecosystems, and broader ecosystem interactions that may influence cancer risk and treatment response. This talk will explore how such determinants contribute to aberrant epigenetic states and how these reversible alterations can be exploited for cancer prevention, early detection, molecular stratification, and precision therapeutics.

Particular emphasis will be placed on epigenetic regulation of tumor suppressor pathways, epithelial–mesenchymal transition, cancer stemness, and the tumor microenvironment, together with emerging evidence for phytochemical-mediated epigenetic modulation, including curcumin and related bioactive compounds.

The integration of epigenomics with genomics, microbiome profiling, metabolomics, liquid biopsy, and artificial intelligence offers opportunities to develop context-specific biomarkers and individualized therapeutic strategies. By linking environmental, microbial, nutritional, and molecular determinants of cancer, this framework positions epigenetic reprogramming as a translational bridge between One Health and precision oncology, supporting a more integrated approach to cancer prevention, diagnosis, and treatment.

Keywords: Epigenetic Reprogramming, One Health, Precision Oncology, Cancer Biomarkers, Phytochemicals, Translational Therapeutics



Title: Long Non-Coding RNAs as emerging and reliable molecular signatures in Oral Squamous Cell Carcinoma

Author: Dr. Shelly Sehgal, Associate Professor, Centre for Molecular Biology, Central University of Jammu

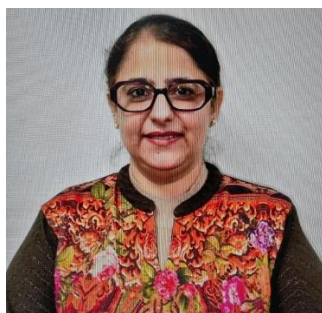
Abstract: Oral cancer often referred to as oral squamous cell carcinoma (OSCC) is a substantial public health concern, defined by the unchecked proliferation of cells in the oral cavity, including the lips, tongue, gums, and other areas. Research studies have shown that more than 75% of the human genome is functional and it is responsible for encoding many non-coding RNAs (ncRNAs). ncRNAs are involved in regulation of gene expression and further divided into two categories- Long non-coding RNAs (lncRNAs), and short non-coding RNAs. Short non-coding RNAs include microRNAs, Piwi-interacting RNAs, small interfering RNAs, promoter-associated RNAs, and enhancer RNAs.

The ENCODE project estimated that the human genome encodes more than 28,000 different lncRNAs and the NONCODEV6 has more than 1,73,000 human lncRNAs. LncRNAs are a subclass of ncRNAs having a length spanning over 200 nucleotides. Alike mRNAs, lncRNAs are synthesized by RNA polymerase II and they too undergo post-transcriptional modifications. Several lncRNAs have been identified and studied in the context of OSCC. These lncRNAs have been shown to influence various aspects of tumor biology, including cell proliferation, programmed cell-death, invasion, angiogenesis, and metastasis. Depending on their precise roles and interactions with other molecules inside the cell, they operate as tumor suppressors or oncogenes. LncRNAs are known to control gene expression, chromatin dynamics, and several aspects of growth and development.

Long non-coding RNAs (lncRNAs) are emerging as key molecular regulators in various cancers, including Oral Squamous Cell Carcinoma (OSCC). Despite their growing recognition, comprehensive and curated resources focusing specifically on OSCC-associated lncRNAs remain scarce. To address this gap, we developed OSCClncDB, a specialized, publicly accessible database that consolidates and organizes lncRNA data relevant to OSCC. This repository integrates experimentally validated and computationally predicted lncRNAs, along with their associated genomic features, chromosomal locations, expression profiles, and clinical relevance.

Data included in OSCClnnoDB were curated from peer-reviewed publications, high-throughput expression studies, and publicly available bioinformatics databases. Each entry is annotated with metadata such as functional roles, interaction networks, and links to supporting literature. The user-friendly interface enables keyword searches, advanced filtering, and downloadable data. OSCClnnoDB provides a focused platform for comprehending the regulatory landscape of lncRNAs in OSCC.

The research aims to accelerate biomarker discovery, therapeutic target identification, and translational research in oral oncology by representing a valuable step toward unraveling the complexity of non-coding RNA involvement in OSCC and promoting data-driven advancements in precision medicine.



Title: Veterinary Science and One Health: Connecting the Dots across Species and Sectors

Author: Simranpreet Kaur, Professor, Centre for One Health, Guru Angad Dev Veterinary and Animal Sciences University, Ludhiana

Abstract Body: The emergence of zoonotic diseases, antimicrobial resistance (AMR), climate change, food-borne hazards and environmental degradation has highlighted the limitations of addressing health challenges through isolated human, animal or environmental perspectives. These interconnected threats underscore the need for a holistic approach that recognizes the complex biological, ecological and societal interactions at the human-animal-environment interface. The One Health approach provides such a framework, and veterinary science occupies a pivotal position in connecting these dimensions.

Veterinarians have traditionally been at the forefront of animal health, disease prevention and population-based surveillance. However, their role has progressively expanded to encompass zoonotic disease prevention, food safety, epidemiology, antimicrobial stewardship, wildlife health, biosecurity and ecosystem health. Livestock, companion animals and wildlife can serve as reservoirs, sentinels and interfaces for pathogen emergence and transmission. Experiences with SARS, COVID-19, West Nile virus, avian influenza, Nipah viral disease and other emerging infections demonstrate the importance of integrating animal and human surveillance, epidemiological intelligence and laboratory systems for early detection and effective response. Increasing interactions among humans, domestic animals and wildlife, driven by land-use change, intensification of animal production, urbanization, climate change, ecotourism and global trade, further emphasize the need for coordinated surveillance and prevention.

Veterinary public health is also central to food safety, extending from farm-level husbandry and biosecurity to slaughter, processing, distribution and consumption. Veterinary expertise contributes to controlling food-borne pathogens and chemical hazards, monitoring antimicrobial residues and strengthening farm-to-fork food safety. The growing challenge of AMR further emphasizes the need to integrate antimicrobial use and stewardship across human, animal and environmental sectors.

Climate and environmental change add further complexity by influencing host-pathogen interactions, vector ecology, wildlife distribution and disease transmission.

Extreme weather events, biodiversity loss, ecosystem degradation and changing patterns of human and animal movement necessitate integrated epidemiological, laboratory, environmental and genomic surveillance for identifying emerging threats and enabling timely interventions.

The One Health paradigm therefore calls for meaningful collaboration among veterinarians, medical and public health professionals, environmental scientists, microbiologists, epidemiologists, agricultural and wildlife sectors, food safety authorities, policymakers, academia and communities. The Centre for One Health, Guru Angad Dev Veterinary and Animal Sciences University, Ludhiana, provides a platform for advancing this integrated vision through education, research, surveillance, capacity building and stakeholder engagement.

Ultimately, veterinary science represents a vital connecting link within One Health-connecting species, connecting sectors and connecting knowledge to action. Strengthening these connections can shift health systems from reactive response towards prevention, preparedness and resilience, while safeguarding the health of humans, animals and ecosystems.



Title: Beyond the patients: A One Health Perspective on Visceral Leishmaniasis in India

Author: Dr. Rajiv Kumar, Centre of Experimental Medicine & Surgery, Institute of Medical Sciences, Banaras Hindu University

Abstract Body: Visceral leishmaniasis (VL), or kala-azar, remains an important neglected tropical disease in the Indian subcontinent. India has made remarkable progress towards eliminating VL as a public health problem, with substantial reductions in incidence through early diagnosis and treatment, vector control and strengthened surveillance. However, sustaining these gains and achieving interruption of transmission will require a broader understanding of the factors that collectively shape VL transmission and persistence.

In India, transmission of *Leishmania donovani* is predominantly anthroponotic, with humans serving as the principal source of infection for the sand-fly vector *Phlebotomus argentipes*. Individuals with visceral disease, asymptomatic infection and post-kala-azar dermal leishmaniasis (PKDL) may contribute differently to the transmission continuum, while vector abundance, infection and insecticide susceptibility influence transmission at the human–vector interface. These biological interactions occur within a wider environmental and socioeconomic context, including housing conditions, local ecology, climate, population movement and access to healthcare, all of which can influence exposure, disease detection and persistence of transmission.

As clinical incidence declines, these interconnected factors become increasingly important for identifying residual transmission and emerging hotspots. Integrated clinical, immunological, entomological, environmental, geospatial and community-based surveillance can help identify individuals and settings that may sustain transmission despite low reported incidence. The potential contribution of animal infection will also be considered, while emphasizing that detection of **Leishmania** in animals alone does not establish a reservoir role.

Achieving the “last mile” of VL elimination therefore requires coordinated attention to human infection, vectors, environment, communities and health systems. Bringing these components together within a One Health framework can strengthen surveillance, guide targeted interventions and help sustain India’s progress towards interruption of VL transmission.



Title: Impact of Fungal Infections on Human Health

Author: Dr. Manjot Kaur, M. Pharm, Ph.D., Department of Science and Technology, DST INSPIRE- Fellow (2018-2023), GNDU

Abstract Body: Fungal infections are significant but often underestimated global health challenge, causing approximately 6.5 million invasive infections and 3.8 million deaths annually.

The WHO has identified 19 fungal pathogens as major public health threats due to their disease burden, emerging resistance, and limited research and treatment options. Immunocompromised individuals, including those with HIV/AIDS, cancer, organ transplantation, or critical illness, are particularly vulnerable.

The emergence of drug-resistant fungi, such as *Candida auris*, azole-resistant *Aspergillus fumigatus*, and resistant dermatophytes, further complicates management. Delayed diagnosis, limited diagnostics, antifungal toxicity, drug interactions, and restricted access to effective therapies remain major challenges.

Strengthening surveillance, diagnostics, antifungal stewardship, equitable treatment access, and development of novel therapies through a One Health approach is essential to reduce the global burden of fungal diseases.



Title: Phytochemicals as Multi-Target Strategies against Antimicrobial Resistance in the One Health Ecosystem

Author: Dr. Sonia Kaushal, Organic Chemist, Assistant Professor, Department of Chemistry, PAU

Abstract Body: Antimicrobial Resistance (AMR) is a top-tier threat to global health, food security, and economic stability. It occurs when microorganisms such as bacteria, viruses, fungi, and parasites evolve resistance to modern medicines making them less effective. It is a major public-health issue because resistant infections can lead to longer illnesses, higher healthcare costs, treatment failures, and increased mortality. AMR does not remain within a single sector.

Resistant organisms and resistance genes can circulate among humans, animals, food, and the environment. Coordinated surveillance and interventions across human health, veterinary medicine, agriculture, food systems, and environmental sectors are therefore essential.

Under a One Health approach, plant-derived products such as essential oils, terpenoids, flavonoids, alkaloids, and polyphenols offer a sustainable strategy to combat AMR across the interconnected human, animal, and environmental ecosystems.

These biodegradable botanical agents feature multi-target mechanisms that disrupt bacterial membranes, block efflux pumps, and dismantle protective biofilms, making it structurally difficult for pathogens to adapt. In human and veterinary medicine, plant extracts function as antibiotic adjuvants that resensitize resistant strains to conventional therapies, while in livestock and aquaculture, they serve as effective phytogetic feed additives to replace routine antibiotic growth promoters.

By substituting persistent synthetic drugs with rapidly degrading plant alternatives, this strategy prevents the accumulation of chemical residues in soil and water runoff, ultimately suppressing the expansion of the environmental resistome.



Title: Targeting the MksB Condensin Complex: Exploiting Novel Structural Vulnerabilities to Block Mycobacterial Chromosome Condensation

Author: Dr. Ravi Kumar, Associate Professor, JNU, New Delhi

Abstract Body: Chromosome organization and segregation are critical for bacterial viability, traditionally driven by canonical Structural Maintenance of Chromosomes (SMC) proteins. However, *Mycobacterium smegmatis* utilizes an alternative condensin, MksB, which operates through fundamentally distinct structural and regulatory mechanisms. Recent studies reveal that MksB functions within a specialized *MksB2E4F2* holo-complex, where MksE and MksF accessory proteins distinctly enhance DNA-binding affinity while suppressing ATPase activity.

Crucially, MksB dimerization is governed not by the conserved glycine residues typical of other SMCs, but by a novel KDDR motif located at a loop near the hinge dimer interface. This structural divergence creates a highly specific therapeutic vulnerability. In vivo and in vitro biochemical profiling demonstrates that disrupting this KDDR motif forces a dimer-to-monomer transition.

This dissociation, or the targeted neutralization of the positively charged central hinge cavity (R603D), completely abrogates the complex's ability to bind DNA and condense the bacterial chromosome. Furthermore, only the fully intact MksB homodimer, executing a precise ATP hydrolysis cycle, can successfully stabilize negatively supercoiled DNA to achieve chromosome compaction.

Because these mechanisms diverge significantly from standard bacterial condensins, MksB represents a highly promising, selective therapeutic target. Developing small molecules to sterically occlude the unique KDDR hinge interface or disrupt MksEF regulatory binding offers a novel antimicrobial strategy to definitively block chromosome condensation and halt mycobacterial proliferation.



Title: Modernising Biomedical Research and Regulatory Policies to Advance Human Health

Author: Dr. Anjana Aggarwal, Scientist & Research Policy Advisor, PETA, India

Co-Author: Emily Trunell

Abstract: Background: Animal experiments' limitations, including low translatability and ethical cost, along with recent scientific advancements, have triggered a global shift towards human-relevant, animal-free research tools. We present evidence advocating a paradigm shift from animal-based methods and recommend a six-point strategy for a faster transition.

Methods: A comprehensive literature review was conducted to identify research areas of animal experimentation. Based on these data, PETA entities have developed the Research Modernisation Deal, containing a six-point strategy for accelerating a shift away from experiments on animals and towards the uptake and further development of non-animal, human-relevant research methods.

Results: The six-point strategy urges immediate cessation of animal use in biomedical areas where they're poor predictors for human health outcomes. It recommends systematic reviews to identify other ineffective areas, transparent evaluations, public commenting periods, global acceptance of non-animal testing methods, fund redirection, and education in non-animal methods.

Conclusion: The mounting evidence against the value of experiments on animals is evident across various domains. The limited predictive value of animal-based methods, increased recognition of animal sentience, and dwindling public support for the use of animals indicate a shift in policies and priorities is needed. Transitioning away from failing animal-based methods will not only spare millions of animals and expedite new treatments and cures for humans, but also open possibilities for economic growth and accelerated returns on investments in drug research and development.

Keywords: Animal experimentation, Human-relevant methods, Roadmap, Strategy, Research Modernisation Deal



Title: Impact of Climate Variability on Disease Patterns and Population Health

Author: Dr. Rashi Sharma, Professor, Faculty of Ayurveda, IMS, BHU

Abstract: Background: Emerging global health challenges are increasingly driven by the complex interactions among human health, animal health, environmental change, climate variability, urbanization, antimicrobial resistance, and changing patterns of infectious and non-communicable diseases. These interconnected challenges require approaches that move beyond conventional, discipline-specific healthcare models. The One Health framework provides an integrated platform for collaboration across human, veterinary, environmental, public health, and allied disciplines.

Objective: To synthesize evidence supporting interdisciplinary One Health approaches for prevention, surveillance, risk assessment, and management of emerging global health challenges and to identify strategies for translating evidence into effective health action.

Methods: A narrative evidence synthesis was undertaken using published literature from multidisciplinary scientific databases and reports from major international health organizations. Evidence related to zoonotic diseases, antimicrobial resistance, climate-sensitive health risks, environmental health, food safety, and integrated disease surveillance was reviewed. Particular emphasis was placed on evidence demonstrating the value of cross-sectoral collaboration, data sharing, community participation, and coordinated prevention strategies.

Results: The available evidence indicates that integrated One Health approaches can improve identification of shared health risks, strengthen surveillance and outbreak preparedness, facilitate coordinated responses to zoonotic diseases, and support antimicrobial stewardship. Environmental monitoring and climate-informed health surveillance can further improve early recognition of emerging risks. Interdisciplinary collaboration also enables integration of epidemiological, clinical, veterinary, ecological, and public health evidence into more comprehensive prevention strategies.

However, implementation remains constrained by fragmented surveillance systems, limited cross-sectoral data sharing, inadequate interdisciplinary training, and differences in institutional priorities. Strengthening One Health governance, digital surveillance, collaborative research, capacity building, community engagement, and evidence-informed policy can facilitate translation of scientific evidence into sustainable action.

Conclusion: The transition ****from evidence to action**** is essential for addressing increasingly interconnected global health challenges. One Health provides a practical framework for integrating knowledge and expertise across disciplines and sectors.

Evidence-based interdisciplinary collaboration, supported by integrated surveillance, innovative technologies, community participation, and responsive policies, can enhance preparedness, prevention, and resilience.

Embedding One Health principles within research, education, healthcare, and public health policy is therefore critical for achieving sustainable and equitable health outcomes.

Keywords: One Health; Interdisciplinary Approach; Evidence-Based Practice; Global Health; Zoonoses; Antimicrobial Resistance; Environmental Health; Disease Surveillance; Health Promotion; Sustainability.



Title: Bridging Epidemiology, Molecular Pathology, Artificial Intelligence (AI) and Biobanking: Building Foundation for Precision Medicine and Digital Health

Author: Dr. Umesh Bhanot, Department of Pathology & Laboratory Medicine, MSKCC, USA

Abstract: The first draft of the human genome was published about quarter of a century ago (2001). This allowed scientists and medical professionals to further explore the molecular basis of human diseases and accelerate the field of new drug discovery.

Next generation sequencing is being used increasingly for mutation detection, novel molecular classification of tumors and therapy selection in human oncology.

Large scale population based biobanking with their associated epidemiologic data, opens new avenues for advancements in molecular epidemiology for example, All of Us Research Program in the US and the UK Biobank. Meanwhile, digital pathology – whole slide imaging (WSI) has taken rapid strides in the post-Covid era.

Leading institutions all over the developed world are undergoing digital transformation. Whole slide images are available and used to train AI models to augment pathologic diagnosis and help accelerate therapeutic decision making for clinical trials.

This has heralded a new era of large language models (LLMs) and multimodal Pathology foundation models.



Title: Identification, Characterization and Evaluation of Indigenous Potential Probiotic Lactobacillus strains for Nutraceutical and health applications

Author: Prof. Ashok Kumar Yadav, Department of Zoology, Central University of Jammu, J&K

Abstract: Probiotics are defined as live microorganisms that, when administered in adequate amounts, confer health benefits to the host (WHO, 2001). This study emphasizes the role of probiotic microorganism in gut health, immune modulation, antimicrobial activity and management of gastrointestinal and other health disorders.

A major focus is the need for indigenous Indian probiotic strains, as Western strains may show limited adhesion, colonization, and adaptation to the Indian gut environment. Indigenous strains may provide better colonization and host-specific health benefits.

Research on Lactobacillus isolates demonstrates important probiotic attributes, including acid and bile tolerance, antioxidant activity, adhesion to intestinal epithelial cells, antimicrobial activity, and immunomodulatory effects. Two indigenous strains LpJ5 and LpJ15 showed strong antimicrobial activity against Staphylococcus aureus and Propionibacterium acnes.

We further explore probiotics in the gut–brain and gut–lung axes, emphasizing microbial metabolites, immune regulation, and potential effects on neurological and respiratory health. It also introduces designer probiotics, using genetic engineering to deliver therapeutic molecules or act as targeted living therapeutics.

Finally, Postbiotics such as metabolites and extracellular vesicles derived from selected indigenous strains LpJ5 and LpJ15 demonstrate antimicrobial activity, supporting their potential as biotherapeutic agents. Overall, the work demonstrates the potential of indigenous probiotics and their derivatives for functional foods, nutraceuticals, and emerging therapeutic applications.



Title: Bridging Waste Utilization and Health: Thermostable Levan Production, Structural Analysis, and Sustainable Bio-Film Fabrication for Food Packaging

Author: Dr. Praveen Kumar Mehta, Professor, Centre for Computational Biology and Bioinformatics, Central University of Himachal Pradesh

Abstract: The one health concept emphasizes the interconnectedness of human health, food systems, and environmental sustainability, highlighting the need for integrated approaches to resource management and health promotion. The food packaging sector is a significant contributor to the global accumulation of plastic waste.

The disposal and end-of-life management of conventional fossil-fuel-derived plastics pose substantial environmental concerns, particularly through microplastic pollution and greenhouse gas (GHG) emissions. In this context, valorization of organic food waste into functional biopolymers offers an environmentally sustainable strategy with potential applications across multiple one health domains.

The present study explored microbial production of the fructan biopolymer levan from organic solid wastes using thermophilic and salt-tolerant *Bacillus* strains. *Bacillus licheniformis* ATS95 and *Bacillus subtilis* AHS57 demonstrated promising levansucrase activity and efficient utilization of waste-derived substrates for levan production. Banana peel extract supported recovery of 9.72 g of ethanol-precipitated polysaccharide from 25 g dry peel under optimized conditions.

Structural characterization using FT-IR, XRD, TGA, SEM, ¹³C-NMR, and TOF-ESI-MS confirmed the formation of high-molecular-weight, predominantly amorphous and thermally stable levan polymers. The recovered levan exhibited antioxidant, anti-inflammatory, emulsifying, and antibiofilm activities, including activity against *Staphylococcus aureus* and *Pseudomonas aeruginosa*, while also demonstrating prebiotic potential for *Lactobacillus plantarum*.

Furthermore, incorporation of levan into polysaccharide-based composite films demonstrated promising biodegradability, with substantial mass loss during soil burial.

Collectively, these findings demonstrate a circular bioeconomy approach in which organic waste can be transformed into value-added biomaterials with potential relevance to food preservation, human health, microbial management, and environmental sustainability.

Further standardized studies on mechanical properties, barrier performance, migration, safety, and biodegradation are warranted to establish their practical applications.

The study illustrates how microbial bioconversion of waste can contribute to an integrated one health framework by simultaneously addressing waste management, sustainable materials production, and health-related applications.



Title: Timing the Clock using photic and non-photoc cues to alleviate circadian disruption in mice

Author: Dr. Dhananjay Kumar, Department of Zoology, School of Life Sciences, Central University of Jammu

Abstract: Exposure to photic and non-photoc cues at odd time of the day disrupts the circadian clock of organisms. This may alter the homeostatic balance (circadian and metabolic), impacts work efficiency, and may cause life-threatening disasters due to cognitive impairment. Timely use of proper lighting schedule and drugs/food intake may mitigate circadian disruption.

Our results using non-photoc cues such as *Bacopa monnieri* and chronic exposure to different diets, high-fat diet (HFD) and low-fat fed diet (LFD), impacted the clock in mice and affected clock genes expression, glucose homeostasis, corticosterone and testosterone levels and cognitive performance in mice.

However, timed treatment with bacoside and *Withania somnifera* extract significantly improved phase–resetting and accelerated the re-entrainment of activity to the newly shifted LD cycle, and it also enhanced cognitive performance in mice subjected to chronic shift-work. Secondly, diet-dependent alterations in clock genes, activity pattern, tau, body composition and energy homeostasis were observed in HFD fed mice. HFD resulted in an immediate deceleration in tau and altered clock genes expression and glucose rhythms compared to LFD fed diet. Our results highlight the importance of timing the light exposure and food intake in maintaining circadian homeostasis.

Thus, timed treatment with light pharmacological agents may attenuate the photic and non-photoc cues induced circadian disruptions at behavioural, metabolic and hormonal levels, and may show positive health benefits and enhance cognitive performance. Such information may prove pivotal in designing appropriate lighting and food intake schedule that may enhance work performance of professionals

Keywords: Circadian clock, *Withania somnifera*, high-fat diet, cognition, shift-work



Title: KNDy/nNOS neurons interplay in GnRH development and regulation in the adult brain

Author: Dr. Jyoti Parkash, Associate Professor, Department of Zoology, School of Basic Sciences, Central University of Punjab

Abstract: The establishment of reproductive competence in mammals depends on the correct projection of gonadotropin-releasing hormone (GnRH) neurons to the hypothalamic median eminence arcuate region (ME-ARC) and the timely release of GnRH into a specialized capillary network for delivery to the anterior pituitary. GnRH neurons and glial cells undergo extensive cytoskeletal plasticity during critical time windows in adulthood, such as at the onset of the preovulatory surge, when massive GnRH release occurs to induce ovulation.

The trend towards lower fertility has increased in the last 50 years worldwide, but even more dramatically in most members of the Indian community. It is also widely accepted that fertility rates will decrease even further in the following decades.

While the emergence of low fertility in India is due to a combination of different factors: institutional, socio-economic, physiological and biologically. They are thus an ideal system in which to analyze the complex relationships involved in neurosecretion and morphological plasticity as well as the role of specific molecules in the homeostasis of the adult nervous system.

In our study we have shown that sex steroid hormones sensitive to KNDy (Kisspeptin, Neurokinin B, and Dynorphin A) neurons convey sex steroid hormones feedback during the reproductive cycle necessary for GnRH surge and pulse generation. Kisspeptin secretion from AVPV neurons during proestrus activates nNOS (Neuronal nitric oxide synthase) neurons and plays a role in the GnRH surge.

The role of the KNDy neurons peptide (NKB) and nNOS interplay is not fully explored in context to the GnRH/LH secretion during the proestrus and diestrus phases in ME-ARC and POA region of the hypothalamus. In this study we found that senktide activates nNOS neurons in the ME-ARC and POA region of the hypothalamus in female rats, depending on the phases of the estrous cycle. The activation of nNOS through the senktide suggests a potential mechanism by which KNDy neurons could activate nNOS neurons in the ME-ARC and POA regions of the hypothalamus through NKB.

Keywords: GnRH, KNDy, NKB, nNOS and LH



Title: The SPRTN Protease and the Molecular Logic of DNA-Protein Crosslink Metabolism

Author: Dr. Swagata Halder, Assistant Professor, Biological Systems Engineering, Plaksha University

Abstract: DNA-protein crosslinks (DPCs) are bulky, chemically heterogeneous lesions that arise when proteins become covalently trapped on DNA. Due to their size and chemical stability, they obstruct essential DNA transactions including replication, transcription, repair and recombination.

Approximately 6,000 DPCs are estimated to arise spontaneously per mammalian genome each day, making them a continuous threat to genomic integrity. Until recently, we lacked clarity about how cells metabolise these toxic DNA lesions.

The discovery and characterisation of the metalloprotease SPRTN has subsequently fulfilled this gap. It is now established that SPRTN acts as a central player in DPCs metabolism and its importance is underscored by Ruijs-Aalfs syndrome, a progeroid disorder that predisposes patients to early-onset hepatocellular carcinoma.

DPC biology is also therapeutically relevant, since many anticancer drugs act by inducing or stabilising these lesions. In this talk, I will discuss how SPRTN resolves DPCs, what its loss reveals about genome stability and disease, and why this pathway may offer new therapeutic opportunities.



Title: From Histones to Ribosomes: Decoding Gene Expression from Chromatin to Cellular Health

Author: Dr. Rohini R. Nair, Assist. Professor, Department of Medical Oncology, Gujarat Biotechnology University

Abstract: Gene expression is a highly coordinated, multi-layered process that integrates chromatin dynamics, RNA regulation, and translational control. In this presentation, titled “From Histones to Ribosomes: A Journey of Gene Expression Control,” I will discuss our work that explores this continuum by uncovering non-canonical roles of histones, the concept of RNA multiplexing, and functional ribosome heterogeneity.

We have identified the role of histones beyond their structural role in chromatin organization, demonstrating that histone levels are dynamic and can be modulated under physiological conditions such as inflammation. Notably, histones released from activated macrophages act as extracellular signaling molecules and contribute to immune responses, highlighting their function as damage-associated molecular patterns (DAMPs).

Building on this, we have introduced the concept of RNA transperons, where subsets of functionally related mRNAs co-localize and coordinate their fate from transcription to translation. Our work identifies a novel role for Histone H4 in facilitating RNA multiplexing through chromatin interactions, thereby linking genome organization to post-transcriptional regulation and cellular processes such as mating in yeast.

Currently we are exploring ribosome heterogeneity as a regulatory layer in gene expression. Using yeast as a model, we demonstrate that ribosomal protein paralogs, particularly RPL12A and RPL12B, exhibit distinct functional roles in TORC1 signalling, lifespan regulation, and stress responses.

Furthermore, we highlight how specialized ribosomes can be harnessed to enhance recombinant protein production without compromising cellular fitness. Together, this work provides a unified perspective on gene expression control, bridging chromatin biology, RNA dynamics, and translational regulation.

Key Words: Histones, DAMPs, mRNA multiplexing, Transperon, Ribosome heterogeneity, TORC1



Title: Mapping the Regulatory Architecture of Ischemic Stroke

Author: Dr. Arti Sharma, Assistant Professor, Dept. of Computational Sciences, Central University of Punjab

Abstract: Ischemic stroke is not a zone of uniform tissue death but a spatially organized, thermodynamically governed survival program operating at both molecular and anatomical scales. Microscale transcriptomic profiling demonstrates that acute ischemia induces deliberate molecular reorganization rather than stochastic degradation. In *Rattus norvegicus*, this follows a three-phase temporal logic gate, from Dynlrb2-associated ATP arrest (acute) to a Neurod1-gated neurogenesis lock (subacute).

In *Homo sapiens*, it appears as coordinated inhibitory locking of ACVRL1 (CSI = 89.21), MADCAM1 (blood-brain barrier), and SLC2A4 (metabolism), regulated by hsa-miR-122-5p across nine functional modules. Despite evolutionary divergence in network topology, both species rely on an identical biophysical requirement: high-affinity thermodynamic clamps defined by hybridization free energy ($MFE_h < -35$ kcal/mol).

Spatially integrating single-cell transcriptomics across four Neurovascular Unit (NVU) lineages (Immune, Endothelial, Smooth Muscle Cell, Platelet) with radiomic coordinates resolves direct anatomical mappings.

The resulting Spatially-Resolved NVU Cascade Atlas showed that MADCAM1 suppression corresponds to endothelial barrier lockdown at the lesion core, and that Cxcl12-driven PI3K-Akt reactivation corresponds to the penumbral rescue window.

The MRVI Index (Imaging_Score 0.6, Molecular_Prior 0.4) unites both layers into a patient-specific fingerprint. Together, these findings define the Ischemic Emergency Protocol, a multi-scale framework for spatially targeted precision therapy.



Title: Unlocking Phytochemical Potential: Gut Microbiota and ER Stress Pathways in Colorectal Cancer Prevention

Author: Dr. Akhilendra Kumar Maurya, Assistant Professor, Department of Zoology, Institute of Science, BHU

Abstract: Chronic intestinal inflammation plays a central role in the pathogenesis of ulcerative colitis (UC) and contributes to the development and progression of colorectal cancer (CRC). CRC remains a global health priority, ranking as the second leading cause of cancer-related mortality. Its pathogenesis is driven by a multifaceted interplay between gut microbiota, host mucosal signaling, dietary intake, and inflammation. Food composition affects colonic health and cancer risk via gut microbiota fermenting complex dietary residues. Though dietary intervention has been shown to reduce disease recurrence and mortality, the elevated intake of whole grains evidences specific attention for modulation of gut microbial communities that diminish multiple hallmark of cancer.

Findings from the study show that rice bran modified gut microbiota from humans confers protection suggesting integrated dietary-FMT intervention from colon carcinogenesis in mice. Results indicated both microbiota dependent and independent mechanisms for rice bran deliberated protective efficacy against CRC, further associated with reduced neoplastic lesion size and local mucosal & systemic inflammation and maintenance of colonic epithelial integrity. Additionally, a longitudinal analysis of fecal microbiota and metabolite changes between diet treatments identified novel mechanisms for rice bran oriented anti-cancer activity.

In another study, persistent inflammation in UC was found to be associated with increased NADPH oxidase 1 (NOX1) and ROS generation, accompanied by activation of inflammation and induction of endoplasmic reticulum (ER) stress signaling. The changes were associated with epithelial injury, increased neutrophil infiltration, loss of goblet cells and disruption of colonic architecture. Further, NOX1 activation was correlated with elevated levels of ERN1, TPT1 and PCNA resulting in inhibition of apoptosis and tumor development in CRC.

Pharmacological inhibition of NOX1 restored the elevated oxidative stress, inflammatory signaling and ER stress, and neutrophil recruitment. Thus, targeting the NOX1-ERN1 axis could serve as a promising intervention for inflammation-driven colorectal cancer.



Title: Antiproliferative effect of some Ayurvedic drugs in the management of psoriasis: A clinical and experimental study

Author: Dr. O.P. Singh, Professor & Former Head, Dept. of Kayachikitsa, FoA, IMS, BHU

Abstract: There are many skin diseases in which there is proliferation of skin tissue leading to thickened and scaly lesions. Among them psoriasis is a common dermatological disease in which there is hyperproliferation of keratinocytes that rapidly multiply causing thick elevated plaques and silvery scales on skin surface. In conventional system of medicine the treatment includes topical steroids, methotrexate, and biologics that slowdown the skin cell division, reduced inflammation and targets the immune mediated effect that was responsible for uncontrolled cell growth.

In Ayurveda, psoriasis has clinical features resembling with Kitibha which is a chronic proliferative skin disease with relapse. There are many medicinal plants that are effective in reducing the proliferation of tissue and mentioned under lekhaneeya mahakashaya in Charak samhita. Daruharidra (*Berberis aristata*) and haridra (*Curcuma longa*) are some of the lekhaneeya medicinal plants that are widely used in treating skin diseases.

A clinical and experimental study was conducted to evaluate the antiproliferative effect of Daruharidra along with Khadir and Nimb mentioned in classical text used for treating skin diseases.

Clinical study has been done on 106 psoriasis patient with CTRI registration in Department of Kayachikitsa, IMS, BHU. Clinical assessment by PASI score and IGA scale was done along with biochemical and photographic analysis. In experimental study that was conducted in Department of Biochemistry, Faculty of Science, BHU, it was observed that a combination of medicinal plants is effective in controlling complex autoimmune and proliferative skin disease psoriasis.

In which some medicinal plants effect the immune mechanism, some have antiproliferative effect and other reduces symptoms like itching, redness etc. Gene expression in the blood sample of treated psoriatic patient was also done that showed reduction of gene expression of pro inflammatory cytokines.

Cell line study has been conduct on spleenocytes, macrophage and HEK 293 cancer cell to evaluate the effect on immune cells, proliferative and antiproliferative action by MTT assay.

In which it was observed that Daruharidra possesses a selective antiproliferative effect on cancer cells without damaging the macrophage cell line. So a holistic approach is followed for the management of psoriasis.

Key words: Kitibha, Daruharidra, cell line, lekahneeya, PASI.

OHC 2026 Oral Abstracts

Title: From Industrial Soil to Sustainable Bioproducts: Bacillus-Derived Functional Exopolysaccharides

Author: Saket Angural, Central University of Jammu

Co-Author: Dr. Ashok Kumar Yadav, Central University of Jammu

Abstract ID: OHC 2026 - 05

Abstract Body: The bioprospecting of thermotolerant Bacillus species from industrial waste contaminated soil revealed potent exopolysaccharide (EPS) producers capable of synthesizing high yields under thermally and chemically stressed conditions. EPS have various applications in pharmaceuticals, food and agriculture field.

In present study 14 Bacillus strains were screened for EPS production using Congo Red Assay. Out of which five isolates showed positive result, further two isolates were selected for production of EPS at different optimised condition. The selected strains Pc₁ and P_{2a3} were exposed at 80 °C during isolation, growth in varying pH ranging 5.50-7.50. Optimization of fermentation parameters like carbon source concentration, pH and incubation time via Response Surface Methodology (RSM) significantly to enhanced EPS production.

We observed a significant increase in EPS yield by Bacillus strain Pc₁ reaching 846.9 mg/mL, followed closely by Bacillus strain P_{2a3} with a yield of 666.45 mg/mL. FTIR analysis revealed complex heteropolysaccharide compositions dominated by hydroxyl, glycosidic and uronic acid functional groups. EPS obtained through Pc₁ and P_{2a3} exhibited pronounced free radical scavenging activity in DPPH. At 1.0 mg/ml, Pc₁ derived EPS scavenged 72.1% of DPPH radicals, while P_{2a3} derived EPS achieved 63.3%. ABTS assay, demonstrated strong antioxidant potential P_{2a3} EPS, with a maximum inhibition of 76.4% at 1.0 mg/ml compared to 67.2% by P_{2a3} EPS.

Hence, these biopolymers demonstrate promising applications as natural emulsifiers in the dairy industry and as antibacterial agents in pharmaceutical formulations, leveraging both their physicochemical and biofunctional attributes.

This study provides comprehensive insight into scalable EPS production from extremophilic Bacillus, establishing a robust framework for exploiting microbial biopolymers as sustainable, multifunctional ingredients in health and industry.

Title: MDSCs as a predictive Biomarker for Implantation failure in women undergoing In- Vitro Fertilization Embryo- Transfer

Author: Dave Prarthana Mahesh, PhD Scholar, Gujarat Biotechnology University

Co-Author: Dr. Rohini Nair, Gujarat Biotechnology University

Abstract ID: OHC 2026 - 07

Abstract Body: According to the World Health Organisation (WHO), Infertility affects around 185 million people, with an estimated 10-15% of couples of reproductive age experiencing difficulties in conceiving. This issue is concerning as it hinders physical, mental and socioeconomic well-being.

The introduction of in vitro fertilisation (IVF) has improved infertility treatment, but successful implantation remains the principal barrier. Emerging evidence suggests that immune dysregulation at the maternal-fetal interface plays a critical role in pregnancy failure.

Myeloid-derived suppressor cells (MDSCs) are a heterogeneous population of immature, circulating myeloid cells with potent immunosuppressive properties. MDSCs typically express CD33 and CD11b, while notably lacking or displaying low levels of HLA-DR. Human subsets are further delineated by lineage markers: M-MDSCs are defined by CD14 expression, whereas Granulocytic MDSCs (G-MDSCs) are identified by the presence of CD15 and CD66b.

We conducted a preliminary study in which a total of 40 peripheral blood samples were collected from IKDRC Hospital, Ahmedabad, from patients on the day of embryo transfer and the flow cytometric analysis was done using MDSCs marker panel.

We found the lower number of MDSCs in patients with Implantation Failure or Unsuccessful pregnancy as compared to normal pregnant females. This confers that MDSCs can be used as a predictive Biomarker for Implantation failure.

Title: Rpl12 paralog dependent TOR-signaling controls the expression of ribosome preservation factor Stm1

Author: Sourav Sharma, PhD Scholar, Gujarat Biotechnology University

Co-Author: Pratyush Kumar Datta, Gujarat Biotechnology University

Abstract ID: OHC 2026 - 11

Abstract Body: Ribosomes are recognized as dynamic regulators of gene expression, but the role of ribosomal protein paralogs in nutrient signaling remains unclear.

In *Saccharomyces cerevisiae*, duplicated ribosomal protein genes often exhibit functional specialization.

Here, we investigated the Rpl12 paralogs, RPL12a and RPL12b and found that *rpl12bΔ* results in reduced TOR signaling compared with *rpl12aΔ* and wildtype strain.

This study provides the first evidence linking Rpl12b to TORC1-mediated Rps6 phosphorylation, a direct link between ribosomal stalk composition and nutrient signaling.

Multi-omics analyses revealed paralog-specific translational and metabolic reprogramming. Notably, RPL12b deletion also reduced the abundance of ribosome preservation factor Stm1.

These findings establish ribosomal paralog specialization as a key regulator of TOR signaling, translation, and cellular longevity.

Title: Genomic Profiling of Differentially Expressed Genes in Thyroid Cancer: A Bioinformatics Approach

Author: Shreya Mangotra, PhD Scholar, Central University of Jammu

Co-Author: Dr Shelly Sehgal, Central University of Jammu

Abstract ID: OHC 2026 - 13

Abstract Body: Thyroid cancer exhibits considerable molecular heterogeneity, with distinct patterns of gene dysregulation underlying differences in tumor behavior and disease progression. Characterizing these molecular alterations can provide insights beyond conventional histopathological assessment and support the development of precision-based approaches to cancer management.

The present study aimed to investigate differentially expressed genes (DEGs) associated with thyroid cancer and explore their functional and pathway-level significance. Transcriptomic expression profiles of thyroid cancer and control samples were analyzed using a bioinformatics-based approach to identify significantly dysregulated genes.

The identified genes were categorized according to their expression patterns, followed by Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) enrichment analyses to characterize their associated biological processes and signaling pathways.

The analysis revealed distinct transcriptional patterns in thyroid cancer, with a range of genes showing significant upregulation and downregulation. Functional enrichment highlighted pathways involved in cellular regulation, metabolism, differentiation, signaling, and cancer-associated processes.

Several differentially expressed genes emerged as biologically relevant candidates with potential implications for thyroid cancer characterization. Overall, the study demonstrates how transcriptomic profiling can uncover molecular signatures associated with thyroid cancer heterogeneity and provide a basis for identifying candidate markers with translational relevance.

Integration of such molecular signatures with clinical and pathological information could contribute to improved patient stratification and facilitate the development of more individualized diagnostic and therapeutic strategies within the framework of precision medicine.

Title: High-depth whole-exome sequencing identifies variants linked to Type 1 Diabetes affected individuals

Author: Shivani, PhD, PGIMER, Chandigarh

Co-Author: Gaurav Sharma 1*, Sheenam Garg 1, Soham Mukherjee 2, Sanjay K Bhadada 2

Abstract ID: OHC 2026 - 15

Abstract: **Objective:** Background: Type 1 diabetes (T1D) is a multifactorial autoimmune disease characterized by progressive destruction of pancreatic β -cells, leading to absolute insulin deficiency. It arises as a result of complex interplay between genetic susceptibility, environmental triggers and immune dysregulation. Though various genetic loci are associated with T1D susceptibility, however the underlying mechanisms remain elusive. Therefore, we analysed genomic variation using high-depth whole-exome sequencing (WES) in relation to T1D vulnerability.

Methods: Five clinically confirmed, unrelated individuals with T1D and ten ethnically matched healthy controls with no family history of diabetes were recruited. High quality genomic DNA extracted from peripheral blood was used to prepare library, followed by exome enrichment and paired-end WES using the Illumina NovaSeq 6000 platform.

Sequencing reads were then aligned to GRCh38, followed by variant calling using GATK best practice workflow and annotated using population, clinical and functional databases. A stringent prioritization strategy was adopted to compare the T1D versus healthy individuals. Variants shared across all five T1D individuals were subsequently evaluated using population allele frequencies, in-silico structural analyses, clinical and functional databases, and pathogenicity prediction tools.

Results: Sequential filtering reduced ~1,50,000 variants per sample to a refined set of 16 high confidence variants consistently observed across all the 5 T1D individuals which were absent from all ten controls. Functional characterization identified loci with strong relevance to immune, metabolic and cellular signalling pathways. Furthermore, among these identified variants, in-silico modelling of variants in ADO and RINL indicated mild destabilizing effects on protein structure.

Conclusion: Exome filtering captured variants mapping to immune signalling, metabolic and regulatory pathways. These observations warrant evaluation in larger prospective cohorts to determine whether such shared variants act as cumulative polygenic modifiers to T1D susceptibility in this population.

Title: Extraction and characterization of probiotic *Lactobacillus* derived- tryptophan metabolites

Author: Shilpa Devi, PhD Scholar, Central University of Jammu

Co-Author: Dr. Ashok Kumar Yadav, Central University of Jammu

Abstract ID: OHC 2026 - 18

Abstract Body: Probiotic *Lactobacillus* species are increasingly recognized for their ability to produce bioactive metabolites such as tryptophan metabolites, SCFAs and bile acids etc that may contribute to host health through modulation of the gut microbiota and gut-brain axis. The present study focuses on the production, extraction, and characterization of tryptophan metabolites (indole derivatives) from selected probiotic *Lactobacillus* isolates.

MRS broth and Tryptophan broth were selected for the production of tryptophan metabolites. Selected *Lactobacillus* isolates were screened for the indole derivatives using qualitative analysis with Salkowski reagent.

All the isolates grown in MRS broth were negative for the production of tryptophan metabolites. While, six isolates (LpJ4, LpJ5, LpJ7, LpJ9, LpJ20 and LfJ21) showed positive results in tryptophan broth for indole derivative production. Six positive isolates were cultured under optimized conditions, and cell-free supernatants were collected for metabolite extraction.

Ethyl Acetate was selected for the extraction of tryptophan metabolites. Extracted metabolites exhibited variable DPPH radical-scavenging activity, with LpJ5 showing the highest activity (52.72%), followed by LpJ4 (50%), LfJ21 (47.72%), LpJ20 (44.09%), LpJ7 (40.45%) and LpJ9 (16.36%).

Based on their antioxidant potential, selected metabolite extracts were further analyzed by thin-layer chromatography and high-resolution mass spectrometry (HR-MS). HR-MS analysis of *L. plantarum* LpJ5 extract showed significant indole-derived compounds, including 5-hydroxyindole, indole-3-carboxaldehyde, indole, and indoleacrylic acid, along with other low-molecular-weight metabolites.

These findings demonstrate the ability of selected probiotic *Lactobacillus* isolates to produce diverse tryptophan-derived metabolites with antioxidant potential and provide a basis for further investigation of their biological activities and possible role in gut-brain axis-mediated neuroprotection.

Title: Biochemical characterization of selected indigenous probiotic *Lactobacillus* isolates

Author: Diksha Sharma, Research Scholar, Central University of Jammu

Co-Author: Dr. Ashok Kumar Yadav

Abstract ID: OHC 2026 - 22

Abstract: The present study aimed to isolate, characterize and evaluate the antioxidant potential of indigenous *Lactobacillus* strains obtained from human faecal samples collected from the Jammu region of Jammu and Kashmir, India. Based on Gram staining, cellular morphology and catalase reaction, 29 isolates showing Gram-positive, rod-shaped and catalase negative, these characteristics were selected as potential *Lactobacillus* strains.

The isolates were further subjected to molecular identification using genus-specific primers, which confirmed their classification within the genus *Lactobacillus*. Based on their characterization, selected indigenous *Lactobacillus* isolates were subsequently evaluated for their antioxidant potential using DPPH and ABTS radical scavenging assays.

The isolates demonstrated considerable free radical scavenging ability, with variations observed among the individual strains. LpJ5 and LpJ8 exhibited strong overall antioxidant potential.

The findings demonstrate that indigenous *Lactobacillus* strains isolated from human faecal samples possess significant antioxidant properties and highlight the potential of these strains as promising sources of antioxidant activity.

In addition, the growth pattern of selected *Lactobacillus* isolates was evaluated at different glucose concentrations using growth and biochemical parameters, including optical density, viable cell count, pH changes and glucose utilization, to assess their growth response and metabolic activity.

Keywords: Probiotics, *Lactobacillus*, antioxidant potential, gut microbiota

OHC 2026 Poster Abstracts

Title: Evaluation of IL-1 β Expression and Its Clinical Significance in Skin Cutaneous Melanoma through Bioinformatics-based analysis

Author: Ishika, Student, GNDU

Co-Author: Dr. Suresh Singh Yadav, Assist. Professor, GNDU

Abstract ID: OHC 2026 - 02

Abstract Body: Skin cutaneous melanoma (SKCM) is the fourth deadliest cancer worldwide. It is a common malignant skin cancer. Chronic inflammation plays a crucial role in many cancer developments and progression. Among the various inflammatory mediators, pro-inflammatory cytokines are major mediators, and SKCM is also closely related to pro-inflammatory cytokines among the cancers.

IL-1 β is known as a potent pro-inflammatory cytokine in tumour-associated inflammation. Therefore, investigating the expression and clinical importance of IL-1 β in SKCM may help to provide a valuable approach for therapeutic purposes.

The present study aims to evaluate the involvement of IL-1 β in SKCM, using various bioinformatics databases. UACLAN, GEPIA, cBioportal, and TIMER are some of the bioinformatics databases used in this study to evaluate gene expression, survival analysis, mutations and the relation between IL-1 β and immune cell infiltration in SKCM. Our findings indicate that IL-1 β is dysregulated in SKCM.

Furthermore, based on the observed data, we can conclude that targeting IL-1 β can be a promising therapeutic strategy for SKCM. In this study, we further hypothesized that extracellular vesicles derived from an anti-inflammatory probiotic can be used to modulate the expression of IL-1 β , thereby suppressing the chronic inflammation that increases the development and progression of SKCM.

Overall, this study provides bioinformatics-based evidence that shows the involvement of IL-1 β in SKCM and suggests a novel therapeutic hypothesis for mitigating chronic inflammation, thereby limiting development and progression of SKCM

Title: Prognostic Significance of Exportins in Colon and Rectal Adenocarcinoma: An In-Silico Analysis

Author: Punita kalia, PhD scholar, GNDU

Abstract ID: OHC 2026 - 03

Abstract Body: Background: Nucleocytoplasmic transport plays an essential role in maintaining cellular homeostasis and is frequently dysregulated during cancer progression. Exportins mediate the nuclear export of proteins and RNA molecules and may contribute to tumor development and prognosis. However, their clinical significance across colorectal cancer subtypes remains incompletely understood.

Objective: To investigate the expression, genetic alterations, prognostic significance, and potential clinical relevance of the seven major exportins in colon adenocarcinoma (COAD) and rectal adenocarcinoma (READ).

Methods: Publicly available datasets and bioinformatics resources were utilized for expression profiling, survival analysis, genetic alteration analysis, immune-cell infiltration, protein–protein interaction, and functional enrichment analyses. COAD and READ-specific findings were obtained from UALCAN, HPA, cBioPortal, Kaplan–Meier Plotter, TIMER, STRING and DAVID,

Results: All seven exportins showed differential expression in COAD and READ compared with normal tissue. Increased expression of XPO1, XPO2, XPO4 and XPOT was associated with poorer overall survival, while XPO1 and XPO2 were significantly associated with reduced relapse-free survival.

Genetic alterations, particularly amplifications involving XPO2, XPO4 and XPO5, were observed and were associated with poorer survival. Exportin expression was also correlated with immune-cell infiltration. In READ, higher XPO1 and XPO6 expression was associated with favorable prognosis.

Conclusion: Exportins demonstrate subtype-specific expression and prognostic associations in COAD and READ. These findings highlight exportins as potential prognostic biomarkers and warrant further experimental investigation of their role in colorectal cancer progression and therapeutic targeting.

Title: Beyond Probiotics: *Saccharomyces boulardii* (SB) as a Living Therapeutic Platform for Human Diseases and Cancer

Author: Garima, PhD scholar, GNDU

Abstract ID: OHC 2026 - 06

Abstract Body: The growing understanding of the relationship between the microbiome and cancer has opened new avenues for probiotic-based therapeutics. *Saccharomyces boulardii* (SB), a non-pathogenic probiotic yeast, has gained attention for its anti-inflammatory, immunomodulatory, antioxidant, and epithelial barrier-protective properties, along with emerging direct anticancer effects.

Studies using SB or its secreted products have demonstrated antiproliferative and pro-apoptotic activity in colorectal and breast cancer models, while its ability to regulate inflammation, oxidative stress, immune responses, and microbiome composition provides a rationale for investigating its therapeutic relevance in other malignancies, including gastric, liver, and inflammation-associated cancers.

SB is particularly promising in colorectal cancer (CRC) because of its natural compatibility with the gastrointestinal tract, where dysbiosis, chronic inflammation, epithelial barrier disruption, and an immunosuppressive tumor microenvironment contribute to disease progression.

SB has been reported to suppress EGFR/Akt and EGFR/ERK signaling, NF- κ B-mediated inflammation, and survivin expression, while promoting apoptosis and modulating intestinal immunity and microbiota. Beyond its intrinsic probiotic activity, SB can be genetically engineered as a live therapeutic delivery platform, enabling localized production of anticancer molecules within the gastrointestinal tract.

Future research could engineer SB for enhanced tumor localization and retention and for delivery of immune-checkpoint inhibitors, nanobodies, cytokines, enzymes, or RNA-based therapeutics. Thus, SB represents a promising bridge between probiotics, synthetic biology, and precision oncology.

Title: Integrated Bioinformatics Analysis of BAX Expression in Acne vulgaris

Author: Shreya Khullar, PG Student, GNDU

Abstract ID: OHC 2026 - 08

Abstract Body: Acne vulgaris is one of the most common chronic inflammatory skin disorders worldwide, affecting adolescents and adults and significantly impacting quality of life. Increasing evidence suggests that dysregulation of apoptosis-related genes contributes to acne pathogenesis.

Among these, the BAX (BCL2-associated X protein) plays a critical role in regulating programmed cell death and maintaining tissue homeostasis. However, the expression analysis pattern and potential role of BAX in acne remain significantly incompletely understood.

Therefore, this study was designed to investigate the expression profile and biological significance of BAX in Acne vulgaris using publicly available gene expression datasets and bioinformatics approaches. Differential expression analysis was performed using the selected Gene Expression Omnibus (GEO) dataset, followed by functional interpretation through Gene Ontology (GO) and pathway enrichment analyses. The relationship between BAX expression and inflammatory processes associated with acne was further explored.

Our findings demonstrated altered BAX expression in acne lesions compared with healthy skin controls, suggesting a potential involvement of apoptosis-related mechanisms in acne development. Functional enrichment analyses indicated that BAX-associated genes were primarily involved in apoptotic signaling pathways, cellular stress responses, and immune-inflammatory regulation.

These results highlight the potential role of BAX as a molecular contributor to acne pathogenesis and suggest that apoptosis-related pathways may represent promising targets for future therapeutic interventions. Further experimental validation is required to confirm the clinical significance of BAX in acne vulgaris.

Keywords: Acne vulgaris, BAX, apoptosis, bioinformatics, gene expression, GEO dataset, inflammatory pathways.

Title: Comprehensive analysis of CRC candidate genes in colorectal cancer using public databases

Author: Navneet Kaur, PG Student, GNDU

Abstract ID: OHC 2026 - 09

Abstract: Colorectal carcinoma (CRC) is the most commonly occurring cancer in adults and second leading cause of cancer-related deaths in America. Majority of CRC cases are associated with lifestyle factors such as physical inactivity, alcohol consumption and smoking, low fibre diet, consumption of processed meats, etc.

Certain mutations that target oncogenes, tumour suppressor genes and DNA repair pathway genes etc, are the drivers of CRC. DNA methylation is abundantly observed in cancers like CRC and is considered as a major epigenetic alteration responsible for cancer progression.

Disturbance in normal gut microbiota or dysbiosis also plays a significant role in the development and progression of colorectal cancer by causing chronic inflammation. This study has been designed to comprehensively analyse the expression and prognostic significance of potential biomarkers of Colon Adenocarcinoma (COAD) and Rectal Adenocarcinoma (READ) using the available web resources.

We have used public databases UALCAN, TNM-PLOT, HPA, MethPrimer, Kaplan Meier Plotter, and STRING Databases to investigate colorectal cancer associated genes, like, IRF4, SLC6A15, SOX21, in COAD and READ patients and data analysis has done.

Our observations showed significant altered expression of genes as well as promoter methylation in colon and rectal adenocarcinoma

This study highlights the potential use of this gene of interest as suitable prognostic biomarker and therapeutic target for colorectal adenocarcinoma progression and management.

Title: NOX1-Mediated Oxidative Stress Promotes Inflammation and Apoptosis in Ulcerative Colitis

Author: Shantanu Singh, Ph.D. Scholar, BHU

Co-Author: Dr. Akhilendra Kumar Maurya

Abstract ID: OHC 2026 - 10

Abstract Body: Ulcerative colitis (UC) is a chronic inflammatory disease characterized by persistent inflammatory responses and abnormal epithelial cell apoptosis resulting in mucosal damage and disease progression. Inflammation and apoptosis are intimately associated in colitis, but the molecular mechanisms mediating their crosstalk have not been fully elucidated.

There is growing evidence that overproduction of reactive oxygen species (ROS) can increase inflammatory signalling and cellular stress leading to apoptotic responses. NADPH oxidase 1 (NOX1) is a major source of ROS in the intestinal mucosa, and may be involved in these pathological processes. Therefore, the purpose of the present study was to examine the role of NOX1 in inflammation and apoptosis and the therapeutic potential of a selective NOX1 inhibitor, ML171, in experimental colitis induced by dextran sulphate sodium (DSS).

DSS administration resulted in severe colonic inflammation, associated with increased expression of NOX1, NOX activity, and ROS generation. These changes were associated with increased inflammatory responses and increased ER stress and activation of apoptotic signalling in colonic tissue. ML171 treatment significantly decreased NOX1-related oxidative stress, inflammation, ER stress, reduced apoptotic signalling and improved colonic tissue damage.

These data together suggest that NOX1 is involved in the inflammatory and apoptotic responses during experimental colitis, potentially through oxidative and ER stress-mediated mechanisms. Hence, inhibition of NOX1 may be a possible therapeutic strategy for control of inflammation and apoptosis in UC.

Keywords: NOX1, ERN1, UC, OXIDATIVE STRESS

Title: Comprehensive Bioinformatics Analysis of Differentially Expressed Genes and Molecular Pathways in Oral squamous cell carcinoma (OSCC)

Author: Preeti Rani, Ph.D. Scholar, Central University of Jammu

Co-Author: Dr. Shelly Sehgal, Central University of Jammu

Abstract ID: OHC 2026 - 12

Abstract Body: Oral squamous cell carcinoma (OSCC) is one of the most prevalent malignancies of the oral cavity and represents a major public health burden due to its aggressive nature, molecular heterogeneity, and poor clinical outcomes. Identification of reliable molecular biomarkers is essential for improving early detection, prognosis, and therapeutic strategies. The present study aimed to identify potential novel genes and biological pathways associated with OSCC using an integrated bioinformatics approach.

Transcriptomic datasets were retrieved from the Gene Expression Omnibus (GEO) database, and differentially expressed genes (DEGs) between OSCC and normal oral tissues were identified using appropriate statistical criteria. The identified DEGs were subjected to Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) enrichment analyses to characterize their associated biological processes and molecular pathways. Protein–protein interaction (PPI) network analysis was subsequently performed to explore functional interactions among DEGs and identify highly connected hub genes with potential biological significance in OSCC.

The integrated analysis revealed differentially expressed genes involved in cellular proliferation, apoptosis, immune regulation, cell adhesion, and cancer-associated signalling pathways. PPI network analysis further highlighted potential hub genes that may contribute to OSCC development and progression. Overall, this study highlights the potential of integrative bioinformatics approaches to identify clinically relevant molecular signatures and key regulatory pathways associated with OSCC, providing valuable insights for biomarker discovery and supporting precision medicine strategies for improved diagnosis, prognosis, and targeted therapeutic interventions.

The identified genes and pathways may serve as potential candidates for further experimental validation and development of diagnostic, prognostic, and therapeutic biomarkers.

Title: Role Of Combination Drug Therapy For Management Of Hypertension With Increasing Age

Author: Partap bir Singh, GNDU

Co-Author: Sukhraj Singh, Assistant Professor, GNDU

Abstract ID: OHC 2026 - 14

Abstract: Objective: In South Asia, hypertension is the third highest factor contributing in public health burden of disease and major risk factor for coronary artery disease especially in women and old age people. The study was aimed to determine the role of gender and age (20–80 years) on severity of hypertension to design an effective schedule for management of hypertension.

Methods: The levels of serum cholesterol, triglycerides (TG), high-density lipoprotein (HDL), low-density lipoproteins (LDL), and blood pressure (BP) of 240 hypertensive patients were monitored. Cholesterol, TG, and HDL levels were detected using ERBA Reagent kit of Transasia Bio-medicals LTD by CHOD-PAP, glycerol phosphate oxidase trinder End point, and polyvinyl sulfonic and polyethyleneglycol-methyl ether based methods, respectively.

Results: The BP and levels of serum cholesterol, TG and LDL were increased in both the genders after 40 years of age. However, the rise in levels of these parameters was more in females in comparison to males.

A hypertension management schedule involving (BP)/Cholesterol lowering drugs and lifestyle changes for period of 60 days showed that combination drug therapy was more effective than monotherapies of same drugs used at higher dosages.

Conclusion: Hypertensive patients strictly followed the prescribed healthy food and exercise schedule showed improvement in their BP and lipid profile even with limited drug intervention.

Keywords: Hypertension, Low-density lipoprotein, Triglycerides, Cholesterol and blood pressure.

Title: High-depth whole-exome sequencing identifies variants linked to Type 1 Diabetes affected individuals

Author: Shivani, PhD, PGIMER, Chandigarh

Co-Author: Gaurav Sharma 1*, Sheenam Garg 1, Soham Mukherjee 2, Sanjay K Bhadada 2

Abstract ID: OHC 2026 - 15

Abstract: **Objective:** Background: Type 1 diabetes (T1D) is a multifactorial autoimmune disease characterized by progressive destruction of pancreatic β -cells, leading to absolute insulin deficiency. It arises as a result of complex interplay between genetic susceptibility, environmental triggers and immune dysregulation. Though various genetic loci are associated with T1D susceptibility, however the underlying mechanisms remain elusive. Therefore, we analysed genomic variation using high-depth whole-exome sequencing (WES) in relation to T1D vulnerability.

Methods: Five clinically confirmed, unrelated individuals with T1D and ten ethnically matched healthy controls with no family history of diabetes were recruited. High quality genomic DNA extracted from peripheral blood was used to prepare library, followed by exome enrichment and paired-end WES using the Illumina NovaSeq 6000 platform.

Sequencing reads were then aligned to GRCh38, followed by variant calling using GATK best practice workflow and annotated using population, clinical and functional databases. A stringent prioritization strategy was adopted to compare the T1D versus healthy individuals. Variants shared across all five T1D individuals were subsequently evaluated using population allele frequencies, in-silico structural analyses, clinical and functional databases, and pathogenicity prediction tools.

Results: Sequential filtering reduced ~1,50,000 variants per sample to a refined set of 16 high confidence variants consistently observed across all the 5 T1D individuals which were absent from all ten controls. Functional characterization identified loci with strong relevance to immune, metabolic and cellular signalling pathways. Furthermore, among these identified variants, in-silico modelling of variants in ADO and RINL indicated mild destabilizing effects on protein structure.

Conclusion: Exome filtering captured variants mapping to immune signalling, metabolic and regulatory pathways. These observations warrant evaluation in larger prospective cohorts to determine whether such shared variants act as cumulative polygenic modifiers to T1D susceptibility in this population.

Title: Antimicrobial Susceptibility pattern of Milk Samples of Dairy Cattles from Jammu Region

Author: Ragni Sharma, Ph. D Scholar, Central University of Jammu, Dr. Ashok Kumar Yadav

Co-Author: Sunaina Devi

Abstract ID: OHC 2026 - 16

Abstract: Antimicrobial resistance (AMR) has emerged as an escalating global health challenge, threatening the effective treatment of infectious diseases and increasing the risk of persistence and transmission of resistant microorganism. Milk, being a widely consumed and nutritionally important food, can serve as a potential vehicle for the transmission of antimicrobial-resistant microorganisms when produced or handled under inadequate hygienic conditions. Raw milk may harbour diverse microorganisms originating from the animal, udder, environment, water, milking equipment, and handling practices.

Commonly reported bacteria associated with raw milk include , *Staphylococcus*, *Streptococcus*, *Escherichia*, *Enterococcus*, *Bacillus*, and *Listeria spp.*, some of which possess important food-safety and public-health significance. The present study aimed to evaluate the antimicrobial susceptibility patterns of microorganisms isolated from raw milk collected from different locations of the Jammu region. The present study was conducted to evaluate the antimicrobial susceptibility pattern of microorganisms present in raw milk samples collected from different locations of the Jammu region. A total of 50 raw milk samples, comprising cow, buffalo, and goat milk, were randomly collected from different locations across Jammu, Samba and Kathua districts of the region, Jammu and Kashmir.

Collected samples were analysed using the Kirby–Bauer disc diffusion method against eight antibiotics namely Azithromycin, Cefepime, Cefixime, Cefuroxime, Cefotaxime, Colistin, Levofloxacin, and Meropenem. The results revealed varying levels of susceptibility and resistance among the tested samples. The highest susceptibility was observed against Levofloxacin (100%), followed by Colistin (96%), and Meropenem (92%), whereas higher resistance was detected against Cefixime (68%) and Cefotaxime (54%). The study indicates the presence of antimicrobial-resistant microorganisms in raw milk and highlights the potential.

Key words: Antimicrobial Resistance, Jammu, Azithromycin, Cefepime, Cefixime, Cefuroxime, Cefotaxime, Colistin, Levofloxacin, Meropenem, Kirby Bauer Disc Diffusion Method.

Title: Isolation and Biophysiochemical Characterization of Exopolysaccharides Derived from Bacillus Species

Author: Komal Bhatia, Research scholar, Central University of Jammu

Co-Author: Dr. Ashok Kumar Yadav

Abstract ID: OHC 2026 - 17

Abstract: Probiotic bacteria, particularly members of the genus *Bacillus*, have gained considerable attention owing to their capacity to produce exopolysaccharides (EPS) with diverse biotherapeutic potential. *Bacillus*-derived EPS are known to exhibit a wide range of bioactivities, including antioxidant, antimicrobial, immunomodulatory, and anti-biofilm properties, making them promising candidates for applications in the pharmaceutical, food, and biomedical industries.

Given their generally regarded as safe (GRAS) status and ability to thrive under diverse environmental conditions, probiotic *Bacillus* strains represent an attractive and sustainable source of functional biopolymers. In the present study, ten indigenous *Bacillus* strains were screened for their EPS-producing potential. Among these, five strains demonstrating comparatively higher EPS production yield were selected for further investigation.

The EPS extracted from these high-yielding strains were subjected to isolation, purification, and biophysiochemical characterization, including analysis of their structural and functional properties. Preliminary characterization confirmed the polysaccharide nature of the extracted biomolecules and provided insight into their composition and physiochemical behavior.

Subsequent evaluation of the bioactive potential of the isolated EPS revealed notable antioxidant activity, suggesting their ability to scavenge free radicals and mitigate oxidative stress. Building on these promising results, the EPS were further assessed for antimicrobial activity against selected pathogenic strains, in order to explore their potential as natural antimicrobial agents.

The findings of this study highlight the biotherapeutic promise of *Bacillus*-derived EPS, particularly their antioxidant and antimicrobial properties, and underscore their potential application as bioactive compounds in nutraceutical, pharmaceutical, and food-preservation contexts.

Further studies are warranted to elucidate the structure-function relationships and mechanisms underlying these bioactivities, paving the way for the development of novel EPS-based therapeutic and industrial products.

Title: Activity Of Licorice Extract and it's Key Component Glycyrrhizin Against Prevalent Microbial Pathogens

Author: Manseerat kaur, Khalsa University, Amritsar

Co-Author: Dr. Partapbir Singh

Abstract ID: OHC 2026 - 20

Abstract: BACKGROUND:

The escalating antimicrobial resistance (AMR) is a serious health concern worldwide against *Candida albicans*, *Rhodococcus*, *Geotrichum*, *Mucor*, and *Micrococcus*, which are causative agents of Rhinocerebral mucormycosis, Disseminated candidemia, *Candida* endocarditis, Cavitory necrotizing pneumonia, and many more serious health issues.

This necessitates the urgent exploration of antimicrobial resources preferably natural alternatives to synthetic drugs. *Glycyrrhiza glabra* (licorice), a traditional Indian medicinal plant, presents a promising solution due to its established biological activities.

MATERIAL AND METHODS:

This study evaluated the antimicrobial potential of crude ethanolic licorice extract and its primary active component, pure glycyrrhizin, against pathogens *Candida albicans*(MTCC 138), *Rhodococcus*(MTCC 2558), *Geotrichum* (MTCC 3998), *Mucor*(MTCC 2713), and *Micrococcus*(MTCC 106). Extract characterization through Chromatography (HPLC) revealed a prominent glycyrrhizin presence at Retention time of 10.2 0.3 minutes using Isocratic Method (Column type: Reversed-Phase C18 Octadecylsilane / ODS and mobile phase: 38% Acetonitrile / 62% Acidified Water). Using the Kirby-Bauer Disc Diffusion method, the antimicrobial efficacy of the crude extract and pure glycyrrhizin was evaluated against standard synthetic controls, including Amphotericin B and Clotrimazole.

RESULTS AND CONCLUSION:

Both the crude licorice extract and pure glycyrrhizin demonstrated selective inhibitory activity specifically against *Candida albicans*, *Rhodococcus*, *Geotrichum*, *Mucor*, and *Micrococcus*. The crude extract yielded mean inhibition zones of 1.2 cm at 400 mcg and 1.9 cm at 600 mcg disc concentrations, whereas pure glycyrrhizin produced zones(mean) of 1.2 cm at 400 mcg and 1.4 cm at 600 mcg.

The superior efficacy of the crude extract at higher doses suggests synergistic interactions among the plant's phytochemicals. Ultimately, these findings highlight licorice as a viable plant-based agent for controlling allergenic fungal growth and mitigating indoor bio-aerosol contamination.

Title: The Burden of Heavy Menstrual Bleeding in Gujarat: Prevalence and Impact on Daily Life Across Educational and Workplace Domains.

Author: Karan Arya, Ph.D. Research Scholar, Gujarat Biotechnology University

Co-Author: Dr. Rohini R. Nair

Abstract ID: OHC 2026 - 21

Abstract: Heavy menstrual bleeding (HMB) is one of the most neglected global health challenges with potentially far-reaching consequences. In clinical terms, heavy menstrual bleeding is defined as “excessive menstrual blood loss which interferes with a woman’s physical, emotional, social or quality of life”.

HMB can lead to iron-deficiency anaemia, and can cause a range of adverse functional outcomes, including reduced productivity and earning capacity, difficulty in performing daily activities, and limitations on social life and relationships.

Despite global prevalence and clinical burden, this study addresses a critical gap by understanding the prevalence and impact of heavy menstrual bleeding on daily life in women of Gujarat, across educational institutions and workplaces. An online/interview-based questionnaire was designed and used to collect information across various societal domains.

Informed consent was taken from all the participants and the study is approved by IHEC committee. The questionnaire was designed into different sections to collect information regarding demographics, menstrual history, clinical history, associated symptoms, SAMANTA tool and impact on life.

The findings will provide evidence on the burden of HMB and its impact across educational and workplace backgrounds, helping identify gaps in awareness and healthcare access. The insights from this study will play a fundamental role in improving and developing targeted public health strategies for early identification, appropriate care and improved menstrual health and quality of life.

Keywords: Heavy menstrual bleeding; Community health; Quality of life; Epidemiology.

Title: Biochemical characterization of selected indigenous probiotic *Lactobacillus* isolates

Author: Diksha Sharma, Research Scholar, Central University of Jammu

Co-Author: Dr. Ashok Kumar Yadav

Abstract ID: OHC 2026 - 22

Abstract: The present study aimed to isolate, characterize and evaluate the antioxidant potential of indigenous *Lactobacillus* strains obtained from human faecal samples collected from the Jammu region of Jammu and Kashmir, India. Based on Gram staining, cellular morphology and catalase reaction, 29 isolates showing Gram-positive, rod-shaped and catalase negative, these characteristics were selected as potential *Lactobacillus* strains.

The isolates were further subjected to molecular identification using genus-specific primers, which confirmed their classification within the genus *Lactobacillus*. Based on their characterization, selected indigenous *Lactobacillus* isolates were subsequently evaluated for their antioxidant potential using DPPH and ABTS radical scavenging assays.

The isolates demonstrated considerable free radical scavenging ability, with variations observed among the individual strains. LpJ5 and LpJ8 exhibited strong overall antioxidant potential.

The findings demonstrate that indigenous *Lactobacillus* strains isolated from human faecal samples possess significant antioxidant properties and highlight the potential of these strains as promising sources of antioxidant activity.

In addition, the growth pattern of selected *Lactobacillus* isolates was evaluated at different glucose concentrations using growth and biochemical parameters, including optical density, viable cell count, pH changes and glucose utilization, to assess their growth response and metabolic activity.

Keywords: Probiotics, *Lactobacillus*, antioxidant potential, gut microbiota

Title: Tobacco Associated Alterations in the Oral-Gut Microbiome and Metabolome linked to proinflammatory response

Author: Khyati Shukla, PhD Scholar, ICMR-NICPR

Co-Author: Kratika Shrivastava, Mushaid Malik, Rishika Singh, Akanksha Vishwakarma, Diksha Saini, Satyendra Kumar Shukla, Pragya Sharma, Anuj Kumar, Deepa Bisht, Pramod Kumar

Abstract ID: OHC 2026 - 23

Abstract: Background: Tobacco use, whether smoked or smokeless, can alter the microbial and metabolic environment of the body, but differences associated with different forms of tobacco exposure remain poorly understood.

This study compared culturable oral and fecal bacteria, microbial taxa, and metabolic profiles among smokers (ST), smokeless tobacco users (SLT), and non-users (TC), focusing on antimicrobial resistance, tobacco-associated metabolic alterations, and potential inflammation-related changes.

Methods: Bacterial isolates from oral and fecal samples were cultured and phenotypically characterized using biochemical tests and antibiotic susceptibility testing. Representative isolates were identified using appropriate identification methods. Metagenomic sequencing data were processed using QIIME, followed by alpha- and beta-diversity and differential abundance analyses across the study groups.

Untargeted metabolomic profiling was performed across the three groups using multivariate analysis, one-way ANOVA, and other statistical tests to identify discriminatory metabolic features. Correlation analyses between microbial and metabolic profiles were performed using statistical tools in R and Python.

Results: Tobacco-exposed groups showed distinct antimicrobial resistance patterns. Compared with non-users, smokers showed higher resistance to erythromycin and amoxicillin-clavulanate, while smokeless tobacco users showed higher resistance to tetracycline and linezolid, indicating form-specific resistance patterns. Phenotypic analysis also demonstrated differences in bacterial characteristics across the study groups, particularly in salt tolerance, motility, and citrate utilization. Metagenomic profiling identified differentially abundant genera, including

Abiotrophia and Aggregatibacter in oral samples and Veillonella and Fusicatenaibacter in fecal samples. Metabolomic profiling showed clear separation according to tobacco-use status, with the greatest divergence observed between smokers and smokeless tobacco users. A total of 52, 73, and 85 significantly altered metabolic features were identified for ST vs TC, SLT vs TC, and ST vs SLT, respectively.

Inflammation-associated metabolites, including calpeptin, capsidiol, N-methylpyridinium, acalyphin, and L-phenylalanine, were identified among the tobacco-use groups, further supporting distinct metabolic profiles associated with inflammation associated metabolites enriched in tobacco users.

Conclusion: Tobacco use was associated with microbial and metabolic alterations that may contribute to changes in the inflammatory and metabolic environment.

These findings highlight the value of integrating culturomic, metagenomic, and metabolomic approaches to better understand tobacco-associated microbial disruption, metabolic alterations, and their potential implications for inflammation, antimicrobial resistance, and disease.

Title: MGMT Promoter Methylation in Breast Cancer: An Epigenetic Biomarker of Tumor Progression and Therapeutic response

Author: Mansi Sharma, Msc. Student, Chandigarh University

Co-Author: Dr. Umesh Kumar

Abstract ID: OHC 2026 - 24

Abstract: Background: O6-methylguanine-DNA methyltransferase (MGMT) is a critical DNA repair enzyme that protects genomic integrity by removing alkyl groups from the O6 position of guanine. Epigenetic silencing of the MGMT gene through promoter CpG island methylation can impair DNA repair capacity and potentially contribute to genomic instability, tumor progression, and altered therapeutic responses.

Although MGMT promoter methylation has been extensively investigated in glioblastoma and other malignancies, its biological and clinical significance in breast cancer remains comparatively less well defined.

Emerging evidence suggests that aberrant MGMT methylation may occur in breast tumors and could be associated with clinicopathological characteristics, molecular subtypes, disease progression, and response to DNA-damaging therapies. Importantly, MGMT methylation may interact with broader epigenetic alterations involving DNA methyltransferases, histone modifications, and other tumor-suppressor genes, thereby contributing to the epigenetic landscape of breast carcinogenesis.

Assessment of MGMT methylation using techniques such as methylation-specific PCR, quantitative methylation-specific PCR, pyrosequencing, or bisulfite sequencing could provide valuable information regarding its potential as a minimally invasive and clinically relevant biomarker. Integrating MGMT methylation status with molecular subtype, hormone-receptor status, treatment response, and patient outcome may help clarify its prognostic and predictive significance.

Future studies involving larger, well-characterized breast cancer cohorts and longitudinal sampling are warranted to establish the clinical utility of MGMT methylation and determine whether epigenetic modulation of MGMT can be exploited therapeutically.

Collectively, MGMT promoter methylation represents a promising area for understanding epigenetic dysregulation in breast cancer and for developing biomarker-driven approaches to precision oncology.

Title: Artificial Light at night alters the antioxidant system, retards growth and development and caused cognitive impairment in silk worm, *Bombyx mori*

Author: Harjot Kaur, Research Scholar, Central University of Jammu

Co-Author: Dr. Dhanananajay Kumar

Abstract ID: OHC 2026 - 25

Abstract: Sericulture, is an important part of rural economies and sustainable textile manufacturing primarily focused on the domesticated silkworm, *Bomby mori*. Recent upsurge in electrification of our villages has witnessed sudden surge in the use of artificial at night (ALAN). Light is the most potent zeitgeber in resetting the circadian clock in most of the living organisms.

Hence, we aimed to evaluate the effects different lighting conditions on the *B. mori*'s growth, physiological development, cocoon features, survival rates and learning and memory. Silk worm larvae were exposed to four different lighting conditions 1.e. 12-h light: 12-h dark (12L:12D; LD), 18 h light: 6 h dark (18L:6 D), constant light (24-h light; LL) and constant darkness (24-h darkness; DD).

Different parameters such as larval weight, cocoon weight, shell weight, shell ratio, oxidative stress, survival rates and learning and memory were quantified. Our results demonstrate that prolonged and chronic exposure to constant lighting conditions altered the circadian clock in silkworm and resulted in significant dysregulation ($p < 0.05$) of antioxidant system (SOD, CAT, GSH and MDA) in *B. mori*, causing significant reduction in the larval, cocoon and shell weight ($p < 0.05$).

Also, prolonged or LL caused significant decline in the learning and memory and caused significant reduction in the survival percentage in *B. mori*.

Together, our data highlights the importance of lighting schedule on the growth, development and cognitive performance in organism, and recommends further investigation using molecular studies to better understand the mechanisms underlying *B. mori*'s photoperiodic sensitivity in maximising silk production

Title: Quercetin Ameliorates Jet-lag/Shift-work induced Oxidative Stress in Rats

Author: Mandeep Kour, Research Scholar, Central University of Jammu

Co-Author: Dr. Dhanananajay Kumar

Abstract ID: OHC 2026 - 26

Abstract: Circadian clock is ubiquitous in nature, and is synchronised by Earth's 24-h light-dark cycle (LD). It regulates various behavioural, physiological, biochemical and metabolic functions. Disruptions of the circadian clock may harm health and well-being of organism.

In today's modern world rapid industrialization and increasing economic demands has forced 24 x7 hour work culture. Such jet-lag/shift-work conditions as a result of trans meridian flight and work schedule in traveller and shift workers has dysregulated physiological, endocrine and reproductive and metabolic system and has resulted into several life style disorders. Quercetin, one of the most abundant flavonoids, has strong antioxidant properties due to its phenolic content.

However, its role in regulating the circadian clock is scarce. We studied the effect of quercetin due to jet-lag/shift-work induced oxidative stress in liver, pancreas and testes of male rats. Rats were subjected to three 8-h chronic advanced jet-lag/shift-work conditions after every 10 days post entrainment to normal LD cycle for two weeks. Twenty-four albino rats were divided into four groups: control rats (n= 6), jet-lag rats (n= 6), quercetin treated (100 mg/kg body weight) jet lag rats (n= 6) and melatonin treated (25 mg/kg body weight).

At the end of the experiment liver, pancreas and testicular tissues and blood were collected and analysed for oxidative stress and antioxidant parameters including SOD, CAT, GSH and MDA and blood glucose, respectively. Quercetin statistically reduced the free radicals produced during jet-lag conditions similar to standard chronobiotic molecule, melatonin and restore blood glucose levels compared to control treated rats.

In summary, quercetin reduces oxidative stress and elevated blood glucose as a result of dysregulated circadian clock. Timed treatment with quercetin is required to explore the molecular mechanism in validating it as a chronobiotic molecule to treat disrupted biological clock.

Title: Cricket as model for circadian rhythm research

Author: Sapana Rani, Research Scholar, Central University of Jammu

Co-Author: Narinder Kumar and Dr. Dhananjay Kumar

Abstract ID: OHC 2026 - 27

Abstract: Circadian clocks are present in nearly all living organisms and consist of self-sustaining oscillators. These oscillators regulate numerous complex physiological processes, ranging from molecular interactions and expression to phenotypic and behavioural responses. Untimed exposure to artificial light at night (ALAN) can affect various biological rhythms in both humans and animals and has emerged as a major environmental concern.

Rapid modernisation and urbanisation of our natural surroundings have disrupted the ecological balance of the animal's natural habitat. Such alterations in lighting conditions have negatively impacted animals' activity patterns, reproduction, and survival. Crickets are used as a model to study the mechanism behind circadian rhythms and photoperiodic responses. *Gryllus bimaculatus* is a primary cricket species that is preferred for its short lifespan, ease of breeding under laboratory conditions, and strong activity patterns.

They have a sensitive nervous system. Hence, they can be used to study the impact of ALAN as a disruptor of circadian organisation in crickets at the molecular level, leading to desynchronization between gene expression cycles and behavioural rhythms such as locomotion, stridulation and learning and memory.

The effects of various pharmacological drugs on resetting the dysregulated circadian clock due to ALAN on melatonin, inflammation, and neurodegeneration, as in humans, can be studied. Our laboratory data, together with other published research on insect and vertebrate models, indicate that circadian disruption negatively affects cognitive processes, including learning efficiency and memory retention.

However, direct experimental studies examining the effects of ALAN on learning and memory in crickets remain limited. Further research is needed to explore the impact of untimed light on the ecological biodiversity. There has been a sudden surge in insect chronobiology research worldwide due to ethical issues involving animals, their short lifespans, lower water consumption, and reduced emissions of harmful gases.

Therefore, crickets may serve as a suitable model in circadian biology to study various ecological, molecular, physiological, and neurological processes that affect numerous circadian rhythms.

Title: Polyphasic Characterization of Bacterial isolate from Garden Soil, Amritsar, Punjab

Author: Reema, PhD Scholar, Guru Nanak Dev University

Abstract ID: OHC 2026 - 28

Abstract: Bacteria are among the oldest forms of life on earth that inhabit nearly every environment, including ocean beds, hot springs, soil, plant surfaces and animal gut.

Their small size, rapid growth and multiplication, minimal survival requirements and diverse biochemical capabilities make them highly valuable in biotechnology, medicine, agriculture and industry.

Among the bacteria studied for industrial applications, the genus *Bacillus* stands out for its ability to produce a wide variety of enzymes, antibiotics and other useful compounds. Its members also form protective endospores that resist heat, desiccation, and other stresses, allowing survival under harsh conditions.

The present study aims to identify a bacteria previously isolated in our laboratory from garden soil, characterize it and screen it for production of useful secreted extracellular enzymes and metabolites.

These may be further exploited at the industrial level. Our results show that the isolate belongs to the genus *Bacillus* as confirmed by various laboratory tests including gram staining, catalase activity, MR-VP test and sporulation test.

Biochemical analysis of its culture supernatant revealed that the isolate secretes lipase (para-nitrophenyl palmitate assay), amylase (starch agar plate) and riboflavin. Experiments for bacterial identification, characterization of secreted enzymes and understanding their potential for industrial usage are underway.

Title: Guarding the Fork: ATR-CHK1-Dependent Regulation of MRE11 Nuclease

Author: Bharvi, Plaksha University

Abstract ID: OHC 2026 - 29

Abstract: Abstract:

Replication stress (RS), characterised by perturbed replication fork progression, aberrant fork stalling and compensatory new origin firing, remains a major source of genome instability and constitutes one of the hallmarks of cancer.

Prolonged RS is also associated with pathological degradation of stalled forks by various nucleases, further promoting genomic instability, cancer aggressiveness and therapy resistance.

RS inherently activates the ATR-CHK1 pathway, which stabilises stalled forks, protects them from nucleolytic degradation and, in the meantime, restrains cell cycle progression, giving cells time to remove lesions and restart forks.

Chronic RS coupled with sustained ATR-CHK1 activity is often addictive in nature and is frequently associated with cancer survival and therapy resistance.

While the interplay between ATR-CHK1 signalling and cell cycle checkpoints is well established, the precise mechanisms underlying fork stabilisation remain poorly understood.

Our preliminary analyses, originating from multiple and diverse cancer cell lines, suggest that the ATR-CHK1 pathway protects stalled forks by regulating MRE11 nuclease activity.

We are presently characterising this pathway through multiple approaches and anticipate revealing specific vulnerabilities that can be addressed clinically.

Title: Exploring the Therapeutic Potential of Next-Generation Probiotics in Type 2 Diabetes

Author: Simrandeep kaur Sandhu, Phd research scholar, Lovely Professional University, Phagwara

Abstract ID: OHC 2026 - 30

Abstract: Type 2 diabetes mellitus (T2D) is a growing metabolic disorder associated with insulin resistance, chronic inflammation, and gut microbiota dysbiosis. Increasing evidence indicates that specific microbial alterations contribute to impaired glucose metabolism, intestinal barrier dysfunction, and metabolic inflammation, highlighting the gut microbiome as a potential therapeutic target.

Next-generation probiotics (NGPs), including *Akkermansia muciniphila*, *Faecalibacterium prausnitzii*, *Roseburia* spp., *Anaerobutyricum hallii*, and *Christensenella minuta*, have emerged as promising candidates for metabolic disease management.

Among these bacteria, *A. muciniphila* has demonstrated encouraging preclinical and early clinical evidence for improving metabolic parameters, while butyrate-producing bacteria such as *F. prausnitzii* and *Roseburia* spp. may contribute to metabolic regulation through anti-inflammatory and barrier-protective effects.

Advances in metagenomics, metabolomics, and integrated multi-omics approaches are facilitating the identification and characterization of disease-associated microbial targets.

However, challenges including strain-specific effects, poor culturability, colonization efficiency, formulation stability, individual microbiome variability, and limited long-term clinical evidence remain. This study examines the therapeutic potential of NGPs in T2D, focusing on their effects on glucose homeostasis, insulin sensitivity, intestinal barrier integrity, inflammation, and microbial metabolite production.

Current evidence suggests that NGPs can influence metabolic health through short-chain fatty acid production, modulation of bile acid signaling, reduction of endotoxin-mediated inflammation, and strengthening of the gut epithelial barrier.

Overall, NGPs represent a promising microbiome-based approach for T2D management. Integrating multi-omics, precision nutrition, and targeted microbial therapies may enable the development of personalized NGP-based interventions and strengthen their translation from experimental research to clinical application.

OHC 2026 Poster Sessions

FINAL ID	TITLE	PRESENTER NAME	COUNTRY
OHC 2026 - 02	Evaluation of IL-1 β Expression and Its Clinical Significance in Skin Cutaneous Melanoma through Bioinformatics-based analysis	Ishika	India
OHC 2026 - 03	Prognostic Significance of Exportins in Colon and Rectal Adenocarcinoma: An In-Silico Analysis	Punita kalia	India
OHC 2026 - 06	Beyond Probiotics: Saccharomyces boulardii (SB) as a Living Therapeutic Platform for Human Diseases and Cancer	Garima	India
OHC 2026 - 08	Integrated Bioinformatics Analysis of BAX Expression in Acne vulgaris	Shreya Khullar	India
OHC 2026 - 09	Comprehensive analysis of CRC candidate genes in colorectal cancer using public databases	Navneet Kaur	India
OHC 2026 - 10	NOX1-Mediated Oxidative Stress Promotes Inflammation and Apoptosis in Ulcerative Colitis	Shantanu Singh	India
OHC 2026 - 12	Comprehensive Bioinformatics Analysis of Differentially Expressed Genes and Molecular Pathways in Oral squamous cell carcinoma (OSCC)	Preeti Rani	India
OHC 2026 - 14	Role Of Combination Drug Therapy for Management Of Hypertension With Increasing Age	Sukhraj Singh	India
OHC 2026 - 15	High-depth whole-exome sequencing identifies variants linked to Type 1 Diabetes affected individuals.	Shivani	India
OHC 2026 - 16	Antimicrobial Susceptibility pattern of Milk Samples of Dairy Cattles from Jammu Region	Ragni Sharma	India
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OHC 2026 - 17	Isolation and Biophysiochemical Characterization of Exopolysaccharides Derived from <i>Bacillus</i> Species	Komal Bhatia	India
OHC 2026 - 20	Activity Of Licorice Extract and it's Key Component Glycyrrhizin Against Prevalent Microbial Pathogens	Manseerat Kaur	India
OHC 2026 - 21	The Burden of Heavy Menstrual Bleeding in Gujarat: Prevalence and Impact on Daily Life Across Educational and Workplace Domains.	Karan Arya	India
OHC 2026 - 22	Biochemical characterization of selected indigenous probiotic <i>Lactobacillus</i> isolates	Diksha Sharma	India
OHC 2026 - 23	Tobacco Associated Alterations in the Oral-Gut Microbiome and Metabolome linked to proinflammatory response	Khyati Shukla	India
OHC 2026 - 24	MGMT Promoter Methylation in Breast Cancer: An Epigenetic Biomarker of Tumor Progression and Therapeutic response	Mansi Sharma	India
OHC 2026 - 25	Artificial Light at night alters the antioxidant system, retards growth and development and caused cognitive impairment in silk worm, <i>Bombyx mori</i>	Harjot Kaur	India
OHC 2026 - 26	Quercetin Ameliorates Jet-lag/Shift-work induced Oxidative Stress in Rats	Mandeep Kour	India
OHC 2026 - 27	Cricket as model for circadian rhythm research	Sapana Rani	India
OHC 2026 - 28	Polyphasic Characterization of Bacterial isolate from Garden Soil, Amritsar, Punjab	Reema	India
OHC 2026 - 29	Guarding the Fork: ATR-CHK1-Dependent Regulation of MRE11 Nuclease	Bharvi	India
OHC 2026 - 30	Exploring the Therapeutic Potential of Next-Generation Probiotics in Type 2 Diabetes	Simrandeep kaur	India



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Thank you all delegates, committee members
and volunteers for making this event a huge success!

We hope you gained valuable insights from the sessions
and enjoyed connecting with other professionals.

– OHIO, New Delhi & GNDU, Amritsar

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