The Gut Microbiota and Probiotic Science Foundation (India)

11th INDIA PROBIOTIC SYMPOSIUM

"Role of Gut Microbiota and Probiotics in Reducing Viral Infections – Mechanisms to Combat Them"

13th & 14th March 2021

Le Meridien, New Delhi

Abstract Book

Welcome Note by Prof. N. K. Ganguly

Dear Colleagues,

Warm greetings from the Gut Microbiota and Probiotic Science Foundation (India).

It gives me immense pleasure to welcome our distinguished participants to the series 11 India Probiotic Symposium that is being held in a hybrid mode on 13th March and 14th March 2021.

The symposium with the theme, " Role of Gut Microbiota and Probiotics in reducing viral infections – mechanisms to combat them" is being organized by the Foundation in association with SRM University, Sonepat, Haryana.

The year gone by came with a lot of learnings but what we learned most was that health cannot be neglected and it is important to focus on interventions that build immunity and keeps us strong to fight infections. Along with nutritional support, one obvious way by which you can build immunity is by controlling the health of the trillions of microbes living in your intestine, collectively known as intestinal microflora. From a clinical view, studies around the world have shown that improving the balance of the microbiota may help in preventing respiratory infections and viral influenza. A Cochrane review of 12 studies that evaluated the benefit of probiotics in preventing upper respiratory tract infections (URTI's) in all age groups including children, adults and the elderly showed a reduction in incidence of URTI's by 30%. A more recent systematic review published in Frontiers in Pharmacology showed that probiotic use was associated with reduced number and duration of influenza like illness. According to her, general probiotic use in the U.S. could save the health care payer and the economy around $1.4 billion in medical bills and lost productivity due to acute respiratory tract infections.

The presentations by International and National experts will delve and provide deeper insights on the benefit accrued by the beneficial components of the gut microbiota and probiotics in reducing viral infections and the unique mechanisms that they employ to impart that benefit.

The symposium will also witness presentations by three young scientists under the age of 40 years who after a rigorous selection were selected for the Young Investigator Awards. They will present their work during the symposium.

I also request you to visit the mobile friendly Foundation website (www.gutfoundation.org.in) which is a valuable source of information for students, scientists and researchers in the area. The presentation of the previous symposia are also archived on the website of the Foundation.

On behalf of the Scientific Advisory Committee of the Foundation, we welcome you to the symposium and hope you will find the two days both exciting and enriching.

Nirmal Kumar Ganguly

Prof. N. K. Ganguly
President
Gut Microbiota and Probiotic Science Foundation (India)

About the Gut Microbiota & Probiotic Science Foundation (India)

The Gut Microbiota and Probiotic Science Foundation (India) was registered as a society on 9th November 2011 by expert scientists under the Presidentship of Professor Nirmal Kumar Ganguly under the Societies Registration Act XX1 of 1860.The objective of the Foundation is to provide a thrust to the science of Gut Microbiota and Probiotics in the country. The Foundation aims to channelize International knowledge and expertise in the field and promote collaborative research for the development of probiotics. It will also foster and maintain research links with scientists of similar interest.

To meets its objective the Foundation will:

- Organize an Annual International symposium for providing a common scientific platform for basic scientists, clinicians, regulators and students to share and exchange knowledge and views and delve into newer areas of research.
- Webcast the symposium for wider viewership.
- Publish the proceedings of the symposium in the form of a book for distribution to libraries and healthcare professionals across the country.
- Publish an Annual newsletter that will capture the latest scientific developments in the area.
- Promote research in the area and felicitate young talent by giving Young Investigator Awards.

Governing Body Members

- **Prof. N. K. Ganguly**
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- **Prof. Ajay Bhalla**

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- **Dr. J. Fujimoto**

PROGRAM

DAY 1 13-03-2021

16:00-17:30 **Inaugural Session**

16:00-16:10 **Inauguration and Saraswati Vandana**

16:10-16:30 **Welcome Address: Prof. N.K. Ganguly**
Former Director General, Indian Council of Medical Research, New Delhi, India
Senior Advisor - Global Health Strategies, New Delhi, India
President, Gut Microbiota and Probiotic Science Foundation (India)

16:30-16:50 **Opening Remarks: Prof. V. Samuel Raj**
Director and Dean Academics, SRM University, Delhi – NCR, Sonepat, Haryana, India

16:50-17:30 **Inaugural address: Prof. Shiv Pillai**
Professor, Medicine and Health Sciences and Technology, Harvard Medical School, Boston, USA
"The Disruption of Adaptive Immunity in COVID-19"

Session One 17:30 – 19:00

Chairperson: Dr. Amulya K. Panda
Director, National Institute of Immunology, New Delhi, India

Co-Chairperson: Dr. Amit Awasthi
Associate Professor, Translational Health Science and Technology Institute (THSTI), Faridabad, Haryana, India

17:30-18:00 **Dr. Kenji Oishi**
Associate Chief Researcher, Microbiological Research Department, Yakult Central Institute, Tokyo, Japan
"Dynamics of Probiotic Strains in Human Small Intestinal Tract"

18:00-18:30 **Dr. Bruno Pot,**
Guest Professor, Vrije Universiteit Brussel, Belgium, Europe
"Probiotics and Immunity: a Long but Interesting Story"

18:30-19:00 **Prof. Jeffrey I. Gordon**
Director of the Center for Genome Sciences and Systems Biology, Washington University School of Medicine, St. Louis, USA
"Microbiota-Directed Foods for Treating Childhood Undernutrition"

DAY 2 — 14-03-2021

Session Two — 10:00 – 12:00

Chairperson: **Prof. G.B. Nair**
Honorary Distinguished Professor, Microbiome Laboratory
Rajiv Gandhi Centre for Biotechnology, Kerala, India

Co-Chairperson: **Prof. Sourabh Dutta**
Professor, Newborn Unit, Post Graduate Institute of Medical Education & Research, Chandigarh, India

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10:00-10:30 — **Dr. Tahmeed Ahmed**
Director, International Centre for Diarrhoea Disease and Research, Bangladesh (icddr,b)
"An Abnormal Gut Microbiota Assembly is Responsible for Environmental Enteropathy and Stunting in Children"

10:30-11:00 — **Dr. Satoshi Hachimura**
Associate Professor, Research Centre for Food Safety, Graduate School of Agricultural and Life Sciences, The University of Tokyo
"Lactic Acid Bacteria in Reducing Infection via the Intestinal Immune System"

11:00-11:30 — **Dr. Stephanie Jeansen,**
Science Activation Senior Manager at Danone Nutricia Research, France

11:30-12:00 — **Young Investigator Presentations**

12:00–13:00 — Panel Discussion

"Gut Microbiota, Probiotics and Immune Response – The Link"

Moderator:
Prof. Anura Kurpad
Physiology and Nutrition Dept, St John's Medical College, Bengaluru, Karnataka, India

Panel Members:

Prof. N K Ganguly
Former Director General, Indian Council of Medical Research, New Delhi, India
Senior Advisor - Global Health Strategies, New Delhi, India
President, Gut Microbiota and Probiotic Science Foundation (India)

Dr. N K Arora
Executive Director, The INCLEN Trust International, New Delhi, India

Prof. B S Ramakrishna
Director, SIMS Institute of Gastroenterology, Hepatobiliary Sciences and Transplantation SRM Institutes of Medical Science, Chennai, Tamil Nadu, India

Dr. B Sesikeran
Former Director– National Institute of Nutrition, Hyderabad, Telangana, India

Prof. A K Srivastava,
Member, Agricultural Scientists Recruitment Board,
Krishi Anusandhan Bhawan-I, New Delhi, India

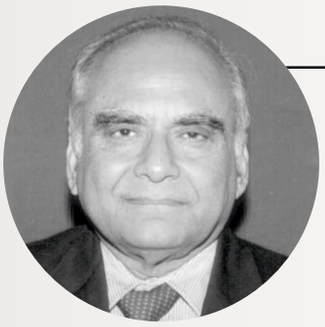
Prof. J B Prajapati
Chairman, VKCoE, Institute of Rural Management, Anand, Gujarat, India

13:00-13:30 Valedictory Session

Chairperson: **Dr. M.S. Chauhan**
Director, National Dairy Research Institute (NDRI), Karnal, India

13:00-13:20 **Ms. Inoshi Sharma,**
Director, Social and Behavioral Change, Food Safety and Standards Authority of India (FSSAI)
"Eat Right for a Better Future"

13:20-13:30 **Vote of Thanks**



Welcome Address: Prof. N.K. Ganguly

'Padma Bhushan'

Former Director General, Indian Council of Medical Research, New Delhi, India
Senior Advisor - Global Health Strategies, New Delhi, India
President, Gut Microbiota and Probiotic Science Foundation (India)

Nirmal Kumar Ganguly, M.D., Ph.D. is a Former Director General of the Indian Council of Medical Research, Former Director PGI Chandigarh and National Institute of Biologicals, Former Presidents of the National Academy of Medical Sciences, Indian Science Congress, JIPMER – Puducherry. He is Fellow of Imperial College and the Royal College of Pathologists and the Tropical School, London, Fellow of all the medical and Science academies in India, third world academy. He is member of the Advisory Committee to the Minister of Health on COVID-19. He was the member of Board of Grand Challenges Canada, Canada Innovation Fund. He is the Chairman of the Research Council of the Institute of Advanced Virology, and Chairman, Indian Pharmacopeia Commission. He was on the Advisory Board of NIH Fogarty International Center, the Health Vaccine Center, the U.S. Centers for Disease Control (CDC). He was in the Scientific Advisory board of IVI, icddr,b Dhaka. Prof. Ganguly is Chairman of the Advisory Committee for Health Research of the World Health Organization-SEARO, the International Vaccine Institute Cholera Board (CHOVI), and the United Nations Children's Fund SAG TDR, NTD Scientific board. He is also the Chair of Scientific Advisory Committee of Eminent Institutes like CCMB, CDFD, CDRI IMTECH, NCCS, RGCB, Bose Institute etc. Currently, he is President of the Gut Microbiota and Probiotic Science Foundation (India), Immunology Foundation of India and Indian Society of Translational Research. He has published more than 775 research papers and supervised or co-supervised 130 Ph.D. candidate dissertations and more than 20 book chapters. Prof. Ganguly has been honoured with the 7 International and 113 National awards along with the prestigious ''Padma Bhushan'' Award in the field of "Medicine" for the year 2008.

Opening Remarks: Prof. V. Samuel Raj

Director and Dean Academics, SRM University, Delhi – NCR,
Sonepat, Haryana, India

Prof. V. Samuel Raj is working as the Professor of Microbiology & Biotechnology; Director of the Centre for Drug Design Discovery & Development (C4D) and Dean (Academic Affairs) at SRM University, Delhi-NCR, Haryana, India. He has established the Centre for Drug Design Discovery and Development (C4D) at SRM University in 2014 with ten years of R&D experience from two major Pharmaceutical giants Ranbaxy and Daiichi Sankyo and also with more than 25 years international & national research experience in the area of infectious diseases including Virology. He has done his PhD in Microbiology from Institute of Medical Sciences, BHU, Varanasi. He has done post doctorates in Academia Sinica, Taiwan, Chiba University, Japan and Thomas Jefferson University & University of Pennsylvania, USA. He was a faculty at the University of Pennsylvania, USA. He is a recipient of many awards including STARS Fellow (Biomedical Leader), Switzerland & Tokyo Biochemical Research Foundation (TBRF) Award, Japan. He is the mentor and reviewer of the scientific research grants, Government of India (India DBT & UKRI, UK; ICMR & Norway). He has been invited to speak in the International Conferences and Universities in USA, UK, Israel, Switzerland, Italy, Japan, Mauritius, China, etc.

THE DISRUPTION OF ADAPTIVE IMMUNITY IN SEVERE COVID-19

Inaugural address: Prof. Shiv Pillai

Professor, Medicine and Health Sciences and Technology,
Harvard Medical School, Boston, USA

Shiv Pillai is a Professor of Medicine and Health Sciences and Technology at Harvard Medical School. He studied medicine at Christian Medical College in Vellore, completed his PhD with Bimal Bacchawat, and was a Postdoctoral Fellow with David Baltimore at the Whitehead institute and MIT. He is the Program Director of an NIH-funded Basic Autoimmune Center of Excellence at Massachusetts General Hospital, the Director of the Harvard Immunology PhD and Master's in Medical Sciences Programs and director of the HMS-HST MD student research program. He has been the recipient of a number of teaching awards at Harvard including the Irving M. London Award for Teaching, the Thomas McMahon Mentoring Award, and has been listed on Harvard Crimson's Professors of the Year.

Dr. Pillai coined the term “surrogate light chains” for proteins that he identified as part of the pre-B receptor, that drives early B cell development. His laboratory postulated and provided evidence for the first ligand-independent signaling model during lymphocyte development and showed that BTK, the product of the gene mutated in X-linked agammaglobulinemia, is functionally linked to the pre-B receptor and the B cell receptor. Btk inhibitors are now widely used in lymphoid malignancies and autoimmunity. Apart from the pro-B to pre-B cell transition, his group developed the concept of the follicular versus marginal zone B lymphoid cell-fate decision, has recently identified a metabolic transitional to follicular B cell switch that is blocked in human common variable immunodeficiency, and identified a block in T follicular helper cell development in COVID-19 that prevents the formation of germinal centers. His laboratory actively studies the dysfunctional extra-follicular B cell response and its link to cytotoxic CD4+T cells in autoimmune and inflammatory diseases that include IgG4-RD, systemic sclerosis, fibrosing mediastinitis, COVID-19 and disorders involving human single gene mutations in CTLA4, NFKB1, PI3KCD and more.

Dr. Pillai is the author of a monograph "Lymphocyte Development" and co-author with Abul Abbas and Andrew Lichtman of two widely used textbooks of immunology.

ABSTRACT

Humoral responses in COVID-19 disease are often of limited durability, as seen with other human coronavirus epidemics. To address the underlying etiology, we examined postmortem thoracic lymph nodes and spleens in acute SARS-CoV-2 infection and observed the absence of germinal centers, a striking reduction in Bcl-6+ germinal center B cells but preservation of AID+ B cells. Absence of germinal centers correlated with an early specific block in Bcl-6+TFH cell differentiation together with an increase in T-bet+TH1 cells and aberrant extra-follicular TNF-a accumulation. Parallel peripheral blood studies revealed loss of transitional and follicular B cells in severe disease and accumulation of SARS-CoV-2-specific “disease-related” B cell populations. These data identify defective Bcl-6+TFH cell generation and dysregulated humoral immune induction early in COVID-19 disease, providing a mechanistic explanation for the limited durability of antibody responses in coronavirus infections and suggest that durable achieving herd immunity through natural infection may be difficult.

The contributions of T cells in the lungs to SARS-CoV-2 clearance and to disease progression are also poorly understood. No previous studies have systematically interrogated T cell subsets in the lungs in severe COVID-19 but some studies on blood and bronchoalveolar lavage cells have suggested that the majority of CD8+ T cells in this disease may be exhausted. We establish here that cytotoxic CD4+ T cells (CD4+ CTLs) are the dominant CD4+ T cell subset in the lungs late in this disease. CD4+CTL expansion is accompanied by widespread HLA-DR expression on lung epithelial and endothelial cells, increased apoptosis of epithelial cells and tissue remodeling. Quantitatively, based on evidence for re-activation in the lung milieu, cytotoxic CD4+ CTLs are as likely to be drivers of viral clearance as are partly exhausted CD8+ T cells and they may also be key contributors to the enhanced lung inflammation and fibrosis seen late in severe COVID-19.

SESSION ONE 17:30 – 19:00

Chairperson: Dr. Amulya K. Panda

Director, National Institute of Immunology, New Delhi, India

Amulya K. Panda is a Scientist at National Institute of Immunology (NII), New Delhi for last 30 years. Currently he is the director of NII. He has master degree in chemical engineering from IIT Madras and Ph. D. in Biochemical Engineering and Biotechnology from IIT , Delhi. He has been a visiting scientist with Prof. Harvey Blanch at the Chemical Engineering Department, University of California at Berkeley, USA and at Department of Pharmaceutical Science at University of Nebraska Medical Centre, Omaha, USA. His research interest includes bioprocess engineering, recombinant fermentation process development, high throughput protein refolding from inclusion bodies and vaccine delivery using biodegradable polymer particles. He has published more than 145 research papers, Twelve book chapters and an inventor of more than 35 issued or pending patents. His honours includes SAMANTA CHANDRA SEKHARA AWARD" from Orissa Bigyan Academy, for the year 2000, Biotech Product and Process Development and Commercialization Award 2001, by the Dept. of Biotechnology, Govt. of India, on May 11th , 2001, Young Asian Biotechnologist Prize from The Society for Biotechnology, Japan for the year 2004, TATA INNOVATION Fellowship, 2010 from the Dept. of Biotechnology, Govt. of India. GB Manjerekar Award of AMI at AMI-2010 conference at BIT-Mesra, Dec. 2010. His research group was also awarded 2nd prize at Intel-UC Berkeley Technology entrepreneurship challenge-2008 and 3rd prize at World Innovation Summit, at Barcelona on June 16th, 2009. He was the President of Association of Microbiologist of India (AMI) for the year 2017. Dr. Panda has the credentials of generating highest number of IPRs while working at National Institute of Immunology. He is a Fellow of Royal Society of Chemistry (Cambridge), Fellow of American Institute of Chemical Engineer, and Fellow of National Academy of Microbiological Sciences, India. Dr. Panda is instrumental in initiating ImmunoEngineering program at NII.

Research Publications: 145	**Patents: 35**	**Research Presentations: 100**	**Book Chapters: 12**
Technologies Developed: 17	**Trademark Products: 3**	**International Awards: 3**	**National Awards: 4**
R&D Projects Completed: 18	**Invited lectures: 125**	**Symposium Organized: 6**	**Ph.D. guided: 17**

Co-Chairperson: Dr. Amit Awasthi

Associate Professor, Translational Health Science and Technology Institute (THSTI), Faridabad, Haryana, India

Dr. Amit Awasthi has significantly contributed in understanding the biology of helper T cell subsets in tissue inflammation in autoimmune diseases, allergic inflammation and infections. He identified the transcriptional signature of pathogenic and nonpathogenic Th17 cells and Tr1 cells (Nature Immunology 2012; 13:991-9, Nature 2013, 25;496:461-8; Nature Immunology 2017, 18:412-421; Cell Reps 2020, 33:108433). He has demonstrated the role of Th9 cells in allergy and anti-tumor immunity (Nature Communications 2017, 8:815; Nature Communications 2021, in press). Amit has contributed significantly in Covid19 pandemic by establishing the animal models to study SarsCov2 infection (bioRxiv, doi: https://doi.org/10.1101/2021.01.11.426080). Using the animal models he established, he has supported vaccine research and drug discovery for covid19.

DYNAMICS OF PROBIOTIC STRAINS IN HUMAN SMALL INTESTINAL TRACT

Dr. Kenji Oishi

Associate Chief Researcher, Microbiological Research Department,
Yakult Central Institute, Tokyo, Japan

Dr. K. Oishi is currently the Associate Chief Researcher at the Microbiological Research Department of Yakult Central Institute. His major research topic is the dynamics and the functions of gut microbes including probiotics. He had belonged to the Yakult Honsha European Research Center for Microbiology in Belgium for 10 years and was involved in a number of clinical trials on the physiological effects of probiotics as the Science Director. He has published 17 original papers and a review article in peer reviewed international journals. He received his Ph.D. from the Tokyo University of Pharmacy and Life Sciences.

ABSTRACT

Kenji Oishi, Ph.D.
Manager of Applied Microbiology Laboratory, Microbiological Research Department, Yakult Central Institute, 5-11 Izumi, Kunitachi-shi, Tokyo 186-8650, Japan

Numerous human clinical studies have shown various benefits of probiotics to the host. These probiotics have been proposed to act by improving the balance of the gut microbiota and enhancing the production of short-chain fatty acids, as well as by interacting with host cells in the gastrointestinal tract, but their dynamics had remained unclear. To investigate what happens in the human gastrointestinal tract after a single ingestion of a fermented milk product containing a probiotic, we periodically collected the small-intestinal fluids. The bacterial composition of the terminal ileum clearly revealed that the ingested probiotics (***Lactobacillus casei*** strain Shirota: LcS and ***Bifidobacterium breve*** strain Yakult: BbrY) occupied the ileal microbiota for several hours in several subjects. Cultivation of ileal fluids showed that more than 1 billion LcS and BbrY cells survived with their colony-forming ability intact after experiencing dramatic pH changes. These results indicate that there is adequate opportunity for the ingested probiotics to continuously stimulate the host cells in the small intestines. As the dynamics of ingested probiotics in the human gastrointestinal tract become clearer, further progress in this research area is expected to elucidate their behavior within the tract, as well as the mechanism of their physiological effects on the host.

1) Takada T, Chinda D, Mikami T, Shimizu K, Oana K, Hayamizu S, Miyazawa K, Arai T, Katto M, Nagara Y, Makino H, Kushiro A, Oishi K, and Fukuda S. Gut Microbes. 11(6) 1662-1676, 2020.

Key Words: colony-forming ability, ileal microbiota, microbiomics, probiotics, small-intestinal fluid perfusion.

PROBIOTICS AND IMMUNITY: A LONG BUT INTERESTING STORY

Dr. Bruno Pot

Guest Professor, Vrije Universiteit Brussel, Belgium, Europe

Prof. Bruno Pot made a PhD in microbiology at the University Gent, Belgium, where he performed research on lactic acid bacteria. In 1997 he joined the company Yakult. In 2001 he became Research Director at the Institut Pasteur in Lille, France. During that time he was also Director at the bioinformatics company Applied Maths NV. Since 2001 Bruno is also Guest Professor at the Vrije Universiteit Brussel for courses in food microbiology. Since 2016 he is back with Yakult as Science Director for Europe. He is a member of the Taxonomic Subcommittee for *Lactobacillus*, *Bifidobacterium* and related taxa, and President of the Pharmabiotic Research Institute, France.

ABSTRACT

Probiotics are widely known to the public. They are available in the supermarket, the drugstore and the pharmacy. They prevent you from getting diarrhoea or respiratory tract infections, solve your constipation problems, and even influence your mood. How is that possible, you are wondering?

The fact is, of course, there is not a single probiotic that can do it all. We know that probiotic activities can be either shared by many different bacteria, like the production of lactic acid, or can be strain-specific. To make things even more complicated, it has become clear from many research results, that specific strains may act in combination only with other species or strains. cross – feeding is a nice example of that.

When looking into beneficial mechanisms of probiotics, it turns out moreover, that a single strain is often active in multiple ways. Microbiologically, by competing for places and nutrients, physiologically, by influencing barrier functions, blood pressure or cholesterol levels, metabolically, by producing vitamins or short chain fatty acids, neurologically, by influencing the nervus vagus, endocrinologically by changing hormonal balances for e.g. satiety or hunger feeling, and, importantly, immunologically, by interacting directly or indirectly with natural killer cells, dendritic cells or other immune mechanisms. Especially the latter immunological functionality is most often strain specific and, obviously, the immune status of the host may also play a role.

All the above considerations should make it clear that finding the “best” probiotic strain for a specific application is a challenging task. In the frame of this conference topic, “microbiota and probiotics in reducing viral infection” the focus of the presentation will be on some of the mechanisms that have been identified to explain how single bacteria can interact with the immune system and the intestinal permeability to increase the resistance against viral infections.

MICROBIOTA-DIRECTED FOODS FOR TREATING CHILDHOOD UNDERNUTRITION

Prof. Jeffrey I. Gordon

Director of the Center for Genome Sciences and Systems Biology, Washington University School of Medicine, St. Louis, USA

Jeffrey Gordon is the Dr. Robert J. Glaser Distinguished University Professor at Washington University in St. Louis. He received his M.D. from the University of Chicago. After completing his clinical training in internal medicine and gastroenterology, and doing a post-doctoral fellowship at the NIH, he joined the faculty at Washington University where he has spent his entire career; first as a member of the Departments of Medicine and Biological Chemistry, then as Head of the Department of Molecular Biology and Pharmacology, and for the past decade as founding Director of the University's interdepartmental, interdisciplinary Center for Genome Sciences and Systems Biology.

ABSTRACT

Jeffrey I. Gordon, Center for Genome Sciences and Systems Biology, and Center for Gut Microbiome and Nutrition Research, Washington University School of Medicine, St. Louis 63110 on behalf of members of the Breast Milk, Gut Microbiome and Immunity (BMMI) Project

Human postnatal development is typically viewed from the perspective of our 'human' organs. As we come to appreciate how our microbial communities are assembled following birth, there is an opportunity to determine how this microbial facet of our developmental biology is related to healthy growth as well as to the risk for and manifestations of disorders that produce abnormal growth. We are testing the hypothesis that perturbations in the normal development of the gut microbiota are causally related to childhood undernutrition, a devastating global health problem whose long-term sequelae, including stunting, neurodevelopmental abnormalities, plus metabolic and immune dysfunction, remain largely refractory to current therapeutic interventions. The journey to preclinical proof-of-concept, and the path forward to clinical proof-of-concept emphasize the opportunities and challenges for developing microbiota-directed therapeutics.

SESSION TWO: 10:00 – 12:00

Chairperson: Prof. G.B. Nair

Honorary Distinguished Professor, Microbiome Laboratory
Rajiv Gandhi Centre for Biotechnology, Kerala, India

Till October 31, 2018, G. Balakrish Nair worked in the Research, Policy and Cooperation Unit of the WHO South-east Asia Regional Office in New Delhi. After superannuation, he shifted to Trivandrum, Kerala and joined the Rajiv Gandhi Centre for Biotechnology as a retired scientist. He was previously the Executive Director of the Translational Health Science Technology Institute (THSTI), an autonomous Institute of the Department of Biotechnology, Ministry of Science and Technology, in Gurgaon, Haryana. Prior to that he was the Director of the National Institute of Cholera and Enteric Diseases (NICED), Kolkata, India. He joined NICED in 1981 and worked there till April 2000 after which he took up a 7-year assignment at the International Centre for Diarrhoeal Diseases in Dhaka, Bangladesh as the Director of Laboratory Sciences Division.

Prof. Nair's research is on enteric pathogens with particular emphasis on *Vibrio cholerae*, the causative agent of the disease cholera. His interest has recently expanded to the Human Microbiome with particular interest in the human gut microbiota and he was instrumental in creating the Centre for Human Microbial Ecology at THSTI.

Prof. Nair is a Fellow of all the major National Academies of India, Foreign Associate of the US National Academy of Sciences, Fellow of the Academy of Sciences for the Developing Nations, Trieste, Italy, Fellow of the American Academy of Microbiology and Member of the German Academy of Sciences (Leopoldina). Under his supervision, 29 students have obtained doctoral degrees. He is the author of over 500 research papers.

Co-Chairperson: Prof. Sourabh Dutta

Professor, Newborn Unit, Post Graduate Institute of Medical Education & Research, Chandigarh, India

Professor, Division of Neonatology, Dept of Pediatrics, PGIMER, India, AND
Adjunct faculty, Department of Pediatrics, McMaster University, Ontario, Canada,
Professor-in-charge, Examination Cell of PGIMER from January 2015
Associate Professor of Neonatology, McMaster University, Hamilton, ON, Canada,
Faculty member in PGIMER
MBBS, MD (Pediatrics) and Senior Residency from AIIMS, Delhi Senior Registrar (Neonatology) from the Children's Hospital at West Mead, Sydney
PhD (Neonatology) from PGIMER, Chandigarh FRCPC (Neonatal-Perinatal Medicine) from Royal College of Physicians & Surgeons of Canada (by academic certification from 2011-13)

Research output

Publications in journals	: 120	**Research guide:**	
Chapters in books	: 19	PhD thesis	: 1
Editorship of books	: 7	DM (doctoral) Neonatology	: 15
Presentations in conferences	: 130	**Theses**	
Awards for best paper	: 12	MD Pediatrics theses	: 15
PI of ongoing funded projects	: 6	Invited talks delivered abroad	: 8
Co-I of funded projects	: 8	Orations	:3

Areas of interest:
Neonatal sepsis, Probiotics, Microbiota, Retinopathy of prematurity, Research methodology

AN ABNORMAL GUT MICROBIOTA ASSEMBLY IS RESPONSIBLE FOR ENVIRONMENTAL ENTEROPATHY AND STUNTING IN CHILDREN

Dr. Tahmeed Ahmed

Director, International Centre for Diarrhoea Disease and Research, Bangladesh (icddr,b)

Dr Tahmeed Ahmed has been working for the last three decades in simplifying the management of childhood malnutrition, childhood tuberculosis, and diarrheal diseases. He leads the BEED (Bangladesh Environmental Enteric Dysfunction) study that attempts to discover non-invasive biomarkers of environmental enteric dysfunction, an important cause of stunting in children. Together with Dr Jeffrey Gordon of Washington University in St. Louis he discovered microbiota directed complementary food (MDCF) - a novel intervention for childhood malnutrition. This discovery was highlighted by the prestigious journal Science as one of the scientific breakthroughs of 2019. He is continuing the research on MDCF with support from the Bill & Melinda Gates Foundation.

Dr Ahmed studied in St. Gregory's High School and Notre Dame College, Dhaka and then obtained his medical degree from Mymensingh Medical College. He received residential training in Dhaka Children's Hospital and subsequently studied at the University of Tsukuba in Japan for his PhD. He has recently been appointed the Executive Director of icddr,b where he has been working for the last three decades. As a member of the Nutrition Guidance Expert Advisory Group of the WHO, Dr Ahmed revised the global guidelines for management of childhood acute malnutrition. He is a member of the international think tank, the Council of Research & Technical Advice on Acute Malnutrition (CORTASAM). He advises the Global Task Force on Cholera Case Control (GTFCC) on case management of cholera in children. Dr Ahmed was awarded the Bangladesh Academy of Science - Dr Sultan Ahmed Choudhury Gold Medal for outstanding achievement in Medical Science in 2003. He received from the Honorable Prime Minister of Bangladesh, Sheikh Hasina, the Islamic Bank Development Transformers' Roadshow Award in 2018. Dr Ahmed works closely with the Ministry of Health of Bangladesh, WHO, UNICEF and the International Atomic Energy Agency in research and training on nutrition. He has more than 370 papers published in international journals and books. Dr Ahmed was the President of the Commonwealth Association of Pediatric Gastroenterology and Nutrition (CAPGAN), an association of professionals in Pediatric Gastroenterology and Nutrition from the 54 Commonwealth nations. He is Professor of Public Health Nutrition of James P. Grant School of Public Health, BRAC University, Dhaka and also Affiliated Professor of School of Global Health, University of Washington, Seattle

ABSTRACT

Stunting, characterized by linear growth faltering of children, is the most common childhood ailment in the world affecting close to 150 million children. These children are more likely to die and those who survive are likely to suffer from impaired brain and intellectual development. Current intervention programs to control stunting have largely been futile attempts. It is believed that environmental enteric dysfunction (EED) is responsible for 40% of childhood stunting. EED is a condition caused by repeated exposure of a child to pathogens that go on to colonize the small intestine, resulting in chronic inflammation, malabsorption and malnutrition. We recently completed the Bangladesh Environmental Enteric Dysfunction (BEED) study to understand the pathogenesis of EED, discover simple and robust biomarkers, assess the impact of feeding on reversal of stunting, and to investigate the role of the gut microbiota in EED.

Children with stunting (length for age <-2) and those who were at risk of stunting (LAZ between -2 and -1) were enrolled for on-site feeding of a nutritious diet as well as a multiple micronutrient supplement once a day for 3 months. Those who did not recover from stunting at the end of intervention were screened for secondary causes of malnutrition such as tuberculosis. Children who did not have any secondary cause of malnutrition were adjudged to have EED and their parents were explained about the need to perform esophagogastroduodenoscopy for the study. Out of 525 stunted children, 104 had small intestinal biopsy confirmed EED. A total of 80 children had duodenal aspirates for microbiota and proteomic analyses. Translational studies were performed to ascertain causal relationship by transfer of enteropathy to germ-free

mouse colonized with cultured duodenal strains obtained from children with EED. A key result of the study was the presence of a core group of 14 bacterial taxa in at least 80% of the aspirates obtained from children with EED. These members of the gut microbiota, not typically classified as enteropathogens, negatively correlated with LAZ and positively correlated with duodenal proteins involved in immunoinflammatory responses. Studies are now planned to investigate the effect of food-based approaches to modulate the abnormal gut microbiota associated with EED. Such an intervention will, of course, be in addition to improving water, sanitation and hygiene among populations where EED and stunting are most prevalent.

LACTIC ACID BACTERIA IN REDUCING INFECTION VIA THE INTESTINAL IMMUNE SYSTEM

Dr. Satoshi Hachimura

Associate Professor, Research Centre for Food Safety, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Japan

Associate Professor Satoshi Hachimura is Vice Director of the Research Center for Food Safety, Graduate School of Agricultural and Life Sciences, The University of Tokyo. He is Secretary Board member the Japanese Association for Food Immunology and Administrative Board member of the Intestinal Microbiology Society. He is the recipient of 'The Food Immunology Award for Basic Research' in 2009. He has published more than 100 research papers in peer reviewed journals. His field of specialization is food immunology, in particular, how food components act on the intestinal immune response.

ABSTRACT

Immune modulation by lactic acid bacteria (LAB) results in many beneficial effects. One important target is enhancement of the immune response, which may lead to host defense. Indeed, many studies have shown that oral administration of LAB can inhibit infections such as influenza in humans and in animal models. At least some parts should be through direct effects on the intestinal immune system, which I would like to focus on.

The enhancement of the antibody response may be useful in preventing infection. Many reports have shown that IgG and IgA responses are enhanced by LAB. Enhancement of IgA secretion may be important in preventing pathogens from invading mucosal barriers. The mechanisms underlying IgA enhancement by LAB have been explored, and it has been reported that LAB can act on cells of the intestinal immune system. We have shown that LAB may act on dendritic cells to produce IL-6, which enhance IgA production. We have also shown that LAB may induce T follicular helper (Tfh) cells.
Another way to augment host defense is through NK cells. Many LAB enhance NK activity, often through IL-12 production. The intestinal immune system may possibly be involved in such cases also. The intestinal immune system may be a key in immunomodulation by LAB.

EFFECTS OF A PROBIOTIC FERMENTED DAIRY DRINK CONTAINING L. CASEI CNCM I-1518 ON COMMON INFECTIOUS DISEASES: RESULTS OF A SYSTEMATIC REVIEW AND META-ANALYSIS

Dr. Stephanie Jeansen

Science Activation Senior Manager at Danone Nutricia Research, France

I have a doctorate of Pharmacy (PharmD) associated with a Master's degree in Toxicology. After a couple of years working in clinical trial departments for pharmaceutical companies, I joined Danone Nutricia Research in 2008 to work on the safety of functional ingredients. My role was to ensure the safety of the voluntarily-added ingredients, including micro-nutrients, macro-nutrients, fibers and strains. Since 2016, I have joined the Dairy and Plant-based R&I department to work on scientific communication around probiotics and gut microbiota.

ABSTRACT

Common infectious diseases (CIDs), which include respiratory and gastrointestinal infections, are a major public health concern with more than 17.5 billion cases of respiratory infections worldwide in 2017. This causes considerable discomfort and economic losses due to missed days at work or medical care.

There is a great interest in the research community in assessing the effects of probiotics in preventing these infections. Systematic reviews and meta-analyses pooling different probiotics from the *Lactobacillus* and *Bifidobacteria* families have previously shown potential to prevent CIDs. Thus, the question of the strain-specific effect may arise.

A systematic review combined with a meta-analysis has been conducted specifically with a probiotic dairy drink containing the *Lacticaseibacillus paracasei* subsp. paracasei CNCM I-1518 and yogurt strains *Lactobacillus bulgaricus* and *Streptococcus thermophilus*.

The effects of this specific probiotic drink were investigated on CIDs, in a pooled data set from people of different age groups. The data quality included was checked according to the criteria of the National Institute of Health. Effects on CIDs incidence, duration and severity have been assessed.

Compared to the control, the consumption of the probiotic dairy drink resulted in (a) a significant reduction in the odds of experiencing ≥1 CID (odds ratio (OR) (with a 95% confidence interval (CI)): 0.81 (0.66, 0.98); p = 0.029); (b) a significant reduction in mean CIDs per subject (−0.09 (−0.15, −0.04); p = 0.001); and (c) a trend towards reduced risk in cumulative CIDs (relative risk (RR): 0.91 (0.82, 1.01); p = 0.082).

The results suggest that the probiotic dairy drink containing the *Lacticaseibacillus paracasei* subsp. *paracasei* CNCM I-1518 and the yoghurt strains may reduce the incidence of CIDs in the general population.

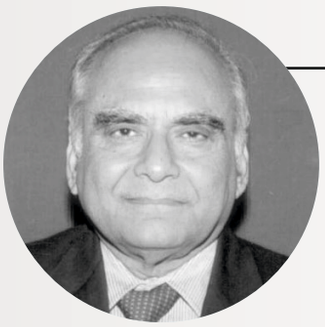
GUT MICROBIOTA, PROBIOTICS AND IMMUNE RESPONSE – THE LINK

Moderator: Prof. Anura Kurpad

Professor, Physiology and Nutrition Dept, St John's Medical College, Bengaluru, Karnataka, India

Anura Kurpad is Professor, Dept. of Physiology and Nutrition at St. John's Medical College, Bangalore, India, and was the Founding Dean of St John's Research Institute, Bangalore, India. He is the Head of the only IAEA Collaborating Centre on Nutrition, located at St John's. He is a Fellow of the Royal College of Physicians (London), the Indian National Academy of Medical Sciences and the International Union of Nutritional Sciences. He is also a Margdarshi Fellow of the Wellcome Trust-DBT India Alliance. He has published over 400 papers, and is co-author of the Asian Adaptation of Guyton's Textbook of Physiology and Co-Editor of the Asia Pacific Journal of Clinical Nutrition. He is the Chairman of the Scientific Advisory Group of the Nutrition Division of ICMR; ICMR Expert Committee on the RDA of Indians; and Nutrition and Fortification Scientific Panel of FSSAI. His interests are in human energy/protein and micronutrient metabolism.

PANEL MEMBERS

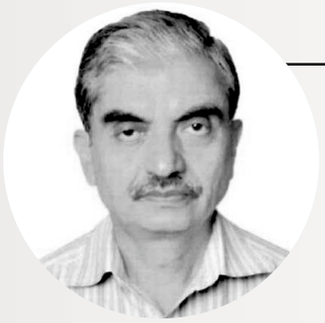


Prof. N K Ganguly

'Padma Bhushan'

Former Director General, Indian Council of Medical Research, New Delhi, India
Senior Advisor - Global Health Strategies, New Delhi, India
President, Gut Microbiota and Probiotic Science Foundation (India)

Nirmal Kumar Ganguly, M.D., Ph.D. is a Former Director General of the Indian Council of Medical Research, Former Director PGI Chandigarh and National Institute of Biologicals, Former Presidents of the National Academy of Medical Sciences, Indian Science Congress, JIPMER – Puducherry. He is Fellow of Imperial College and the Royal College of Pathologists and the Tropical School, London, Fellow of all the medical and Science academies in India, third world academy. He is member of the Advisory Committee to the Minister of Health on COVID-19. He was the member of Board of Grand Challenges Canada, Canada Innovation Fund. He is the Chairman of the Research Council of the Institute of Advanced Virology, and Chairman, Indian Pharmacopeia Commission. He was on the Advisory Board of NIH Fogarty International Center, the Health Vaccine Center, the U.S. Centers for Disease Control (CDC). He was in the Scientific Advisory board of IVI, icddr,b Dhaka. Prof. Ganguly is Chairman of the Advisory Committee for Health Research of the World Health Organization-SEARO, the International Vaccine Institute Cholera Board (CHOVI), and the United Nations Children's Fund SAG TDR, NTD Scientific board. He is also the Chair of Scientific Advisory Committee of Eminent Institutes like CCMB, CDFD, CDRI IMTECH, NCCS, RGCB, Bose Institute etc. Currently, he is President of the Gut Microbiota and Probiotic Science Foundation (India), Immunology Foundation of India and Indian Society of Translational Research. He has published more than 775 research papers and supervised or co-supervised 130 Ph.D. candidate dissertations and more than 20 book chapters. Prof. Ganguly has been honoured with the 7 International and 113 National awards along with the prestigious ''Padma Bhushan'' Award in the field of "Medicine" for the year 2008.



Prof. Narendra Kumar Arora

Executive Director, The INCLEN Trust International, New Delhi, India

Professor Narendra Kumar Arora is a paediatrician and public health expert. He was on the faculty of AIIMS New Delhi between 1983 and 2005. Since 2005 he is the Executive Director of the INCLEN Trust International (INCLEN) based in New Delhi-India. In 2018, he was appointed President, AIIMS-Patna and AIIMS-Deoghar, (Two new National Institutions of Eminence) to steer these to national centers of excellence in clinical care, research and training.

Professor Arora has made major contributions to the Immunization sector at both national and global levels. He has been involved in the research related to Pulse Polio Immunization Program, vaccine hesitancy and active & passive AEFI surveillance since 1997. Prof Arora is currently the Chairman of the National Certification Committee for Polio Eradication and the National Verification Committee for Measles, Rubella and CRS.

Dr Arora was on the WHO SAGE (Strategic Group of Experts-Immunization) from 2010 to 2016 and SEAR-ITAG between 2009 and 2017. He has been chair/member of seven SAGE working groups. He is currently serving as a member of the WHO Global Advisory Committee on Vaccine Safety (GACVS).

Prof. B S Ramakrishna

Director, SIMS Institute of Gastroenterology, Hepatobiliary Sciences and Transplantation SRM Institutes of Medical Science, Chennai, Tamil Nadu, India

Balakrishnan S. Ramakrishna is Director, Institute of Gastroenterology, Heptobiliary Science & Transplantation at the SIMS Hospitals, Vadapalani, Chennai. Formerly Professor and Head of the Gastroenterology Department at the Christian Medical College, Vellore, he continues to be an active practicing clinician and endoscopist besides conducting research targeting intestinal disease and the gut microbiome. He is a fellow of several National Academies and he served as President of the Indian Society of Gastroenterology and as Editor-in-chief of the Indian Journal of Gastroenterology. He has served on committees in the World Gastroenterology Organization, the Asian Pacific Association of Gasteroenterology, and the Wellcome Trust, UK. He has more than 160 peer-reviewed publications, 20 book chapters, several GenBank submissions and a patent application to his credit.

Dr. B Sesikeran

Former Director– National Institute of Nutrition, Hyderabad, Telangana, India

Dr. Sesikeran is the Former Director of NIN, ICMR Hyderabad. He is a Pathologist by training and has carried out research in the area of Nutrition, Food Safety, and Toxicology for 30 years. He has over 120 publications and Chapters in 3 Books. He has developed guidelines for Probiotics in foods, Guidelines for GM food safety, Guidelines for Biosimilar Drugs, Recommended Dietary Allowances and Dietary Guidelines. He was the Director NIN between 2006 and 2012. He is a Fellow of the National Academy of Medical Sciences and Fellow of the International Medical Scientists Academy. He is Fellow of AP & Telangana Academies of Sciences. Past President Nutrition Society of India. He is Public Trustee of ILSI India. Member Governing Body of Nutrition Foundation India, Member- Advisory Council on Science -Coca Cola India. Member Scientific Advisory Committee Gut Microbiota and Probiotic Science Foundation (India). He is also the Chairman of the Scientific Advisory Committee of PFNDAI.

Prof. A K Srivastava

Member, Agricultural Scientists Recruitment Board, Krishi Anusandhan Bhawan-I, New Delhi, India

Prof. (Dr.) A.K. Srivastava, a distinguished pharmacologist and former Professor and Head, Pharmacology, and Toxicology, PAU, Ludhiana is presently working as Member, ASRB. Before joining ASRB, DARE, Ministry of Agriculture and Farmers Welfare, GoI, Prof. Srivastava was Director and Vice Chancellor at ICAR-National Dairy Research Institute, Karnal, Dean, Director Resident Instructions and Dean PGs at Sher-e-Kashmir University of Agricultural Sciences & Technologies, Jammu. He is Post Doctorate from Institute of Toxicology, München, Germany. Prof. Srivastava is Vice President of National Academy of Agricultural Sciences (NAAS), President National Academy of Dairy Science (India), and Patron of Indian Dairy Association. He is President, Association of Mastitis and President of Probiotic Association of India. Earlier, Prof. Srivastava was Secretary, NAAS, and also the President, Indian Society of Pharmacology and Toxicology. He was also Chairman, FAD 19, Bureau of Indian Standard Committee, BIS, Govt. of India. Dr. Srivastava was Founder Authority Member of Food Safety and Standard Authority of India and member of International Dairy Federation. Prof. Srivastava is distinguished Member of National Academy of Sciences, fellow of National Academy of Agricultural Sciences, fellow of National Academy of Dairy Sciences and fellow of National Academy of Veterinary Sciences, fellow of National Academy of Biological Sciences. He is Member, Board of Governing Council of "Agriculture Skill Council of India", Ministry of Skill Development. Member, Advisory Committee of Indian Institute of Packaging, Ministry of Commerce and Industries, Govt. of India and Chairman R&D Committee of Ministry of Food Processing Industries, GoI, New Delhi.

He has been decorated with numerous prestigious awards and honours including ICAR Jawaharlal Nehru Award; International NOCIL Award; National Alarsin Awards in 1987-88 and 1999-2000; Prof. S. Kannaiyan Memorial Award-2019, by National Academy of Biological Sciences. Dr. V. Kurien Memorial Oration Award and many more. He has more than 250 research papers in his credit and has guided more than 30 PhD and MVSc/MS/MD students.

Prof. J B Prajapati

Chairman, VKCoE, Institute of Rural Management, Anand, Gujarat, India

Professor Jashbhai B. Prajapati is a Dairy Technologist from Anand with Ph.D. in Dairy Microbiology from NDRI. He retired as the Dean of the Faculty of Dairy Science at AAU, Anand. He is Chairman of Indian Dairy Association, Gujarat State and Coordinator of SASNET-Fermented Foods. He is a renowned academician and scientists in the area of probiotics and fermented foods who has handled 22 projects financed by various organization and has guided 32 MTech and 9 PhD students and has more than 500 publication including 2 books. He had Fellowship award from Erasmus Mundus (EU) as well as Indian National Science Academy. He is a Fellow of Indian Dairy Association as well as National Academy of Dairy Science. He is a recipient of several awards and is member in executive bodies of several universities and scientific organizations. At present he is the Chairperson of Verghese Kurien Centre of Excellence at Institute of Rural Management, Anand.

EAT RIGHT FOR A BETTER FUTURE

Dr. M S Chauhan

Director, National Dairy Research Institute (NDRI), Karnal, India

Dr. Manmohan Singh Chauhan is the Director, National Dairy Research Institute, Karnal, India. He has been the Principal Investigator of 11 externally funded projects and Co-PI of 9 inter-disciplinary and inter-institutional externally funded projects. Besides research, he has also contributed in teaching and developed 4 courses of animal physiology and animal biotechnology for post graduate students.

Dr. Chauhan is a Fellow of National Academy of Agricultural Sciences (FNAAS) Fellow of National Academy of Dairy Sciences (FNADS), Fellow Society of Extension Education.

Dr. Chauhan is recipients of Rafi Ahmed Kidwai Award by ICAR, 2015; Dr. P. Bhattacharya Memorial Award by NAAS 2020; Rao Bahadur B. Viswanath Award 2019 by IARI, New Delhi; and many more.

Dr. Chauhan has published over 155 original research papers and cited, 7 books, 44 scientific and technical publications have been authored or co-authored, 34 lectures delivered in National and International conferences

EAT RIGHT FOR A BETTER FUTURE

Ms. Inoshi Sharma

Director, Social and Behavioral Change, Food Safety and Standards Authority of India (FSSAI), New Delhi, India

Ms. Inoshi Sharma, Director (Social and Behaviour Change and Food Fortification Resource Centre) is a civil servant-an officer of the Indian Revenue Service. Her current assignment at FSSAI involves leading the Eat Right India initiative and extending support to scaling up of Fortification across the country. She has previous work experience as Director, National Health Mission in Haryana where she was looking after the supply chain management of drugs & equipment and adolescent health pertaining to Menstrual Hygiene & Weekly Iron Folic Acid Supplementations. She has an interest in area of Public policy, Administration and Social Sector.

ABSTRACT

As the apex food regulatory body in the country, the Food Safety and Standards of Authority of India (FSSAI) has the mandate to ensure safe and wholesome food for all citizens. In addition to scaling up its core regualtory activities, through the vision of Eat Right India, it is also promoting healthy food through sustainable food systems.

Food that is not safe is not food. Our vision aims to achieve food safety and hygiene for the people of India to prevent food borne illnesses that have a huge impact on the health and economy of the nation.

For this, Eat Right India has adopted a systems approach that is aligned with the UN's Sustainable Development Goals. Our strategy is to work across the food value chain and forge partnerships with various stakeholders ranging from the State Food Safety Department, to professionals in food and nutrition, various civil society organizations and citizens.

Eat Right India has devised FIVE key actions to implement in the next three years to achieve our Vision. The first action is to formulate new regulations to promote healthy eating. Second, we will train and build capacity of various stakeholders. Third, based on benchmarks for food safety and hygiene, we will certify various clusters of street food vendors to restaurants to schools and campuses. Fourth, we will nudge food businesses to reformulate packaged foods into healthier options and to use safe and sustainable packaging materials. And finally, we will ignite large-scale social and behavioral change among the people of India.

SENSORY PROTEIN SIGNATURES IN GUT MICROBIOME AS BIOMARKERS FOR EARLY DETECTION OF ASYMPTOMATIC DISEASES

Subhrajit Bhar *(First Prize)*

Authors: Subhrajit Bhar, Rashmi Singh, Nishal Kumar Pinna, Tungadri Bose, Anirban Dutta, Sharmila S. Mande

Affiliation: TCS Research, Tata Consultancy Services Ltd., 54B Hadapsar Industrial Estate, Pune 411013, Maharashtra, India

Email of submitting author: *subhrajit.bhar@tcs.com*

Mr. Subhrajit Bhar earned his M.Tech from the Central University of Hyderabad, and is currently employed as a Researcher in TCS Research, Tata Consultancy Services Ltd. His research focus lies in areas of biomarker discovery, host-microbe interactions, biological networks analysis and functional foods. During his 5 years of association with TCS Research, he has been a part of multiple research projects focussed on the microbiota and is a co-inventor in 8 patents filed across multiple geographies. In a recent publication, he has presented a novel metric for assessing the pathogenic potential of uncharacterized microbes based on their sensory protein repertoire.

ABSTRACT

Introduction: Dysbiotic gut-microbiome has been shown to be associated with multiple diseases/disorders. Bacterial community utilizes its repertoire of sensory proteins (SPs) to sense and gradually acclimatize to changes in environment/host physiology. We hypothesized that SP-signatures could be indicative of such changes associated to health status, even in early/asymptomatic stages of diseases.

Objectives: We evaluated whether SP-signatures from gut-microbiomes of colorectal cancer (CRC) and diabetes patients are indicative of their health status.

Methods: A database of bacterial SPs was generated and was subsequently used for analysing metagenomic data from previously published 'case-control' (case: different disease stages; control: healthy) studies on CRC (healthy, adenoma, carcinoma samples), and diabetes (healthy, pre-diabetes, diabetes samples). SP-abundance matrices for each dataset were generated to depict the SP-content of constituting bacterial species corresponding to each of the metagenomic samples. Finally, Random-Forest (RF) classifiers were built using features from the SP-abundance matrices for testing the potential of SPs to distinguish between healthy and disease associated samples.

Results: SP-based RF-classifiers were observed to be reasonably efficient in segregating the disease and healthy samples, especially those in early disease stages. These RF-classifiers exhibited better accuracies (AUC of 0.67 for adenoma and AUC of 0.7 for pre-diabetes cases) when compared to earlier reported microbial taxonomy-based classifiers.

Discussion: Timely diagnosis of asymptomatic diseases is often challenging and may result in higher morbidity/mortality and treatment costs. Our study suggests that SP-based techniques could aid in early detection/risk-assessment, thus enabling timely intervention. We also expect these SP-signatures to be universal and not confounded by geography/diet/ethnicity-associated taxonomic variations in the gut-microbiome.

Conclusion: SP-signatures in gut-microbiome samples may be used for non-invasive risk-assessment and as companion diagnostics.

Key Message: Sensory protein signatures from gut-microbiome is indicative of the onset (and progression) of certain diseases/disorders. These could act as biomarkers for early diagnosis of such asymptomatic diseases.

SKIN, ORAL AND GUT SHARE PHYLOTYPES TO URINARY MICROBIOME AND ITS DIVERGENCE MAY ASSOCIATED WITH TYPES OF URINARY KIDNEY STONES

Mangesh Vasant Suryavanshi *(Second Prize)*

Mangesh Suryavanshi[1], Muhammed Manzoor[1], M Mujeeburahiman[2], A.B. Arun[1], Yogesh Shouche[3], Punchappady-Devasya Rekha1
[1]Yenepoya Research Centre, Yenepoya Deemed to be University, Mangalore 575018
[2]Urology Department, Yenepoya Deemed to be University, Mangalore 575018
[3]National Centre for Microbial Resource, National Centre for Cell Science, Pune 411021

Presenting Author Email: mangeshnccs@gmail.com

He is a science enthusiast with a masters in microbiology and PhD degree in biotechnology from National Centre for Cell Science, Pune. He has recently been awarded the SERB-NPDF fellowship and currently working as PI for the NPDF project. He wants to explore the intrinsic relationship between the human associated microbes and their genetic, metabolic and responsive capacities. The different ecological aspects, right from the association between the microbes to the host suffering with metabolic disorders; he envisions to disseminate interspecies interactions through genomics. He has to his credit of total 36 research publications and, looking for decent faculty positions.

ABSTRACT

Background/Aims: The present study is aimed at understanding the link between Kidney stone disease (KSD) and urogenital microbiome (UMB) in disease progression and management. We performed a cross-sectional study involving total 369 patients with KSD and age-sex matched non-KSD controls.

Objectives: Cross-talk for gut-urinary axis phylotypes and accessing divergence in urinary microbiome for KSD status.

Methods: UMB was studied through 16S rRNA gene sequencing from the healthy (HLT) and KSD subjects. Metabolic capabilities of the bacterial community were inferred by PICRUSt software. SourceTracker was applied treating the different human body sites like human gut, skin and oral cavity phylotypes from Indian population. Surgically removed stones were identified using FTIR and X-ray powder diffraction methods. WGS of urine culture bacterial isolates to test the in-vitro capabilities.

Results: The mean age of the KSD group was 46.34 ±12.34 years and represented four stone types (calcium oxalate, struvite, uric acid and mixed). Among KSD population, positive stone culture and urine culture were seen in 16 (39.02%) and 15 (36.5%) patients subject respectively. In HLT cohorts 12 (29.2%) urine samples showed the growth of bacteria. A difference in the total community composition between HLT and KSD cohorts ($p < 0.05$) was observed. Metabolic reconstructions of the UMB revealed the significant abundance of many functional categories that may have influence on stone formation. Similarities in viz. skin, oral and gut were been recorded with (11.7%, 0.6% and 9.4% respectively for KSD group and, with (13.3%, 0.2% and 10.3% respectively for HLT group.

Discussion and Conclusion: The results show that UMB may play a role in KSD and alterations in the UMB may be a risk factor for KSD. Supports gut-urinary axis hypothesis to show translocation of phylotypes from gut to urine. There may be a few key species that give protection against stone disease, while, some phylotypes like *Kalamiella piersonii* MCC 3118 may facilitate the stone accumulation due to their specific metabolic pathways or modify the stone composition. To establish this fact, thorough studies across geographical regions and diverse population is essential.

Key message: First report of urinary microbiome from India and, which has characteristic of divergence in disease state.

PROBIOTIC *Lactobacillus fermentum* MEDIATES ITS IMMUNOREGULATORY FUNCTION BY TARGETING EPIGENOMIC MODULATIONS

Ankita Kumari *(Third Prize)*

Ankita Kumari,
Shalaka Bhawal, Suman Kapila and Rajeev Kapila
Division of Animal Biochemistry, National Dairy Research Institute (NDRI)
Karnal, Haryana-132001

My name is Ankita Kumari and I have recently submitted my Ph.D. thesis. My Ph.D. research work is based on the study of epigenetic modifications of intestinal cells in presence of probiotic bacteria. I have a desire to develop a research career in the area of the role of epigenetic modifications in host-microbiome interactions in the gut.

ABSTRACT

Introduction: Probiotic *Lactobacillus fermentum* (MTCC 5898: LF) isolated from the faeces of a 10-month-old infant have a role in the maintenance of gut homeostasis through the regulation of the immune response of the host. Besides, LF can attenuate *E.coli* or LPS induced inflammatory response in intestinal epithelial cells. Hence, it is important to know the mechanism of action of probiotics before their use.

Objective: The present study aimed to investigate whether probiotics *Lactobacillus fermentum* (MTCC 5898: LF) regulate immunomodulatory activities functions through epigenetic mechanisms.

Methods: Human colonic epithelial (Caco-2) cells were treated with *L. fermentum* and *E. coli* for 24 h and mRNA expression of HDAC1 was analyzed by RT-qPCR. Further, HDAC1 was inhibited followed by incubation with LF and *E. coli* and mRNA expression of immune genes and H3 histone acetylation of the promoter region of immune genes was analyzed by using RT-qPCR and Chromatin Immunoprecipitation (ChIP) assay respectively.

Results: RT-PCR analysis showed that LF induced the mRNA expression of HDAC1 while *E. coli* suppressed it. Post-treatment with *L. fermentum* to inhibitor-treated cells significantly resisted the earlier strongly induced expression of innate immune genes opposite to *E. coli* which synergistically enhanced the expression of immune genes. Chromatin immunoprecipitation analyses showed a decrease in histone H3 acetylation at innate immune gene promoters during LF incubation and corresponded to transcriptional activity.

Discussion: *L. fermentum* regulated immune genes by activating HDAC1 which reduces H3 acetylation in opposite to inflammatory E. coli which increases the levels of H3 acetylation by suppressing the mRNA expression of HDAC1.

Conclusion: From the above results, it was concluded that probiotics regulate the immune response of host cells through histone acetylation.

Key messages: The regulation of immune genes by probiotics through epigenomic mechanisms further aided the existing understanding of cellular and molecular pathways that regulate host-commensal interactions.

EVALUATION OF EFFECT OF PROBIOTICS ON CYTOKINE LEVELS IN CRITICALLY ILL CHILDREN WITH SEVERE SEPSIS: A RANDOMIZED, DOUBLE-BLIND, PLACEBO-CONTROLLED TRIAL

Suresh Kumar Angurana

Authors: Suresh Kumar Angurana, Arun Bansal, Sunit Singhi, Ritu Aggarwal, Jayashree Muralidharan, Manila Salaria, Navdeep Kaur Mangat.

Department and institute: Department of Pediatrics, Advanced Pediatrics Centre, Department of Immunopathology, Postgraduate Institute of Medical Education and Research (PGIMER), Chandigarh, India 160012.

Dr Suresh Kumar Angurana My academic qualifications include MD Pediatrics, DNB Pediatrics, DM Pediatric Critical Care, FCCP, and FIMSA. I am currently working as Assistant Professor in the Division of Pediatric Critical Care, PGIMER, Chandigarh. I have published >130 papers in national and international journals and presented >40 papers in national and international conferences. Our group has a special interest in role of probiotics in critically ill children and published several papers on this topic. The role of probiotics on the modulation of inflammation was tested in an RCT (Published in Critical Care Medicine 2018) and we demonstrated that the use of a multi-strain probiotic mix for 7 days resulted in a reduction in pro-inflammatory cytokines and an increase in anti-inflammatory cytokines in critically ill children with severe sepsis. Earlier, in an RCT (Critical Care Medicine 2013) we demonstrated that probiotics were effective in reducing candida colonization in GIT in critically ill children on broad-spectrum antibiotics. In a before-after study (Pediatric Critical Care Medicine 2013), we noted that probiotic mix for 7 days resulted in a significant reduction in candiduria and invasive candidiasis in critically ill children on broad spectrum antibiotics. These studies are major breakthroughs and important contributions to literature in demonstrating the role of probiotics in critically ill children in the modulation of inflammation; and reduction of GIT candida colonization, candiduria, and invasive candidiasis. The 2 review articles published by our team regarding the role of probiotics in critically ill children (Role of probiotics in prevention of Candida infection in critically ill children, Mycoses 2013; and Probiotics in critically ill children, F1000 Faculty Reviews 2016).

ABSTRACT

Introduction: Sepsis is characterized by hyperactive and dysregulated endogenous inflammatory response, the excess of which is associated with multiorgan dysfunction syndrome (MODS) and mortality. Administration of probiotics have been shown to modulate inflammatory response in experimental studies and in critically ill adults. There is paucity of data on the role of probiotics in modulation of inflammation in critically ill children. So, we conducted this trial to investigate the effect of a multi strain probiotic VSL#3 on critically ill children with severe sepsis with the hypothesis that supplementation with probiotics may reduce inflammation in critically ill children with severe sepsis.

Objective: To evaluate the effect of probiotics on cytokines in children with severe sepsis.

Methods: This randomized, double-blind, placebo-controlled trial was conducted in Pediatric intensive care unit (PICU) of a tertiary care teaching hospital in North India involving children aged 3 months-12 years with severe sepsis. Enrolled children were randomized to probiotic (n=50) and placebo (n=50) groups. Probiotic group received VSL#3® (*Lactobacillus paracasei*, *L. plantarum, L. acidophilus, L. delbrueckii, Bifidobacterium longum, B. breve, B. infantis, Streptococcus salivarius*; maltose; and silicon dioxide) and placebo group received maltose and silicon dioxide. Dose was 1 sachet BD for 7 days. Blood was collected on day 1 and 7 for estimation of IL-6, IL-12p70, IL-17, TNF-α, IL-10, and TGF-β1. Primary outcome: Change in cytokine levels in probiotic and placebo group from day 1 to 7. Secondary outcomes: Sequential organ failure assessment (SOFA) score, health care associated infections (HCAIs), ICU stay, and mortality.

Results: On day 7, probiotic group had significantly lower levels of pro-inflammatory cytokines [IL-6 (80 vs. 186 pg/ml, p=0.001), IL-12p70 (44 vs. 79 pg/ml, p=0.001), IL-17 (217 vs. 293 pg/ml, p=0.01, and TNF-α (192 vs. 348 pg/ml, p=0.01)] and higher levels of anti-inflammatory cytokines [IL-10 (320 vs. 240 pg/ml, p=0.02) and TGF-β1 (311 vs. 221 ng/ml,p=0.01)] than placebo group. From day 1 to 7, probiotic group showed significant decrease in pro-inflammatory cytokines [IL-6 (196 to 80 pg/ml, p=0.001), IL-12p70 (71 to 44 pg/ml, p=0.01), IL-17 (258 to 217 pg/ml, p=0.01, and TNF-α (347 to 192 pg/ml, p=0.001)] and increase in anti-inflammatory

cytokines [IL-10 (198 to 320 pg/ml, p=0.001) and TGF-β1 (216 to 311 ng/ml, p=0.001)] as compared to placebo group. SOFA score on day 7 was significantly less in probiotic group (1 vs. 3). There was a non-significant trend towards lower incidence of HCAIs (14% vs. 20%) and duration of ICU stay (6.5 vs. 9 days) in probiotic group. Mortality was similar in two groups.

Discussion: This study demonstrated that administration of probiotics for 1 week to critically ill children with severe sepsis resulted in decrease in level of proinflammatory and increases in anti-inflammatory cytokines. There was no effect on mortality with probiotics supplementation. These results are similar to various experimental and critically ill adult studies, which demonstrated that probiotics were effective in modulating immune response and reducing inflammation. This is the first double-blind, placebo-controlled randomized trial that evaluated effect of probiotics on cytokine levels in critically ill children with severe sepsis. This is also the only study comparing multiple cytokines in this group of children.

Conclusion: Probiotics supplementation for 7 days resulted in significant decrease in pro-inflammatory and increase in anti-inflammatory cytokines in children with severe sepsis. Key Messages: Probiotics have potential to modulate inflammation in critically ill children with severe sepsis. Further studies are needed to support the use of probiotics as an adjunctive therapy in critically ill children with severe sepsis.

LACTOBACILLI SIGNATURES FOR PRETERM BIRTH IN THE INDIAN WOMEN

Shakti Kumar

Shakti Kumar, Naina Kumari, GARBH-Ini study group, Shinjini Bhatnagar, Souvik Mukherjee, Bhabatosh Das

Molecular Genetics Laboratory, Translational Health Science and Technology Institute (THSTI), NCR Biotech Science Cluster, 3rd Milestone, Faridabad-Gurgaon Expressway, PO Box #04, Faridabad, Haryana 121001, India

Dr. Shakti Kumar is working as Senior Technical Officer in the ongoing project at Translational Research Programme at Molecular Genetics Laboratory, Translational Health Science and Technology Institute (THSTI) under the supervision of Dr. Bhabatosh Das and Prof. Shinjini Bhatnagar. Dr. Kumar has expertise in genomics and metagenomics data analysis by using open-source bioinformatics tools/software to develop pipelines based on Perl programming. Currently, Dr. Kumar is analyzing the vaginal microbiome of the GARBH-Ini cohort, a Department of Biotechnology (DBT) funded project â€œInterdisciplinary Group for Advanced Research on Birth Outcomes â€“ A DBT India Initiative (GARBH-Ini)â€ .

ABSTRACT

Introduction: Different species of *Lactobacillus* are most commenly probiotics aross the world. Reproductive tract of healthy women and small intestine are enriched with Lactobacilli. It has been well established that differential abundance of Lactobacillus species may act as marker of vaginal health. Lower abundance of *Lactobacillus* and increased microbial diversity are potential risk factors of Preterm birth (PTB). Ample number of vaginal microbiome studies have been performed globally but very limited in India. The present study was designed to explore abundance and genomic contents of *Lactobacillus* species isolated from the vaginal milieu of Indian women delivered term (TB) and preterm (PTB) babies.

Objectives: (i) To understand the vaginal microbiota of GARBH-Ini enrolled TB and PTB delivered mothers and differential abundance of *Lactobacillus* species, (ii) Whole genome analysis of dominant *Lactobacillus* species to identify potential genomic features that may have role in TB and PTB and (iii) Pan- and -core genome based phylogenetic study to explore evolutionary diversities among *Lactobacillus* species.

Methods: (i) 115 vaginal swabs were collected from 38 demographically defined pregnant Indian women enrolled in GARBH-Ini cohort who delivered spontaneous term (n=20) and preterm (n=18) for each trimesters: 1st (V1: 1-12 weeks), 2nd (V2: 13-26 weeks) and 3rd (V3: 27 week – birth). (ii) paired-end raw reads from V3-V4 region of 16S rRNA gene were generated by targeted next generation sequencing of DNA isolated from collected smaples during all the three trimesters. (iii) Whole genome based analysis and identification of genomic features of associated bacterial taxa with birth outcomes was done by shotgun sequencing method and using various bioinformatics tools respectively. (iv) Pan- and core based phylogenetic analysis by open source tools/softwares to look into their genome diversification.

Results: Vaginal microbiome of both term and preterm samples has similar alpha diversity indices. However, relative abundance of *L. gasseri* (p-value3rd_Trimester =0.009) was observed significanly high in 3rd Trimester in term samples. The relative abundance of *L. crispatus* was also high but statistical non-significant throughout all Trimesters. In case of preterm samples, significantly higher abundance of *L. iners* (p-valueAll_Trimesters <0.02), *Megasphaera cerevisiae* (p-value1st_3rd_Trimesters <0.02), *Gardnerella vaginalis* (p-value2nd_Trimester=0.014) and *Sneathia sanguinegens* (p-value2nd_Trimester <0.0001) were identified. The range of open reading frames (ORFs) from 1462 to 2249 obtained by analysis of whole genome of fifteen Lactobacillus species i.e.*L. crispatus* (n = 8), *L. gasseri* (n = 6) and L. iners (n = 1) that encode various types of antibacterial peptides (i.e. bacteriocin, helveticin, helveticin J and bacteriocin transporters) to protect the vaginal milieu from the invasion of non-indigenous microbiota. Pan- and core genome based phylogeny have shown that each species has made separate clade. This analysis reveals that each Lactobacillus species have diverse genome compositions.

Discussion: Vaginal microbiota of asymptomatic, otherwise healthy women are mostly dominated by the different species of Lactobacillus. Such similar results have been also reported by analysis of the vaginal microbiome of White American, Asian, Black American and Hispanic women. Analyses of the representative genomes of *L. crispatus* and *L. gasseri* indicate presence of secretory

transcriptional regulator and several ribosomally synthesized antimicrobial peptides correlated with anti-inflammatory condition in the vagina. In addition, culture supernatant of *L. crispatus* inhibits the growth of opportunistic bacterial pathogens *Klebsiella pneumoniae* and *Acinetobacter baumannii*. These findings indicate protective role of *L. crispatus* and *L. gasseri* that reduced the risk of preterm birth.

Conclusion: Our findings indicate that the some *Lactobacillus* species such as *L. crispatus*, *L. gasseri* and *L. iners* are present in all three trimesters but their relative abundance have significantly variation except *L. crispatus*. Few other non-lactobacillus bacterial taxa significantly vary in TB and PTB outcomes. Lactobacillus species encode protective elements to drive off other pathogenic microbes.

Key Message: Lactobacillus species is the most abundant taxa in vaginal microbiota. Their relative abundance vary in TB and PTB. Genomic composition of *Lactobacilli* have beneficial elements to maintain the healthy female reproductive tract.

ASSESSMENT OF EFFECTS OF A PROBIOTIC-BACILLUS CLAUSII UBBC07 IN INDIAN INFLAMMATORY BOWEL DISEASE (IBD) PATIENTS: A DOUBLE-BLIND RANDOMIZED PLACEBO CONTROLLED STUDY

Divya Pandey

D Pandey[1], V D Bamola[1], P Samanta[1], S Kedia[2], V Ahuja[2], R Chaudhry[1]*
[1] Department of Microbiology, [2]Department of Gastroenterology,
All India Institute of Medical Sciences, New Delhi, India

Graduated in B. tech (Biotechnology) from Amity University and M. Tech (Industrial Biotechnology) from DTU, Delhi. In 2017, I have joined the Department of Microbiology as researcher and working in the area of Probiotics and Gut microbiome.

ABSTRACT

Introduction: The effects of probiotics are strain specific and certain probiotics have shown efficacy in Gastrointestinal (GI) disease including inflammatory bowel disease (IBD). Etiology of IBD is multi-factorial which involves individual's genetics, ethnicity, lifestyle, immunity and gut microbiota. Alteration in the gut microbiota (dysbiosis) plays an important role in the pathogenesis of IBD. Probiotic intervention is evolving as an important approach for treatment and health restoration in GI disorders including IBD. This study was aimed to assess the effect of a probiotic-*Bacillus clausii* UBBC07 (MTCC 5260) in Indian IBD patients and therefore, a double blind, randomized placebo controlled study was conducted (Ref-CTRI/2019/11/022087).

Objective: To assess the effect of *Bacillus clausii* UBBC07 (MTCC 5260) in IBD patients.

Methods: A double blind, randomized placebo controlled study was conducted at All India Institute of Medical Sciences, New Delhi to assess the effect of Bacillus clausii UBBC07 in Indian IBD patients (18–60 years) under standard Medical treatment (SMT) with

Methods: A double blind, randomized placebo controlled study was conducted at All India Institute of Medical Sciences, New Delhi to assess the effect of Bacillus clausii UBBC07 in Indian IBD patients (18–60 years) under standard Medical treatment (SMT) with ethical approval from Institute Ethics Committee (Ref – IEC.478/07.10.2016.OP-7). After screening as per inclusion and exclusion criteria, 150 subjects were recruited in the study. The enrolled subjects were provided the trial drug and placebo as per blinding and randomization along with SMT. One probiotic capsule (CFU-2X10^9 per capsule) / placebo twice in day for the duration of 4 weeks were given to each enrolled subject. Survival of *B clausii* UBBC07 in GI of enrolled subjects, change in gut microbiota, clinical features, physical and psychological symptoms, cytokines and other biochemical parameters were assessed before and after intervention.

Results and Discussion: *B clausii* UBBC07 showed good survival in IBD patients without any reported adverse event. The probiotic treated group showed significant increase of beneficial *Lactobacilli* after intervention as compared to placebo group ($p < 0.001$).
B clausii UBBC07 showed potential to modulate the secretion of serum cytokines in IBD patients. Anti-inflammatory IL-10 was increased significantly ($p < 0.01$) and pro-inflammatory cytokines (IL-6, IL-1β, TNF- α, IL -17 and IL -23) were decreased variably in the probiotic treated group. B clausii UBBC07 was significantly able to decrease the severity of symptoms of IBD to various degrees in the treatment group. *B clausii* UBBC07 also showed the significant improvement in the psychological parameters of IBD patients to various degrees in the treatment group.

Conclusion and Key findings:

- *Bacillus clausii* UBBC07 was able to survive in the gut of IBD patients.
- *Bacillus clausii* UBBC07 was able to enhance the presence of beneficial Lactobacilli in IBD patients in the treatment group.
- *Bacillus clausii* UBBC07 was significantly able to reduce the severity of symptoms to various degrees and showed the significant improvement in the psychological parameter in IBD patients in the treatment group.
- The modulations of pro and anti-inflammatory cytokines were varied and significant in treatment group as compared to placebo group.
- *Bacillus clausii* UBBC07 have shown significant beneficial outcomes in IBD patients when administered along with SMT.

DEAD OR ALIVE? - 'SITAR', A FRAMEWORK FOR ONE-STEP ASSESSMENT OF TAXONOMIC ABUNDANCE AND VIABILITY OF GUT MICROBIOMES USING AMPLICON-SEQUENCING

Dr. Anirban Dutta

Authors: Anirban Dutta, Tungadri Bose, Nishal Kumar Pinna, Subhrajit Bhar, Sharmila S. Mande

Affiliation: TCS Research, Tata Consultancy Services Ltd., 54B Hadapsar Industrial Estate, Pune 411013, Maharashtra, India

Dr. Anirban Dutta is working as a Senior Scientist in Life Sciences R&D, TCS Research. A biotechnologist by training, he has over 10 years of experience in the field of bioinformatics and data-analytics. His primary research interests include metagenomics, biomarker discovery, modelling complex biological systems and management of â€˜omicsâ€™-scale data. Anirban has authored multiple scientific articles spanning the fields of genomics, metagenomics and systems-biology, and has filed over 40 patents as an inventor/co-inventor. He maintains a strong connect with academia through his teaching and research collaborations with many reputed universities, institutions and hospitals worldwide.

ABSTRACT

Introduction: Our understanding of gut-microbiomes is heavily reliant on NGS-technologies. Intriguingly, sequenced DNA can come from both live and dead bacteria (or those with contrasting growth-rates). This can confound our ability to derive correct taxonomic estimates of viable bacteria, and consequently make it difficult to gauge/predict their influence and interactions. Though longitudinal sampling can potentially overcome these concerns, it unfortunately entails additional costs.

Objectives: We aimed at designing a low-cost amplicon-sequencing framework/protocol (SITAR) to allow simultaneous investigation of taxonomic abundance and replication-rates in a microbiome.

Methods: Bacterial chromosomal-replication is characterized by bidirectional 'replication-forks' progressing from the origin of replication (ori). Consequently, sequencing an actively replicating bacteria would exhibit relatively higher read-coverage for genes located closer to 'ori'. Drawing inspiration from this phenomenon, SITAR protocol targets 16S rRNA (V4) and CPN60 (UT) genes for a 'duplex' amplicon-sequencing experiment. Post sequencing, the reads are mapped back to a pre-populated reference-database of locations (and copy-numbers) of the targeted taxonomic-markers, to derive taxonomic abundance estimates. Further, for every bacterial species/strain, read-coverage at 16S and CPN60 loci are fit into a piecewise-linear function, wherein the derived slope serves as a proxy-measure for replication-rate/viability.

Results: In-silico simulations of SITAR protocol, based on data from 82 deep-WGS experiments, show significant correlation between predicted and experimentally observed bacterial growth-rates across microbiome samples (Spearman $\rho = 0.55$; $p=6.52E-08$). Additional wet-lab validation and calibration experiments are underway.

Discussion: Simultaneous evaluation of bacterial population-diversity and population-dynamics can help decipher more meaningful health-microbiome associations (biomarkers) and enable easy monitoring of post-therapeutic effects (e.g. probiotic efficacy).

Conclusion: Besides taxonomic profiling, SITAR framework unlocks another relevant dimension of growth-rates, at no additional cost, and has the potential to become de-facto standard in amplicon-sequencing based microbiome studies.

Key Message: SITAR framework enables understanding both diversity and dynamics of microbiome populations from a single amplicon - sequencing experiment.

ASSESSMENT OF IMMUNOMODULATORY PROPERTIES OF INDIGENOUS *Lactobacillus acidophilus* AND ITS PEPTIDOGLYCAN AND SURFACE PROTEINS AGAINST *Salmonella Typhimurium*

Projoyita Samanta

Projoyita Samanta[1], V Deepak Bamola[1], Bimal K Das[1], Pawan Malhotra[2], Partho Chattopadaya[3], Rama Chaudhry[1]*

[1]Department of Microbiology, [3]Biochemistry, All India Institute of Medical Sciences, New Delhi, India. [2]ICGEB, New Delhi India
*Corresponding author-Prof. Rama Chaudhry (drramach@gmail.com)

Projoyita Samanta, currently working as a ICMR SRF in the department of Microbiology, AIIMS New Delhi. My main area of research is probiotics and gut microbiota.

ABSTRACT

Introduction: The concept of microbial intervention through probiotics in human body for health benefits has gained significant importance in recent times. Probiotics modifies the enteric microflora, suppress the overgrowth and translocation of pathogens in the gut and also enhances immune function. They are used to prevent and treat various gastrointestinal (GI) diseases. Various studies have reported that the population specific indigenous probiotics are more effective because of strain-specificity. Therefore, the probiotics should be well characterized for preventive and therapeutic application.

Aim & objectives: Evaluation of immuno-modulatory properties of indigenous *Lactobacillus acidophilus* (La5) (with good probiotic properties) and its surface components: peptidoglycan and cell surface proteins against S Typhimurium.

Methodology: Indigenous *Lactobacillus acidophilus* (La5) was isolated from healthy Indian gut after ethical clearance from Institute Ethics Committee of All India Institute of Medical Sciences (AIIMS), New Delhi (Reference - IECS/T-13401-04-2015). The isolation was performed using De Maan Rogosa and Sharpe (MRS) medium and identified by API 50CH and 16 S r RNA sequencing using universal primer and BLAST match. The strain was screened for various probiotic properties (Acid and Bile resistance, antagonistic properties, antibiotic resistance, and adherence to gastrointestinal (CaCo-2) cell lines). Surface components peptido-glycan and Cell surface proteins were Isolated from *Lactobacillus acidophilus* (La5) and characterized by Electron microscopy and FTIR (fourier transform infrared spectroscopy), LC-MS. *L acidophilus* (La5) and its surface components were evaluated for immuno-modulatory properties against S Typhimurium using Caco-2 cells. Various immuno-modulatory parameters evaluated were: surface IgA and IgG receptors by flowcytometry, relative expression of TLR2, TLR4, Pro-inflammatory cytokines (Il-8, IL17, IL23) and anti-inflammatory cytokine (IL10) by Real Time PCR (qRT-PCR).

Result & Discussion: Out of 5 *Lactobacillus acidophillus*, La 5 exhibited good probiotic properties and was the most potent immuno-modulatory strain against S Typhimurium. It increased the expression of IgA receptors, up-regulated the expression of TLR 2 and IL10 and down-regulated IL 8, IL17, IL23 expressions (p value < 0.01). The surface component (peptidoglycan) of La5 was chemically characterized by FTIR which showed the presence of C=o stretching, Amide I, Amide II, O-H, CH2 asymmetric band. The Peptidoglycan of L acidophilus (La5) exhibited good anti-inflammatory properties against S Typhimurium. Around 50 different Surface proteins were identified in cell surface extract of La5 which mainly includes moonlighting proteins. The surface proteins of La5 exhibited immunomodulatory properties in IEC (stimulated with S Typhimurium). Results demonstrated that the *Lactobacillus acidophilus* La1, down-regulated the pro-inflammatory cytokines and up-regulated the expression of anti-inflammatory cytokines in S Typhimurium induced IEC. *L acidophilus* (La5) exhibited significant (p value < 0.01) anti-inflammatory properties both as a whole and its purified components including peptidoglycan and surface proteins.

Conclusion and Key findings:

- Indigenous Lactobacilli *L acidophilus* (La5) exhibited good anti-inflammatory properties both as a whole and its purified components including peptidoglycan and surface proteins against S Typhimurium therefore can be used for therapeutic and preventive applications.
- La 5 can be used for future application in preventing dysbiosis and restoring and maintaining gastrointestinal homeostasis to prevent and treat the gastrointestinal anomalies caused by S typhimurium infections.

A GUT SIGNATURE FOR NON-ALCOHOLIC FATTY LIVER DISEASE IN THE INDIAN PATIENTS

Ayushi Purohit

Ayushi Purohit, Sanjay Banerjee, Bhabatosh Das

Translational Health Science and Technology Institute, NCR Biotech Science Cluster

The primary focus of my research is Non-alcoholic fatty liver disease (NAFLD) is a chronic metabolic disorder, which primarily affects the liver by inducing accumulation of extra fat. We are interested in the identification of proinflammatory microbial taxa Collinsella aerofaciens that are normal commensals in the gut and mouth but due to increased alpha diversity are acting as dysbiotic pathobionts. We are trying to correlate this genus to NASH progression. Preliminary data from our lab and previously published reports show the link between Collinsella and obesity. The pro-inflammatory dysbiotic commensal has been known to metabolize bile acids to oxo-bile acid intermediates that may contribute to increased intestinal permeability. The intestinal epithelial cells linked together through tight junctions underlying lamina propria are pivotal in maintaining intestinal immune homeostasis. Exploring some dominant microbial taxa from NASH patients by next-generation DNA sequencing will identify functions that may modulate inflammation and fatty acid accumulation. I am more fascinated by the work that you are currently investigating the efficacy of a novel microbiome to restore microbiota-mediated colonization in the gut. We can use MAM as a novel therapeutic target that increases the anti-inflammation cascade in the gut and restore the microbiota-mediated colonization resistance. Increasing the cascade of anti-inflammatory function in the gut can significantly inhibit intestinal permeability and decolonization of dysbiotic pathobionts that can curtail the levels of translocation of pro-inflammatory endotoxins, LPS, and other bacterial metabolites and evaluate the levels of anti-inflammatory endotoxins, LPS, and metabolites that can restore gut mucosal barrier (â€œleaky gutâ€) via the gutâ€“liver axis probably playing a decisive role in the pathogenesis of liver diseases can be an attractive therapeutic avenue for the development of a novel treatment for NASH.

ABSTRACT

Introduction: The human gastrointestinal tract (GIT) harbors a complex microbial ecosystem with more than 700 bacterial species or phylotypes in each individual. The composition of the microbial species in the GIT ecosystem varies among individuals and throughout development depending on various factors. Both environmental factors as well as host genetics influence the homeostasis and composition of GIT microbiome. A plethora of conditions, from obesity to anxiety, appear to be linked to the microbes inside us. Several factors can affect the homeostatic equilibrium of GIT microbiome and lead to dysbiotic microbiome configuration. Taxonomic and functional dysbiosis in the GIT microbiome is associated with numerous health disorders like non-alcoholic fatty liver disease NAFLD. In the present study, we investigate the composition and functions of gut microbiota of Indian subjects with or without NAFLD.

Aim: Identification of gut microbial signature in the Indian NAFLD patients.

Objectives:

- Identify bacterial taxa associated with NAFLD.
- Decipher the whole genome sequences of bacterial taxa associated with NAFLD.
- Functional evaluation of the anti- pro-inflammatory signature encoded by the pathobiont in the prognosis of disease.

Methods: (i) Community microbial genomic DNA was extracted from the fecal samples of subjects by THSTI method. 16S rRNA genes (V1-V5) region was amplified using 0.1 ng of template DNA specific primers. (ii) C. aerofaciens strain indica was isolated from a fecal sample of NASH patients (iii) Whole genome of C. aerofaciens was sequenced and analyzed to identify potential inflammatory functions.

Result: We have identified 2.30-Mb genome sequence of C. aerofaciens with 60.1% GC content. The genome has 276 subsystems and is enriched with protein 135 ORFs, carbohydrate 120 ORFs, and vitamin 102 ORFs metabolic functions. However, the C. aerofaciens genome has 29 genes are detected for the subcategory of virulence, pathogenicity, and disease development.

Discussion: Recent studies have reported changes in the microbiota in the gut of NAFLD patients compared to the healthy subjects.

Conclusion: The current study, for the first time, reported significant association between Collinsella abundance in the metabolic health in overweight and obese people, which may be affected by dietary fiber intake.

Key Message: The insights from the current findings will help us to understand the importance of Collinsella in health and disease.

FUT GENOTYPES, SECRETOR STATUS, H.PYLORI ANTIBODY LEVELS AND VITAMIN-B12 CONCENTRATIONS IN INDIANS

Krishna Kishore Sukla

Sukla KK[1], Kunte PS[1], Kamat R[1], Raut D[1], Bhat DS[1], Dedaniya A[3], Chaphekar A[2], Chandak GR[3], Yajnik CS[1]

I am a postdoctoral researcher working in the domain of nutrigenomics. Multi-omic (genomic, metabolomic, transcriptomic, epigenetic, and metagenomic) approach is currently employed in my research to understand the impact of one-Carbon metabolites on chronic disease susceptibility and general health in PMNS cohort.

ABSTRACT

Background: The FUT2 gene is responsible for the secretion of ABO blood type antigens into the body fluids (saliva, mucous, urine, tears, breast milk, sweat, and semen). Those who secrete the antigens into body fluids are call secretors, those who do not are called non-secretors. Circulating Vitamin-B12 concentrations are governed by diet, genotype and gut microbiome.

Hypothesis: GWAS studies have reported FUT gene variants to be associated with circulating vitamin-B12 concentrations. Missense mutations in FUT2 gene results in non-secretor phenotype. Thus, secretory status of an individual may effect circulating vitamin-B12 concentrations over and above the genotype.

Materials and Methods: We included 780 participants (271 children, 282 mothers and 227 fathers) from Pune Maternal Nutrition Study (PMNS). We measured secretor status of individuals in saliva by hemagglutination test. A total of eight genetic variants including six SNPs from FUT2 gene (rs492602, rs681343, rs281377, rs601338, rs1800027 and rs602662) and two SNPs from FUT6 gene (rs3760776 and rs3760775) from our previous GWAS study were correlated with circulating vitamin-B12 levels. We tested the associations of FUT gene variants with secretors status phenotype, and of the secretors phenotype with circulating vit-B12, folate and ferritin concentrations in addition to H.pylori antibody levels.

Results and Discussion: We found 33% of participants were non-secretors compared to 20 % reported in Western Caucasian populations. Non-secretors had higher vitamin-B12 concentrations but not of folate and ferritin, vitamin-B12 associations were over and above FUT genotypes. Non-secretors showed higher response to vit-B12 supplementation. We found a FUT2 haplotype () to be strongly associated with vit-B12 concentrations and non-secretor status. Non-secretors had lower H.pylori antibody concentrations. FUT6 genotype and haplotype was associated with vit-B12 concentrations but not with secretor status and H.pylori antibody levels.
Our data suggests that secretor status may influence vit-B12 concentrations though susceptibility to H.pylori infection and possibly through other gut microbiota. The association of gut microbiome (metagenomics) with secretor status vis-à-vis circulating vitamin-B12 concentrations is in progress. Higher frequency of non-secretors in Indians could offer a selective advantage against vit-B12 deficiency.

MULTI-OMIC ANALYSIS TO EXPLORE THE MICROBIAL AND METABOLITE DIVERSITY OF DAHI (TRADITIONAL INDIAN FERMENTED MILK PRODUCT)

Rashmi H M

Rashmi Hogarehalli Mallappa, Amrita Tigga, , E. Shree Niharika, Santhosh Kumar Muniyappa Chandrasekhar B, Saurabh Kadyan, Diwas Pradhan and Sunita Grover

***Molecular Biology Unit, Dairy Microbiology Division, ICAR-National Dairy Research Institute, Karnal-132001, Haryana, India.**

I am working in the area of probiotics and gut microbiota from past 10 year. During this period, myself explored the potential of indigenous probiotic strains spanning isolation, identification (16S based & Whole genome), strain typing (MLST), characterization (for probiotic and health attributes in in vitro and in vivo models), deposition and maintenance of the repository of probiotic strains (~100), transfer of technologies related to probiotic strains besides working in several externally funded projects (Development traditional probiotic fermented milk products (MoFPI), screening probiotics for GLP-1 secretion ability (ICMR), against Persistent Diarrhea (ICMR), and currently working with AIIMS (ICMR project) to study efficacy of oral probiotics supplementation in children with Autism Spectrum disorders (ASDs). In addition, I investigated the gut microbial diversity of North and North-East Indian population under DBT project besides studying the gut microbial dysbiosis in malnourished children.

ABSTRACT

High-Throughput Integrative Omics approach is widely used to study the microbiome (composition) and metabolome (function) of various econiches including gut. This Multi– Omics approach has been employed in the present investigation to study the bacterial and metabolite profile of traditional Indian fermented milk product "*Dahi*" prepared by traditional back slopping method in Haryana region of India. Bacterial profile was explored with the employment of metagenomics (16S Amplicon sequencing using Oxford Nanopore technology platform) and culturomics (70 culturomics conditions using ten different media, three different atmospheric conditions and different temperatures) approaches. Metaboloimc profile was determined by the GS-MS analysis of the derivatized metabolites extracted from Dahi samples. In metagenomics study, the total DNA from 12 individual samples of Dahi were extracted, pooled (4:1), amplicon sequenced and analysed for bacterial taxonomy, The bacterial taxonomics clearly indicated Firmicutes as the major phyla (88.32–92.48% abundance) followed by Proteobacteria (1.37-5.38%). Further analysis revealed Streptococcus, *Lactobacillus, Bacillus, Enterococcus, Lactococcus, Staphylococcus, Pseudomonas, Oscillospira, Cupriavidus, Bacteroides, Clostridium, Serratia* and *Prevotella* as the major bacterial genera of Dahi samples. Through initial culturomics study, 18 culture conditions were selected based on the maximum growth of *Dahi* bacteria and were subsequently isolated for identification using Polyphasic taxonomy. Dahi samples were found to have majority of bacteria that belonged to Lactococcus lactis group (34.14%), followed by *Lactobacillus delbrueckii* (19.5%), *Streptococcus thermophillus* (17%), *Leuconostocspecies* (7.31%), *Staphylococcus species* (7.3%), *Macrococcus caseolyticus* (4.87%), *Bacillus subtilis* (4.8%) and *Enterococcus* strains (2.4%). On comparing metagenomics and culturomics data, we find quite similarities in both data sets, as in both approaches *Firmcutes*, most of which have gram-positive cell wall structure appeared as major phyla. *Lactobacillus delbrueckii* that emerged as the major species (19-26%) in metagenomics was also found to be present at 19.5% in culturomics study. Besides *Streptococcus thermophillus* and *Lactococcus lactis* also emerged as other major Dahi lactic acid bacteria whereas *Staphylococcus, Bacillus, Macrococcus* and *Enterococcus* were observed as environmental contaminants in both approaches.

In metabolomics, the compounds identified in the traditionally fermented Dahi samples comprised largely of amino acids (7), fatty acids and lipids (14), carbohydrates and sugars (17) and 25 compounds related to or part of intermediary metabolism. The most important metabolites which included Valine, Oxoproline, Alanine, Glycine, Linoelaidic acid, Butyric acid, Oleic acid, Caprylic acid, GABA (Gamma Aminobutyric Acid) lactic acid / gluconic acid and glutamic acid that can provide health benefits.

From the data that emerged out the study, it is quite clear that, both metagenomics and culturomics are highly complementary approaches and can push forward the field of microbiota research in the field of tranditional fermented milk products. The application of metabolomics can determine the functionality and uniqueness of traditional fermented milk products. However, substantial improvements need to be made by using the metagenomic data to improve the efficiency of culture methods by having more supplements which may enhance metagenomics efficiency and metabolomics studies needs to be conducted on large sample size and validated to yield more meaningful insights.

INSIGHTS INTO THE GENOME OF LACTOBACILLUS SPECIES FOR DEVELOPING INDIGENOUS PROBIOTIC FOR FEMALE REPRODUCTIVE HEALTH

Dr. Jyoti Verma

Jyoti Verma, Shakti Kumar, Daizee Talukdar, Akansha Kothidar, Bhabatosh Das

Translational Health Science and Technology Institute, NCR Biotech Science Cluster, 3rd Milestone, Faridabad—Gurgaon Expressway, PO Box #04, Faridabad, Haryana 121001, India

Dr. Jyoti Verma is actively engaged in the study of vaginal microbiome of Indian women and their potential role in the birth outcomes. She carried out her PhD under the supervision of Dr. Bhabatosh Das at Translational Health Science & Technology Institute. Her doctoral research work involved to have molecular insights into the antibiotic resistance traits of enteric pathogens and to re-sensitize the multidrug-resistant enteric pathogens against commonly used antibiotics. She has been awarded the Young Investigator Award at the 9th and 10th India Probiotic Symposium, 2018 (IIIrd prize) and 2020 (Ist prize) respectively.

ABSTRACT

Introduction: *Lactobacillus* species are the dominant inhabitants of the lower reproductive tract of healthy women. They maintain a lower vaginal pH (<=4.5) and protect against sexually transmitted infections. However, dysbiosis may lead to bacterial vaginosis, marked by higher pH, inflammation and vaginal discharge. The dysbiosis may have some adverse impacts and have been implicated to result in adverse pregnancy outcomes such as Pre Term Birth (PTB). PTB is one of the leading health challenges that are responsible for 40% of neonatal deaths annually in the developed as well as in the developing countries. Developments of various interventions such as probiotics that include *Lactobacilli* have been investigated to improve the adult female reproductive health. The findings from our group depict higher abundance of *L. crispatus* and *L. gasseri* in the vaginal microbiota of Indian pregnant women who gave term birth. However, their abundance was lower in case of PTB. Hence, in the pursuit of candidate probiotic we explored the genome of *L. crispatus* (n= 10) and *L. gasseri* (n= 10) isolated from the vaginal swabs of pregnant Indian women.

Objectives: (i) Isolation of *Lactobacillus* species from the vaginal swabs of pregnant Indian women. (ii) Analysis of the genome of *Lactobacillus* species. (iii) To study the abundance and linkage of antibiotic resistance genes (ARGs) with various mobile genetic elements (MGEs).

Methods: (i) 50 µl of Amies transport medium with the swab samples were used to isolate discrete colonies onto a de Man-Rogosa-Sharpe (MRS) agar plate incubated in an anaerobic workstation (Whitley A95TG, UK) at 37°C for 48 hrs. (ii) Distinct colonies that appeared were picked up and grown in MRS broth under anaerobic growth conditions at 37°C for 48 hrs and were subjected to genomic DNA extraction and phylogenetic identity analysis by16S rRNA gene sequencing. (iii) Whole genome sequencing was done using a high-throughput Illumina MiSeq sequencing platform. (iv) FastQC and Trimmomatic programs were used to review the quality of raw reads and remove adapter sequences and low quality reads followed by genome assembly using Unicycler pipeline. (v) After assembly Rapid Annotation Subsystem Technology (RAST) was used for annotation. (vi) To investigate the ARGs in the genome of Lactobacillus species, the ORFs were compared with the already catalogued ARGs available in the publically PATRIC 3.6.5 and CARD database (Comprehensive Antibiotic Resistance Database).

Results: The genome of *Lactobacillus* is enriched with horizontally acquired fitness traits including bacteriocins, CRISPR-Cas system, metabolic functions, metal and antibiotic resistance. The strains were found to harbor fewer antibiotic resistance genes and their linkage was not observed with any MGEs.

Discussion: The area of vaginal health and its associated microbiome with respect to Indian context has limited studies on probiotics for female reproductive health. Thus, there is an unmet need for the development of well-designed probiotics for reproductive health. The ideal strain for the probiotic should not be carrying ARGs to prevent their dissemination to other microbes in its vicinity. In this study, we analyzed the genome of vaginal *Lactobacillus* strains in pursuit of a potential probiotic. Based on the genomics, the candidate probiotic strain need further in-vitro and in-vivo validation.

Conclusion: This study has an important translational value for the selection and development of potential probiotic for vaginal health as well as an intervention to prevent PTB. It is important to understand the genetic repertoires involved in fitness, antimicrobial, antiviral and immunomodulatory functions of the candidate probiotic strains.

Key Message: Exploring the genome of Lactobacillus species will assuredly pave the way further for the development of candidate probiotic.

REGARDLESS OF THE NATURE OF EXOGENOUS ASSAULT, LOWERING OF GUT MICROBIAL BUTYRATE DECLINES RNA BINDING PROTEIN AUF1 TO INDUCE HYPERCHOLESTEROLEMIA

Moumita Bhaumik

Authors: Oishika Das, Debmalya Mitra, Rahul Gajbhiye, **Moumita Bhaumik**

Affiliation: ICMR-National Institute of Cholera and Enteric Diseases, Kolkata

Email: *drmoumitabhaumik@gmail.com*

Moumita Bhaumik, is a Scientist in ICMR-National Institute of Cholera and Enteric Diseases, Kolkata. After completing her PhD from CSIR-IICB, she joined ICMR-NICED as a Scientist C in 2017. Her research interest is to study the â€œcomplex rulesâ€ by which gut microbiome or microbial metabolites regulate the host physiology. Her group focuses on how gut microbial products link to disease profile and therapy outcome in multiple non-infectious diseases that originate from gut.

ABSTRACT

Introduction: Growing evidences highlight the effect of butyrate, one of the SCFA on hepatic cholesterol biosynthesis, the mechanism of which is still not clear.

Objective: The aim of this investigation is to gain information on the mechanistic molecular details of butyrate mediated cholesterol balance in murine models of HFD induced obesity, antibiotic induced gut dysbiosis as a surrogate of germ-free mice and DSS induced colitis.

Methods: We exploited high fat diet (HFD) induced obesity model in mice to understand the comprehensive role of butyrate in cholesterol regulation. We explored the three domains of cholesterol homeostasis- cholesterol synthesis, catabolism and efflux. We examined the effect of butyrate by measuring status of serum cholesterol, fat droplet formation and gene expression of cholesterol metabolising enzymes in mice liver. To get into the mechanistic details of butyrate action on cholesterol homeostasis, we undertook studies with Huh7 cells. Finally the molecular link of butyrate mediated cholesterol regulation was validated in three independent mice models i) HFD-induced obesity ii) prolonged antibiotic treatment and ii) DSS induced colitis.

Results and Discussion: We report butyrate causes reduction in serum cholesterol with decrease in hepatic fat droplets and gene expression of enzymes related to cholesterol synthesis in HFD fed mice. Furthermore, butyrate treatment increases hepatic gene expression of cholesterol catabolising enzyme and efflux proteins in HFD fed mice. Upon dissection of molecular pathway in Huh7 cells we show that butyrate modulates selective isoforms of RNA binding protein AUF1leading to down-regulation of Dicer1, miR122 and resulting in down-regulation of cholesterol. We also show that in HFD, antibiotics and colitis mice the lowering of fecal butyrate can be linked with hyper-cholesterolemia mediated through a tentative axis “butyrate-AUF1-Dicer1-miR122-cholesterol”.

Conclusion: The study lies on a new sphere of understanding the molecular details of butyrate mediated cholesterol metabolism in variety of intestinal pathology.

Key message: Our study proposes a paradigm of common axis of butyrate-AUF1-Dicer1-miR122-cholesterol resulting in other pathological effects.

IN SILICO ANALYSIS OF METABOLIC FUNCTIONAL CAPABILITIES OF GUT MICROBIOTA AND ITS IMPLICATION(S) IN HEALTH AND DISEASE

Harrisham Kaur

Harrisham Kaur is a bioinformatics scientist currently working with Bio-Sciences R&D unit of TCS research. She has an extensive experience in NGS data analysis, 'omics' (genomics/metagenomics/metatranscriptomics) data analysis, microbiome research, machine learning and bio-marker discovery. Her current research interests focus to understand the interplay of gut microbial communities with host health and well-being. With seven plus years of industrial experience in discovering simple, smart and effective microbiome solutions for disease-diagnostics, therapy and other industrial applications, Harrisham has a strong aptitude for research and innovation. Her scientific portfolio is excellent and her research caliber is backed by peer-reviewed publications and patents.

ABSTRACT

Introduction: Trillions of microbes inhabiting the gut (gut microbiota) contribute significantly towards host health. An imbalance in their composition is associated with various metabolic/gut-associated disorders. Recent studies reveal that compositional changes in gut microbiota are markers/signatures of physiological changes occurring under disease conditions. However, the utility of compositional biomarkers is limited by inter-individual variations (diet/age/geographical factors).

Objectives: The present study addresses the above-mentioned limitations by analyzing/utilizing the metabolic functions of gut microbiota which often remain similar despite taxonomic differences. The study evaluates specific functional capabilities as potential biomarkers for gut-health assessment/improvement.

Methods: Systematic literature mining was used to shortlist the beneficial and damaging metabolic roles/pathways of gut microbes. Further, ~8000 gut bacterial genomes were investigated for presence/absence of these metabolic pathways. A 'gut-genome-pathway' matrix was collated, and gut-health assessment scheme was devised. Publicly available gut microbiota datasets were evaluated for distribution of metabolic pathways in healthy and disease states.

Results: The results show differential enrichment of metabolic pathways in gut commensals and pathogens. While commensals harbour the beneficial butyrate-production pathways, the pathogens have only harmful ammonia-releasing pathways. Further, gut commensals and pathogens are observed to utilize different pathways to produce the same metabolite. This emphasizes the significance of pathway evaluation. Additionally, the proposed scheme (validated on publicly available case/control gut microbiota datasets) could predict gut-health status >95% accuracy.

Discussion: The identified function-based biomarkers are robust and diet/age/geography agnostic. These can be utilized for non-invasive screening/diagnosis of gut-associated diseases and for design of personalized therapeutic regimes. Further, the method can help evaluate the treatment efficiency (e.g., pre-/pro-biotic treatment, etc.) for gut-related diseases.

Conclusion: The insights from the study can be utilized for gut-health screening and management.

Key Message: The gut-health assessment utilizing function-based biomarkers serves as a promising non-invasive, health monitoring and risk evaluation method for gut-associated and other metabolic diseases.

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MODULATION OF HIGH FAT DIET INDUCED METABOLIC COMPLICATIONS BY NOVEL SYNBIOTIC (LACTOBACILLUS PENTOSUS GSSK2 + ISOMALTO-OLIGOSACCHARIDES) IN SPRAGUE DAWLEY RATS

Sakshi Khanna

Sakshi Khanna[1], Kanthi Kiran Kondepudi[2], Geeta Shukla[1]*
Email: khannasakshi1507@gmail.com

[1]Department of Microbiology, Panjab University, Chandigarh, India
[2]National Agri-food Biotechnology Institute (NABI), S.A.S. Nagar, Punjab, India

Sakshi Khanna has completed her M.Sc. Microbial Biotechnology, from Panjab University, Chandigarh with distinction and gold medal. She has qualified UGC NET, ARS-NET, GATE and ICMR-JRF exams. Presently, she is pursuing PhD under the supervision of Professor Geeta Shukla (Department of Microbiology, Punjab University) and Dr. Kanthi Kiran Kondepudi (National Agri-food Biotechnology Institute). She is working for her Ph.D. on isolation, characterization and evaluation of probiotics for the management of metabolic syndrome.

ABSTRACT

Introduction: Metabolic syndrome, a lifestyle disease, where diet and gut microbiota play a prodigious role in its initiation and progression. As both diet and gut microbiota can be modulated, therefore employing probiotics and prebiotics as prophylactic bio-interventions may offer an alternate nutritional approach to attenuate the progression of metabolic syndrome.
Objective: The study aimed to evaluate the protective potential of synbiotic (*L. pentosus* GSSK2 + IMOs) in comparison with commonly used antiobesity drug, orlistat, in experimental metabolic syndrome.

Methods: Male SD rats were divided into nine groups (n=6/ group) i.e. Control (fed with standard pellet diet, 6% calories as fat), HFD (fed with HFD, 60% calories as fat), L. pentosus GSSK2, *L. pentosus* GSSK2 + HFD, IMOs, IMOs + HFD, Synbiotic, Synbiotic + HFD and Orlistat + HFD. All the groups were administered with respective treatments for 12 weeks following which systemic adiposity, blood glucose level, serum lipid profile, liver function tests, fecal lactobacilli count, gut bacterial abundance, gene expression and histological alterations in liver, adipose tissue and colon were studied.

Results: It was observed that supplementation of synbiotic for 12 weeks to SD rats fed with HFD, ameliorated the anthropometric parameters, visceral fat deposition, increased lactic acid bacteria count, lipid excretion in feces and Bacteroidetes to Firmicutes ratio, elevated population of *Lactobacillus spp*., *Akkermansia spp*., *Faecalibacterium spp*., *Roseburia spp*. and reduced the Enterobacteriaceae. Additionally, synbiotic administration to HFD animals led to improved glucose tolerance, lipid biomarkers and alleviated oxidative stress, serum lipopolysaccharides, modulated the inflammatory (TNF-α, IL-6), lipid (FASN, HSL) and glucose (GLUT-4, glucokinase) metabolism genes along with restored histomorphology of liver, adipose tissue and colon compared with HFD animals.

Conclusion and key message: It is proposed that such novel synbiotic intervention may be employed for combating the growing incidence of metabolic syndrome that could be considered as a promising and alternative prophylactic live bacteriotherapy for maintaining the immune- metabolic homeostasis.

GENOMICS AND PHYSIOLOGICAL SIGNATURES FROM ALPHA-AMYLASE INHIBITOR PRODUCING *Lactobacillus sp.* FROM HOME-MADE *DAHI*

Ranjan Kaushal Tirwa

Ranjan Kaushal Tirwa[1], Buddhiman Tamang[1], Mangesh Suryavanshi[2],

[1]Department of Microbiology, Sikkim University, Tadong - Gangtok, Sikkim 737102
[2]Yenepoya Research Centre, Yenepoya Deemed to be University, Mangalore 575018

Presenting Author Email: rtirwa8@gmail.com

I am a Research Scholar in the Dept of Microbiology, Sikkim University. I have submitted my thesis Entitled 'Isolation and Characterization of Lactic acid Bacteria having alpha-amylase inhibitor activity. Currently, I am serving at Sikkim Professional University as Assitant Professor in the Arts and Science College.

ABSTRACT

Background/Aims: Rising additional burden in diabetes by 'Postprandial Hyperglycemia (PPG)' is alarming; this disorder perpetuates blood glucose levels immediate after the food intake. Amongst all, Inhibitors of α-amylase, enzymes responsible for carbohydrate digestion, have emerged as the molecules of choice due to their unambiguous and unique mechanism of action on PPG. Some of inhibitors from microbial origin had been the alternate biological treatment and, inhibitors are mostly reported from species of *Streptomyces* and *Lactobacillus* among bacteria. To maintain the homeostasis, gut microbes can be effective solutions though these researches are still naive and elusive. We aimed to explore the metabolic possibilities of GRAS bacteria, *Lactobacillus* isolates for the alpha-amylase inhibitory roles.

Objectives: Deducing the phenotypic expression for alpha-amylase inhibitory activity and genomic characterisation of *Lactobacillus* sp. from home-made *Dahi.*

Methods: Primary screening was done on 332 LAB isolates for AAI activity as described by Feng et al. with some modifications. Screened, total 07 LAB isolates were utilized for secondary screening to facilitate the production of α-amylase inhibitor quantitatively and followed with stability studies. Amongst other, selectively 02 *Lactobacillus* sp. i.e. DMR09 and DMR17 isolates were exploited well for additional probiotic traits and genomic characterization through Whole Genome Sequencing.

Results: Seven isolates were found to produce α-amylase inhibitory activity; the inhibitory percentage was similar to that of acarbose and copper sulfate was used as control. Phenotypic analysis, DMR09 (90.1 ± 2.8%) and DMR17 (83.8 ± 1.8%) had the highest inhibitory activities. These two has been characterizing well with probiotic traits and metabolic capacities have been evaluated through the WGS. And, proposal of potential probiotic candidate chart has been explored along with median protein count: 2926.

Discussion and Conclusion: Essentially, prevention of the onset of diabetes and for an excessive rise in blood glucose in diabetic individuals, control of PPG is gaining much importance. The *Lactobacillus* spp. was able to produce amylase inhibitors and, had the potential to adhere to the hydrocarbons indicating their potential to attach to the intestinal epithelium. None of the isolates was hemolytic and neither could hydrolyze gelatin. Being able to resist the oro-gastric-intestinal environment, isolates showed the ability to cope with the harsh environment of the GI tract and genotypic signatures for probiotic genes were recorded. Therefore, these isolates can be the potential probiotic candidate which can be used in the control of PPG and the management of diabetes.

Key message: Metabolic potentials of GRAS bacteria, *Lactobacillus* sp. might involved in circulatory glucose homeostasis.

Keywords: Diabetes, α-amylase inhibitor, Probiotic, *Lactobacillus*

PROSPECTS OF PROBIOTIC LACTOBACILLI IN GUT-BRAIN AXIS FOR AMELIORATION OF LEAD INDUCED NEUROTOXICITY IN RAT MODEL

Hemlata Singh

Hemlata Singh[1] and Chand Ram[2]
[1] Ph.D. Scholar; [2] Principal Scientist
Synbiotic Functional Food and Bioremediation Laboratory, Dairy Microbiology Division,
ICAR-National Dairy Research Institute (Deemed University), Karnal – 132001 Haryana, India
Email: hemlatasingh0591@gmail.com

Ph.D. Scholar Synbiotic Functional Food and Bioremediation Laboratory, Dairy Microbiology Division, ICAR-National Dairy Research Institute.

ABSTRACT

The emergence of gut brain axis has fascinated the world to envision the gut as a second brain of human body. Lead, a common food contaminant can cross the blood brain barrier leading to neurotoxicity, particularly in children. Based on this approach, the current research was designed to evaluate the mechanism of probiotic bacteria for ameliorating lead induced neurotoxicity in rat model due to its metal binding potential.

Objectives:

- Screening of probiotic lactobacilli strains for lead bioadsorption.
- Evaluation of selected probiotic strain against lead induced neurotoxicity in rat model.

Methods: Lead bioadsorption potential of lactobacilli strains were analyzed by Atomic Adsorption Spectrophotometer (AAS). Further in-vitro digestion of the selected probiotic lactobacilli strain for lead-bioaccessibility reduction potential was carried out. ELISA was used to evaluate the biomarkers of neurotoxicity in the brain, i.e., glutamate, GABA, dopamine and serotonin, as well as oxidative stress biomarkers, i.e., plasma corticosterone. In addition, microbial fecal counts have also been carried out.

Results & Discussion: Based on *in-vitro* evaluation the probiotic *Lactobacillus plantarum* HD-51 was selected for ameliorating lead induced neurotoxicity in-vivo as a preventive approach. Rats fed with lead acetate showed a decrease in GABA, dopamine and serotonin level and an increase in glutamate level compared to *L. plantarum* HD-51 fed group. Similarly, the plasma corticosterone levels were higher in lead fed group compared with *L. plantarum* HD-51 fed group. The coliform and E. coli count was higher in lead fed group compared to L. plantarum HD-51 fed group.

Conclusion & way forward: Probiotic *Lactobacillus plantarum* HD-51 has been proved to be a potent lead adsorbent, helping in sustaining neurotransmitters level, reducing oxidative stress and restoring gut balance. In neurodegenerative disorders such as Depression, Autism and Parkinson's disease, such probiotic strains can be used as supportive therapy to advance our way of understanding the role of probiotics in the brain beyond our imagination.

COMPARATIVE METAGENOME ANALYSIS OF TRADITIONAL DAHI VS INDUSTRIAL CURD

Shruti Nayyar

[1]**S. Nayyar**, [2]Hirak J Chakraborty, [1]S. Kadyan, [1]Rashmi HM, [1]S. Grover, [1]D. Pradhan
[1]ICAR-National Dairy Research Institute, Karnal, Haryana, India
[2]ICAR-Central Inland Fisheries Research Institute, Barrackpore, West Bengal, India

Shruti had done B.Tech in Dairy Technology afterwards completed her M.Tech in Dairy Microbiology from National Dairy Research Institute, Karnal. She participated in various poster competition and have been selected for Bill and Melinda Gates Foundation, lower middle income grant for complimentary Registration to attend the ASM Conference on Rapid Applied Microbial Next Generation Sequencing and Bioinformatics pipelines and received participation certificate for e poster presentation.

ABSTRACT

Introduction: *Dahi,* a top dietary source of live microorganisms, is traditionally prepared by backslopping due to which its microflora is highly diverse. The number of microorganisms in *Dahi* can differ significantly depending on the enviroment and hygeine levels. Hence, a comparative Dahi-metagenome analysis can shed light on its underlying community dynamics in relation to human health care.

Objectives: Comparative assessment of the microbial community of traditionally and industrially manufactured Dahi and their antibiotic resistome was carried out using shotgun metagenomic approach.

Methods: 4 pools of Metagenome samples comprising of traditional *Dahi* (sample A & B) and industrial Dahi (Sample C- local & D- multinational companies). Good quality DNA library was sequenced using Illumina HiSeq platform. *De novo* assembly followed by Taxonomic binning of Illumina paired end reads were performed using metaSPAdes assembler, after which the filtered contigs were annotated for gene prediction and antibiotic resistome detection using MetaGeneMark tool and CARD database, respectively.

Results & Discussion: Total contigs generated after *de novo* assembly of sample A, B, C and D were 156492, 99815, 125111 and 208113, respectively. Analysis of microbial taxonomy revealed that Proteobacteria then Terrabacteria group was two most dominating phylum in sample A and B, whereas Firmicutes were the prominent microbial phylum in the industrial samples. Species level classification exposed high levels of oppurtunistic pathogens in samples A, B and D, at the same time sample C contained majorly lactic microflora. Eukaryotes of filamentous fungi group and bacteriophages (Caudovirales) were also detected in all samples. Analysis of antibiotic resistome revealed a total of 35, 35, 36 and 226 numbers of ARGs against 15 drug classes in samples A and B, C and D, respectively. Abundance analysis revealed resistance-nodulation-cell division antibiotic efflux pump and beta-lactam resistance genes were highly abundant in the Dahi samples. As high as 43 different metabolic functional pathways that belonged to biosynthesis, metabolism, degradation etc. were also detected in traditonal *Dahi*, the diversity of which was sufficeintly low in industrial *Dahi.*

Conclusion: Dahi is a rich source of essential nutrients and diverse microflora, however, metagenomic analysis shows it also carry a large number of pathogens and ARGs.

Key Messages: Traditional Dahi prepared in hygeinic environment is a great source of diverse live microorganisms.

CHARACTERIZATION AND PRODUCTION OF NOVEL ACE-INHIBITORY BIOACTIVE PEPTIDES DERIVED FROM FERMENTED GOAT MILK USING POTENT LACTOBACILLUS CULTURES

Heena Parmar

Heena Parmar*, Subrota Hati, Amar A. Sakure and J B Prajapati
Dept. Dairy Microbiology, Anand Agricultural University, Anand-388110, Gujarat, India

***Corresponding author:** heenaparmar18@gmail.com

PhD student, Dept., Dairy Microbiology, SMC College of Dairy Science, Anand Agricultural University, Gujarat, India

ABSTRACT

Introduction: Goat milk is popular for its beneficial attributes on the human beings. Lactic Acid Bacteria (LAB) is an important friendly bacteria exist in all the fermented milk products. Fermented goat milk has multiple therapeutic and nutritional effects. Goat milk has lot of health benefits like antihypertensive, antioxidant and antimicrobial activity. But there is scanty information on ACE-inhibitory activity of fermented Surti goat milk (Indian breed).

Objective:

- To evaluate the proteolytic activity, di and tripeptidase activity and ACE-inhibitory activity of lactobacillus cultures.
- To optimise the growth conditions for the production of peptides.
- To determine the relative proteolytic activity of lactobacillus cultures.
- To purify and separate the novel ACE-inhibitory peptides from fermented goat milk.

Material and Methods: The LAB cultures used in the study i.e. *Lactobacillus casei* (KR732325) (NK9) and *Lactobacillus fermentum* (TDS030603) (MTCC 25067) (LF) were obtained from the Culture Collection of Dairy Microbiology Department, SMC College of Dairy Science, Anand, India. The proteolytic activity of the selected Lactobacillus cultures was expressed as the absorbance of free amino groups measured at 340 nm. The peptide content was expressed as mg/ml. Di and Tipeptidase activity was also determined (Donkor et al. 2007). Growth conditions (i.e., inoculation rate and incubation periods) for the production of peptides were optimized according to o-phthaldialdehyde (OPA) method (Donkor et al. 2007). ACE-inhibitory was determined according to Hati et al. (2015) and Solanki et al. (2017). Relative proteolytic activity was carried out following Vasiljevic and Jelen (2002). Identification and Characterization of Purified ACE-Inhibitory Peptides Derived from Fermented Goat Milk through RPLC/MS analysis (Solanki et al. 2017).

Result and Discussion: In the study, two *Lactobacillus* cultures i.e. *L. casei* (NK9) and *L. fermentum* (LF) were studied for their proteolytic activity, di and tripeptidase activity, ACE-inhibitory activity and peptides production under optimized growth condition from fermented goat milk (*Capra aegagrus hircus*). NK9 and LF were found to be a strong proteolytic culture with 2.0% rate of inoculation after 48 h. LF (10 kDa retentate) produced maximum peptides among all the retentates of the fermented goat milk. Goat milk fermented with NK9 (10 kDa permeates) exhibited peptide sequence i.e. AFPEHK which had ACE inhibitory activity, matched with goat milk protein databases of AHTPDB. Goat milk fermented with NK9 (3 kDa permeate) showed peptides sequence DERFFDDK. This peptide sequence derived from CASK_CAPHI Kappa-casein which has encrypted the hypertensive peptides (DERF, RFF and FFD). However, *L. casei* (NK9) and *L. fermentum* (LF) could be explored for the production of ACE inhibitory peptides from fermented goat milk.

Conclusion: Fermented goat milks with two selected *Lactobacillus* cultures i.e. NK9 (*L. casei*) and LF *(L. fermentum*) with 2% rate of inoculation were used for production, purification and characterization of ACE-inhibitory peptides for 48 h at 37ºC. Various antihypertensive bioactive peptides were characterized and their similarity with different goat milk proteins were confirmed against goat milk protein databases of AHTPDB. From the study, it has been concluded that, fermented goat milk could be a best source of ACE-inhibitory peptides.

Key words: Fermented goat milk, *Lactobacillus*, Proteolytic, ACE-inhibitory, Peptide AHTPDB

PROBIOTIC PROPERTIES OF LACTIC ACID BACTERIA ISOLATED FROM NATURALLY FERMENTED MILK PRODUCTS OF SIKKIM

Ranjita Rai

Ranjita Rai and Jyoti Prakash Tamang

DAICENTER (DBT-AIST International Centre for Translational and Environmental Research) and Bioinformatics Centre, Department of Microbiology, School of Life Sciences, Sikkim University, Tadong, Gangtok 737102, Sikkim, India

Email: skmeseranjurai@gmail.com

I have completed my Ph.D. Thesis title: Diversity of Lactic Acid Bacteria and Their Probiotic Properties in Some Naturally Fermented Milk Products of Sikkim under the supervision of Professor Jyoti Prakash Tamang, Sikkim University. I have published four papers with high impact factor and attended national and international seminars. Participated and presented a poster at 6th AIST International Imaging Workshop & DAILAB PINNIKH series XXXII held at Biomedical Research Institute, AIST, Tsukuba Science City, Japan supported by AIST & JST (Govt. of Japan) and DBT (Govt. of India).

ABSTRACT

Introduction: Natural fermentation is the oldest method for the fermentation of naturally fermented milk products. Lactic acid bacteria are dominant microflora present in milk products and it has probiotic potential which exerts various health benefits on a host. Probiotic cultures should demonstrate the following properties to be recognized as functional food components such as acid and bile stability, resistance to digestive enzymes, adhesion to intestinal surface, antagonistic activity and cholesterol lowering effects.
Objectives: The present study aimed to document the diversity of lactic acid bacteria from naturally fermented milk (NFM) products and to analyse their probiotic properties.

Methods: In this study both culturable and non-culturable approach have been applied. The genomic DNA were extracted and sent for 16S rRNA sequencing. Illumina MiSeq amplicon sequencing was done to evaluate metagenomic DNA. To check the potential probiotic attributes, basic probiotic screening of selected LAB were validated with some probiotic gene detection using PCR method.

Results: Five different types of NFM products were analyzed and their microbial load (cfu/ml) was ranges from ($3.5x10^4$ to $5.3x10^8$). *Leuconostoc* sp. was found dominant in culture dependent analysis. However, relative abundance of phyla *Firmicutes* and *Proteobacteria* were found higher in metagenomic analysis. Further, seventy LAB strains were selected for probiotic analysis. Most of the strains showed high tolerance of bile salt, low pH, hydrophobicity activity and antimicrobial activity against pathogenic strains.
Discussion: The present study revealed that the NFM of Sikkim harbor diverse species of lactic acid bacteria with potential probiotic properties which may be applicable for food industries.

Conclusion: Some lactic acid bacteria showed probiotic attributes in NFM of Sikkim which may possibly impart health benefits to the consumers..

Key message: Recent tools for study microbiota are more efficient and cost effective. Further extensive research has to be done in this field in the near future.

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