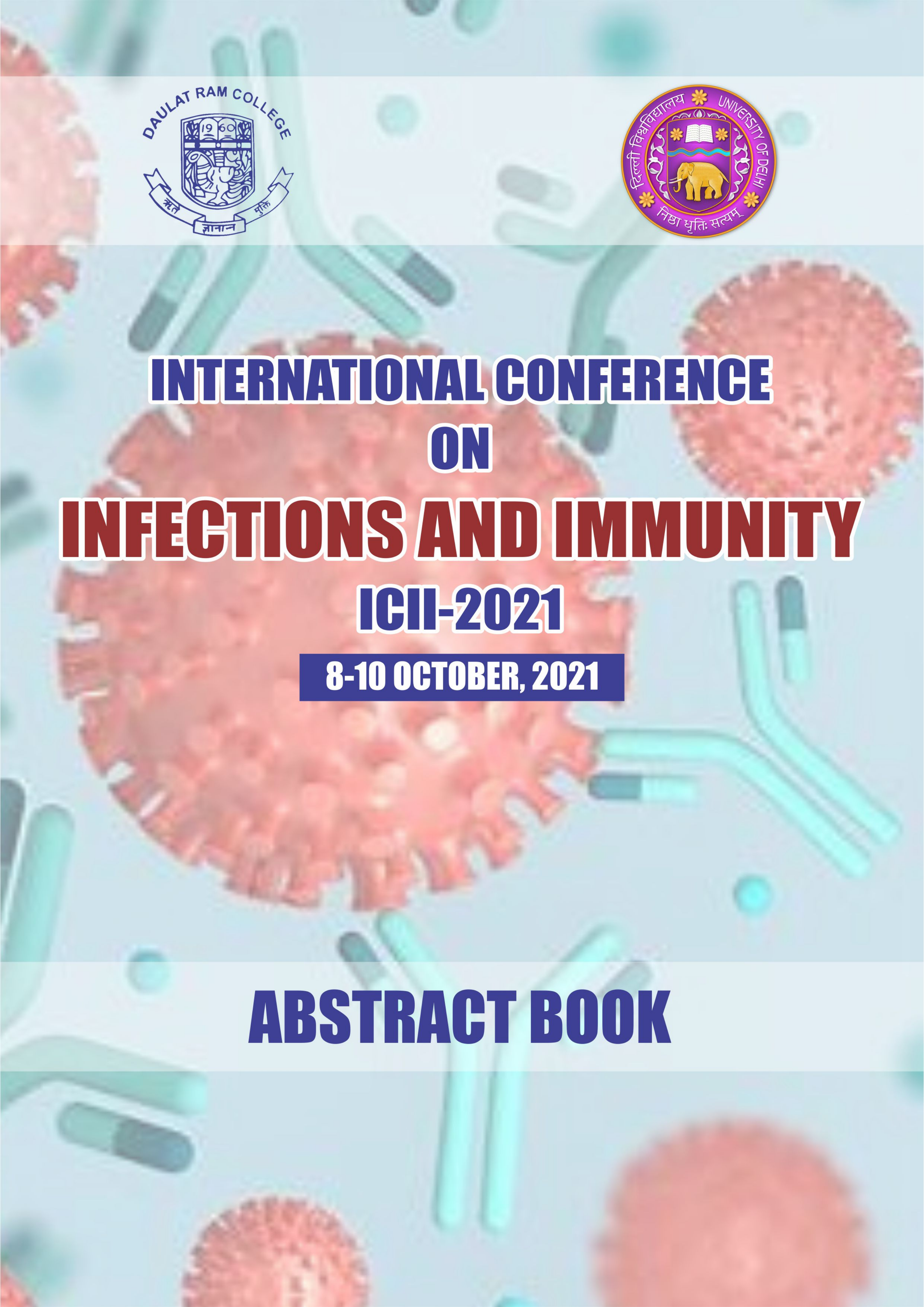

DAULAT RAM COLLEGE

UNIVERSITY OF DELHI

INTERNATIONAL CONFERENCE
ON
INFECTIONS AND IMMUNITY

ICII-2021

8-10 OCTOBER, 2021

ABSTRACT BOOK

INTERNATIONAL CONFERENCE

ON

INFECTIONS AND IMMUNITY

ICII-2021

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ABSTRACT BOOK

Convened By
Dr. Jyoti Taneja
Dr. Sonika Sharma

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PREFACE

ॐ सर्वे भवन्तु सुखिनः सर्वे सन्तु निरामयाः ।
सर्वे भद्राणि पश्यन्तु मा कश्चिद्दुःखभाग्भवेत् ।

May everyone be happy, may everyone be free from all diseases may every one see goodness and auspiciousness in everything, may none be unhappy or distressed!

Department of Zoology, Daulat Ram College, University of Delhi is organizing a Three-day International Conference on “Infections and Immunity” The conference has been planned to address the various aspects of emerging infectious diseases, problems, and solutions to deal with possible infections of the future.

The conference will host speeches from some eminent scientists and industry experts, on recent therapeutic and diagnostic tools in tackling infections, and developmental challenges in vaccines and immunity.

The major goal of any research is to increase scientific knowledge. This conference will bring all the knowledge collected by our eminent speakers and scientists to a single platform. This Pandemic has been a major outbreak in the world; hence we want our future scholars and scientists to be aware of evolving microbes and vaccine design. Conference will include open discussions on the enlisted themes where the participants will have an opportunity to exchange their opinions, ideas and update their existing knowledge.

The conference will have the following scientific sessions for specific discussions:

- Infections: Bacterial, Viral and Parasitic
- Vaccine design and efficacy of immune system
- Immune system and cancer
- Genomic surveillance of infective agents
- Role of Artificial Intelligence in disease treatment
- COVID Treatment and Management

We offer our sincere thanks to Prof. Savita Roy, Principal, Daulat Ram College, University of Delhi for her constant guidance, support and motivation. We thanks all faculty members of Daulat Ram College, non-teaching staff and Student Volunteers for their unending support and making this conference a successful event.

We thank all members of our Advisory board, Editorial board and organizing committee for their tireless efforts in the efficient management of this Conference.

We welcome all to share their knowledge and expertise and help to disseminate it amongst the faculty, researchers and students.

Dr. Jyoti Taneja
Convenor & TIC Zoology

Dr. Sonika Sharma
Convenor

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MESSAGE FROM CONVENORS

On behalf of the organizing team it is our pleasure to invite you all to attend the International Conference "Infections and Immunity" between 8-10 October 2021 which aims towards a global collaboration between scientists, research scholars and students working on various aspects of immunology from different research organizations, medical institutions, NGOs, and reputed Universities, to share their ideas and discuss the solutions. This conference will bring all the knowledge collected by our eminent speakers and scientists to a single platform. This Pandemic has been a major outbreak in the world, hence we want our future scholars and scientists to be aware of emerging viruses and vaccine design. The Conference will include open discussions on the enlisted themes where the participants will have an opportunity to exchange their opinions, ideas and update their existing knowledge.

We wish to extend our heartiest gratitude to Prof. Savita Roy, Principal, Daulat Ram College, all faculty members of Daulat Ram College, Student Volunteers and Staff for their unending support. A special thanks goes to the organizing team for their tireless efforts in the efficient management of this Conference.

Last but not the least, we thank all delegates from India and Abroad for their contribution to Infections and Immunity 2021.

Dr. Jyoti Taneja

Dr. Sonika Sharma

MESSAGE FROM CHAIRMAN

"The immune system, is a collection of organs, tissues, cells and enzymes, all united under one goal - to protect the body. The key player in the acquired immune response, include T cells, B cells and Antibodies, which our most knowledgeable patrons, present with us, would elaborate and discuss upon. One can, in short, understand one basic synopsis of Nature's bounty, rendered to all living beings, that

"INFECTION IS THE MOTHER OF IMMUNITY BUILD UP, THROUGH CREATION OF ANTIBODIES."

T cells, B cells and Antibodies, create an Immunilogical memory or Immune system for future attacks by the same Pathogen. It is equipped with the specific machinery to protect the body.

I pass on the discussion to our enlightened patrons.

Thanks

Mr. Mukul Gupta

MESSAGE FROM PRINCIPAL

Daulat Ram College (DRC), University of Delhi, is a premier educational institute for women established in 1960. The institution since then has acquired a strong identity and has evolved into a prestigious women's college with its own distinct culture and traditions. It is engaged in imparting holistic and quality education at undergraduate level in all disciplines viz Science, Commerce and Humanities to about 4500 students through its distinguished faculty. The college was accredited with 'A' Grade by National Assessment & Accreditation Council (NAAC) in April 2017 and recently it was ranked 26 by NIRF for two consecutive years. It was awarded Star status by the Department of Biotechnology (DBT), Government of India (GOI) for undertaking innovative practices in the science department. The college promotes interaction of students with experts in their respective fields. Thus, the College regularly organizes conferences, seminars, symposiums and workshops at national and international levels.

It is a matter of pride that the Zoology Department, Daulat Ram College, is organizing a 3-day International Conference on “Infections and Immunity” on October 8-10, 2021. The theme of the conference is very relevant in the current scenario. In the past one and half years we have faced several unprecedented situations. The need of the hour is a platform where the scientific community can come together to decipher and understand the various aspects of immunology.

I extend my best wishes to the organizing team of my College for the conference. Also my heartiest welcome to all the esteemed Speakers, distinguished Scientists and participants from India and abroad for a meaningful interaction on this platform in the next few days. My best wishes for the success of this Conference.

Prof Savita Roy

MESSAGE FROM GUESTS OF HONOR

I would like to congratulate and compliment the team which has put together this seminar under this important theme of "Infection and Immunity" and the consequent bringing together of leading Academicians, Clinicians, Researchers and students to exchange and share their experiences and research results on all aspects of Immunology and Infectious Disease. The complex paradigm of infection and consequent immune response has been worked upon extensively and still there are many intricacies about our body's natural defense system which are hitherto unknown. This three days of intense dialogue on the latest ideas, data, insight, models and methods in immunity and infectious disease dynamics will help for advancement and dissemination of fundamental knowledge concerning Infection and Immunity. DBT also encourages research in the area and solicits a wide array of projects on bacterial, viral, parasitic, and fungal diseases spanning the spectrum from basic biology of human pathogens and their interaction with human hosts, through translational and clinical research toward the development of new and improved diagnostics, drugs, and vaccines for infectious diseases.

Dr. Anamika Gambhir

Covid -19 pandemic was a surprise to most of us due to a common belief that the infectious diseases are in control since the beginning of the 21st century, precisely because of the advancements in the science and technology. Surprisingly, Corona virus infection presented itself differently in people depending on age, sex, and body weight. The severity of Covid-19 was more in people with comorbidities like cardiovascular disease and diabetes mellitus type II. An important aspect which came to light was that the males were more adversely affected that females. This has been observed in other infectious diseases such as MERS, hepatitis, and TB, however it became more evident during Covid-19 pandemic because multiple waves of infection. Therefore, it is important to understand the correlation of hormones and immunity in a gender-based manner. In addition, it is also relevant to emphasize the importance of healthy lifestyle, and exercise to avoid comorbidities and to build immunity to fight against corona virus like environmental threats.

Prof. Rita Singh

About the College

Daulat Ram College (DRC), University of Delhi is a premier educational institute for women founded by an educationist, late Shri Daulat Ram Gupta in 1960. Originally started as “Pramila College” the college in 1964 shifted to its present premises in North Delhi University Campus and was re-named as “Daulat Ram College”. The institution since then has acquired a strong identity and has evolved into a prestigious women's college with its own distinct culture and traditions. It is engaged in imparting holistic and quality education at undergraduate level in all disciplines, Science, Commerce, and Humanities to about 3600 students via distinguished faculty. The college was accredited with 'A' Grade by National Assessment & Accreditation Council (NAAC) in April 2017.

About the Department

The Department of Zoology was awarded Star status by the Department of Biotechnology (DBT), Government of India (GOI) for undertaking innovative practices in the science department. The Department has a team of young and talented faculty members with diverse specializations in various fields.

Department seeks to set high academic and intellectual standards for students. It provides an atmosphere for blended learning where every student can accommodate and express themselves. Apart from teaching, faculty members also mentor students in undergraduate research and encourage them to participate in conferences and workshops. Every year, the department organizes various In-house Skill Development Program for undergraduate students for enhancing E-Learning through ICT tools and methodologies and techniques in academic research.

About the Conference

Department of Zoology, Daulat Ram College, University of Delhi is organizing a

Three-day International Conference

on

“Infections and Immunity”

between 8-10 October 2021

which aim towards a global collaboration between scientists, research scholars and students working on various aspects of immunology from different research organizations, medical institutions, NGOs, and reputed Universities, to share their ideas and discuss the solutions.

The conference has been planned to address the various aspects of emerging infectious diseases, problems, and solutions to deal with possible infections of the future.

The conference will host speeches from some eminent scientists and industry experts, on recent therapeutic and diagnostic tools in tackling infections, and developmental challenges in vaccines and immunity.

Scopes and Themes

The major goal of any research is to increase scientific knowledge. This conference will bring all the knowledge collected by our eminent speakers and scientists to a single platform. *This Pandemic has been a major outbreak in the world, hence we want our future scholars and scientists to be aware of emerging viruses and vaccine design*. Conference will include open discussions on the enlisted themes where the participants will have an opportunity to exchange their opinions, ideas and update their existing knowledge.

Major themes of the conference are but not restricted to:

- **Infections: Bacterial, Viral and Parasitic**
- **Vaccine design and efficacy of immune system**
- **Immune system and cancer**
- **Genomic surveillance of infective agents**
- **Role of Artificial Intelligence in disease treatment**
- **COVID Treatment and Management**

CHIEF GUEST

DR. Seema Kapoor

Director Professor, Paediatrics
In-charge, Division of Genetics & Metabolism
Maulana Azad Medical College, New Delhi
(DRC Alumni)

Dr Seema Kapoor is a practicing pediatrician with a rich experience in research in the field of metabolic disorders, reproductive health and pediatric health. She is the coordinator of the center for excellence in Biochemical Genetics. Author of many publications, she has bagged many awards to her credit in medical research.

Keynote Speakers

Talk Title:
SARS-CoV-2 Genomic Surveillance and its future applications

Dr. Rajesh Pandey's lab at CSIR-IGIB works toward Integrative Genomics of Host-Pathogen. This includes pathogens genome architecture, host response, single cell genomics, 3D Organoids and role of co-infections in disease severity and clinical outcome. His lab has been integral to the Genomic Surveillance of SARS-CoV-2.

DR. RAJESH PANDEY
Associate Professor
Principal Scientist
(CSIR-IGIB), Delhi

DR. PRAVEEN GUPTA
M.D. (Medicine), D.M (Neurology)
Director & HOD
FORTIS Memorial Hospital, Gurugram

Talk Title:
Covid and its management

Dr. Gupta is best neurologist, widely recognised for his skill and competence. He has been instrumental in the treatment and management of Covid -19. Dr. Gupta established the first stroke center in Gurugram, was also pioneer in the use of solitaire for mechanical thrombolysis. He is involved in active research in randomized controlled trial in migraines and other neurological disorders.

Talk Title:

Artificial Intelligence for Covid-19 solutions

Dr. Tavpritesh Sethi is a physician-scientist and Associate Professor of Computational Biology at IIIT Delhi, India and a fellow of the Wellcome Trust India Alliance at AIIMS, New Delhi, India. His research is focused on development and deployment of machine-learning based solutions to enable decisions and policy in pressing healthcare questions such as antimicrobial resistance, sepsis and health inequalities in intensive care and public health settings.

Talk Title:

Emerging viruses and future strategies for interventions

Dr. Manu Anantpadma, is expert scientist in infectious viral disease in Integrated Research Facility at National Institute of Allergy and Diseases, National Institute of Health, USA. An accomplished scientist with focus area in virology, high throughput drug screening, microbiology and immunology. Has expertise in working in the laboratories of biosafety level- 4 (BSL-4).

Talk Title:

Semi Invariant Natural Killer T-cells in Pulmonary tularemia: an approach to rational vaccine design

Dr. Amrendra Kumar is Research Scientist in Pathology at The Ohio State University, USA. Dr. Kumar is an expert immunologist with focus on understanding development and function of innate lymphocytes such as NKT, NK and MAIT cells in infectious diseases as well as cancers.

Publish your Paper!

The selected full length articles from participants and other scholars will be published in special thematic issue on *'Infections and Immunity'* of Chemical Biology Letters after peer-review.

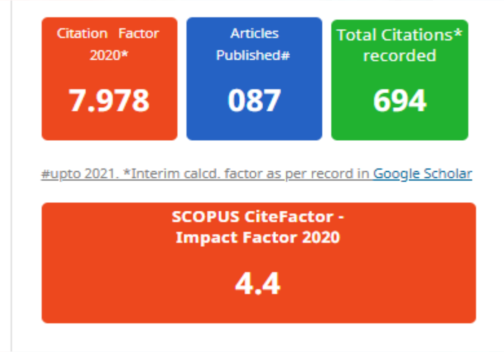
'Infections and Immunity'

A Special issue meant to cover aspects of emerging infectious diseases, problems, and solutions to deal with possible infections of future, including conference proceedings will be published.

About the Journal

The **Chemical Biology Letters** is a peer reviewed international journal that provides a rapid forum for publication of quality original research at the interface of chemistry and biology. The journal accepts research articles from the community of chemical biologists.

Scopus Index & Impact Factor



Citation Factor 2020*
7.978

Articles Published#
087

Total Citations* recorded
694

#upto 2021. *Interim calcd. factor as per record in Google Scholar

SCOPUS CiteFactor - Impact Factor 2020
4.4

Note:

- **Publication is subjected to acceptance by the journal.**
- **Link for submission of full-length articles will be provided upon registration.**

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https://pubs.thesciencein.org/author-guidelines-chemical-biology-journal/

DEPARTMENT OF ZOOLOGY
DAULAT RAM COLLEGE, UNIVERSITY OF DELHI
NAAC ACCREDITED 'A' GRADE COLLEGE ; NIRF RANK 26

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cordially invites you to the

Inaugural Function

of

International Conference

on

"INFECTIONS AND IMMUNITY"

8th OCTOBER | 2PM ONWARDS

Chief Guest
PROF. BALRAM PANI
PRINCIPAL, BCAS
DEAN OF COLLEGES, UNIVERSITY OF DELHI

Keynote Speaker
DR. SEEMA KAPOOR
DIRECTOR PROFESSOR, PAEDIATRICS IN-CHARGE,
DIVISION OF GENETICS & METABOLISM,
MAULANA AZAD MEDICAL COLLEGE

Guest of Honour
DR. ANAMIKA GAMBHIR
SCIENTISTS F, DBT

Chief Patron
MR. MUKUL GUPTA
CHAIRMAN
GOVERNING BODY
DAULAT RAM COLLEGE

Patron
PROF. SAVITA ROY
PRINCIPAL
DAULAT RAM COLLEGE

CONVENOR
DR. JYOTI TANEJA
TIC, Dept of Zoology, DRC

CONVENOR
DR. SONIKA SHARMA
Dept of Zoology, DRC

IQAC CONVENOR
DR. SARITA NANDA
Vice Principal, DRC

Zoom Meet Link: https://zoom.us/j/96592426716?pwd=WXlGNEFpUE1kd0R1Tkl0MG82djNGUT09

✉ zoologyambrosia@gmail.com

🌐 http://dr.du.ac.in/Zoology_Int_Conf.php

Department of Zoology, Daulat Ram College
University of Delhi

International Conference on "Infections and Immunity"

8 - 10th to Oct. 2021

Conference Schedule

DAY 1: 8th Oct 2021

2:00 pm: Inaugural Session	
2:00 pm	**College Prayer and Lighting of Lamp**
2:10 pm	**Welcome of Guests and Participants**
2:15 pm	**Welcome Remarks by Mr. Mukul Gupta, Chairman, Governing Body, Daulat Ram College**
2:25 pm	**Introductory Remarks by Prof. Savita Roy, Principal, Daulat Ram College**
2:35 pm	**Address by Chief Guest, Prof. Balram Pani, Principal, BCAS, Dean of Colleges, University of Delhi**
2:50 pm	**Address by Guest of Honor, Dr. Anamika Gambhir, Dept. of Biotechnology, Govt. of India**
3:05 pm	**Keynote Address by Chief Guest of Conference, Dr. Seema Kapoor, Maulana Azad Medical College**
3:20 - 3:30 pm	**Cultural Program**
Vote of Thanks	

4:00 pm: Technical Session - 1	
Session Theme: Genome Surveillance of Infective Agents	**Session Chair**: **Dr. Sunita Jetly** Associate Professor Department of Biomedical Sciences Acharya Narendra Dev College
4:00 - 5:00 pm	**Invited Talk: Dr. Rajesh Pandey** Associate Professor Principal Scientist (CSIR - IGIB), Delhi **Title: SARS-CoV-2 Genomic Surveillance and its Future Applications.**
5:00 - 5:30 pm	**Open Discussion on Theme**

DAY 2: 9th Oct 2021

2:00 pm: Technical Session - 2	
Session Theme: Role of Artificial Intelligence in Disease Treatment	**Session Chair**: **Dr Hare Ram Das** Associate Professor Department of Zoology Zakir Husain Delhi College
2:00 - 3:00 pm	**Invited Talk: Dr. Tavpritesh Sethi** Associate Professor Computational Biology - IIIT Delhi **Title: Artificial Intelligence for Covid-19 Solution.**
3:00 - 3:30 pm	**Open Discussion on Theme**
3:30 - 4:00 pm	**e-Posters Display**
Tea-Break	
4:30 pm: Technical Session - 3	
Session Theme: Vaccine Design and Efficacy of Immune System	**Session Chair**: **Prof. Seema Makhija** Professor Department of Zoology Acharya Narendra Dev College
4:30 - 5:30 pm	**Invited Talk: Dr. Amrendra Kumar** Research Scientist Department of Pathology, Ohio State University, USA **Title: Semi Invariant Natural Killer T-cells in Pulmonary tularemia: An Approach to Rational Vaccine Design**
5:30 - 6:00 pm	**Open Discussion on Theme**

DAY 3: 10th Oct 2021

2:00 pm: Technical Session - 4	
Session Theme: Infections: Bacterial, Viral and Parasitic	**Session Chair: Dr. Indrakant Singh** Associate Professor Department of Zoology Deshbandhu College
2:00 - 3:00 pm	**Invited Talk: Dr. Manu Anantpadma** Study Director National Institute of Allergy and Infections National Institute of Health MD, USA **Title: Emerging viruses and future strategies for interventions**
3:00 - 3:30 pm	**Open Discussion on Theme**
Tea-Break	
4:00 pm: Technical Session - 5	
Session Theme: COVID Treatment and Management	**Session Chair: Dr. Padamshree Mudgal** Associate Professor Department of Biochemistry Daulat Ram College
4:00 - 5:00 pm	**Invited Talk: Dr. Praveen Gupta** M.D. (Medicine), D.M. (Neurology) Director & HOD, Neurology- FORTIS Memorial Research Institute Gurugram **Title: COVID-19 and its Management**
5:00 - 5:30 pm	**Open Discussion on Theme**

DEPARTMENT OF ZOOLOGY
DAULAT RAM COLLEGE, UNIVERSITY OF DELHI
NAAC ACCREDITED 'A' GRADE COLLEGE ; NIRF RANK 26

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cordially invites you to the

Valedictory Function

of

International Conference

on

"INFECTIONS AND IMMUNITY"

10th OCTOBER | 6:00 PM ONWARDS

Chief Guest

PROF. SUMAN KUNDU
DIRECTOR
SOUTH CAMPUS
UNIVERSITY OF DELHI

Guest of Honour

PROF. RITA SINGH
DIVISION OF MOLECULAR ENDOCRINOLOGY AND REPRODUCTION, DEPARTMENT OF ZOOLOGY
UNIVERSITY OF DELHI

Chief Patron

MR. MUKUL GUPTA
CHAIRMAN
GOVERNING BODY
DAULAT RAM COLLEGE

Patron

PROF. SAVITA ROY
PRINCIPAL
DAULAT RAM COLLEGE

CONVENOR
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CONVENOR
DR. SONIKA SHARMA
Dept of Zoology, DRC

IQAC CONVENOR
DR. SARITA NANDA
Vice Principal, DRC

Zoom Meet Link: https://zoom.us/j/93614299502?pwd=SVR0TjNySy9hRE5pY2duUFZ6bE95dz09

✉ zoologyambrosia@gmail.com

http://dr.du.ac.in/Zoology_Int_Conf.php

6:00 pm: Valedictory Session	
6:00 pm	**Saraswati Vandana**
6:05 pm	**Welcome of Invited Guests**
6:15 pm	**Conference Report, Release of Conference Proceedings Booklet**
6:25 pm	**Concluding Remarks by Guest of Honor, Prof. Rita Singh, Division of Molecular Endocrinology and Reproduction, Dept. of Zoology, University of Delhi**
6:40 pm	**Concluding Remarks by Chief Guest, Prof. Suman Kundu, Director South Campus, University of Delhi**
7:00 pm	**Valedictory Address by Prof. Savita Roy, Principal, Daulat Ram College**
7:30 pm	**Award Ceremony**
7:35 pm	**Vote of Thanks**

Keynote Address

Words from the Chief Guest

वो राह थी जिसपर चली, वह नीव थी गहरी बड़ी!

वो दौलत राम से दूर थी, पर उसके धड़कनों की नूर थी!

यह राह शिशु से अग्रिम हुई, एक शहर मे पूरित हुई!

य़ह जंग है अब तक नयी, मैं सोच मे हूँ पड़ गई!

इन्फेक्शन ईम्मयूनिटी की जंग में, इस से सही अवसर नहीं!

नतमस्तक हो ईश की अर्चना करे, इस समन्जस्य के इस समय

हर वृक्ष को कोविड से परे, इस धरा को हरा करे!

- डा. सीमा कपूर

The journal of evolution has moved from the primates with inmate immunity to the complex of adaptive immunity. The initial mechanisms have unfolded from the basic defense mechanisms to more intricate molecular mechanisms. The move to a complex interplay of both the mechanisms of immune regulation is closely linked to each other. The molecular targets to disease are phenotypes currently unexplored.

Dr. Seema Kapoor
(Chief Guest)

Invited Lectures

IL - 1

SARS-CoV-2 Genomic Surveillance and its Future application

Dr. Rajesh Pandey, CSIR-IGIB, Delhi

Abstract

Genome, Genomics and Genomic Surveillance has been part of real-time global conversation which has percolated into public vocabulary at large. The learning's from the Integrative Genomics of SARS-CoV-2 towards better understanding of the COVID-19 pandemic has helped to elucidate the myriad of factors responsible for observed diversity of disease severity and clinical outcome. The investigation ranges from SARS-CoV-2 genome architecture vis-à-vis spectrum of mutations for their role in identifying Variants of Interest (VOI) & Variants of Concern (VOC), immune escape potential, their transmissibility, protein & RNA structure modulation, and possible association with disease severity. From the host perspective, the differential immune response and the genetic make-up has been helping to uncover the factors underlying differential disease response. At the same time, the role of co-infections has been emerging as an important area of research wherein microbial diversity and abundance has been associated with disease sub-phenotypes – mild, moderate severe and mortality. All of the above factors in combination with the clinical parameters are being used for developing Artificial Intelligence (AI)/ Machine Learning (ML) based models for identifying factors associated with risk stratification and mortality prediction. As we make progress with vaccination for SARS-CoV-2, in India and globally, it is possibly the time to think whether genomic surveillance would be useful for other diseases of concern caused by pathogens, inclusive of *Mycobacterium tuberculosis* (MTB), Human papilloma virus (HPV), Dengue, Chikungunya and Japanese encephalitis. These have been endemic to India and South-Asia in general with seasonal as well as perennial pattern. A ***Genomics-based Pathogen Surveillance (GPS)*** can be an effort which will facilitate better disease management, pre-emptive response and targeted healthcare support for sub-group of patients with predicted severe disease outcome.

IL - 2

Artificial Intelligence for Covid-19 Solution.

Dr. Tavpritesh Sethi
Assistant Professor,
Computational Biology, IIIT, Delhi

Abstract

COVID-19 has revealed the need to put intelligent data and decision systems in place. In this talk, I will showcase some of the areas where AI can be applied in designing COVID-19 solutions. These include molecular, clinical, epidemiological and public solutions created by our lab in addressing the multi-dimensional challenges posed by COVID-19. Finally I will showcase a genomic surveillance platform based on reading the book of virus using natural language models and its potential in predicting surges.

IL - 3

Semi-invariant natural killer T (iNKT)-cells in pulmonary tularemia: an approach to rationale vaccine design

Dr. Amrendra Kumar
Department of Pathology, The Ohio State University, Columbus, OH, USA

Abstract

The respiratory mucosa represents a major port of invasion by pathogens and, therefore, has highly specialized immune-surveillance mechanism. *Francisella tularenisis (Ft)* either invades the lung mucosa directly or through systemic spread from the primary site of infection such as skin or intestine, often causing fatal form of pulmonary tularemia. Tularemia is an inflammatory, sepsis-like disease. Type B *Ft* subspecies holarctica, which causes a milder disease in humans has been developed into an attenuated live vaccine strain (LVS). However, LVS is not FDA approved due to its poor efficacy. Type 1 semi-invariant natural killer T (iNKT) are innate-like lymphocytes that recognize microbial glycolipids or microbe-induced self-lipids presented by MHC-like CD1d-molecules. Despite being one of the major T cell subsets in lungs, role of iNKT cells in respiratory infections such as pulmonary tularemia is poorly understood. We have found that iNKT cells exacerbate features associated with *Ft* LVS induced pulmonary tularemia. Infection of mice through the intranasal route activate NKT cells in TCR dependent manner. Furthermore, *Ft* LVS derived lipids activated NKT cells in CD1d-dependent manner in the in-vitro studies. Since mice lacking NKT cells have better protection against intranasal infection with *Ft* LVS, understanding and knowledge of NKT cell agonist(s) and its/their biosynthetic pathway could have direct implications for design of NKT cell vaccine/vaccination strategies against pulmonary tularemia.

IL - 4

Emerging viruses and future strategies for interventions

Dr. Manu Anantpadma
National Institute of Allergy and Infection
National Institute of Health, MD. USA

Abstract

Unless we are prepared to tackle them today, the increasing frequency of infectious pandemics point to a bleak tomorrow. The current Coronavirus crisis has augmented the need for research on infectious diseases, antivirals, and vaccine development. So far, most viral outbreaks have involved reactionary approaches. Scientists and administrators are always found scrambling to find a 'quick cure.' While the pace of research is unprecedented and promising leads are quick, reactionary approaches almost always fail to deliver timely results. This lost time leads to a devastating loss of life and an extraordinary economic impact on society. While prophylactic strategies like vaccine development have been relatively fast against some viruses (like Coronaviruses), other viruses have required a long time (Dengue, RSV, Ebola). Even after approval, mass availability, administration, and subsequent herd immunity from vaccines can be challenging. Unlike vaccines, the development of therapeutics to manage viral infections is even more challenging. Very limited antivirals are approved for human use. Many antivirals that are promising *in vitro* and even in animal models fail in human trials.

The presenter will discuss how experiences from past epidemics are helping to drive and shape the current approaches to tackling present and future epidemics.

IL - 5

COVID-19 and its Management

Dr. Praveen Gupta
M.D. (Medicine), D.M (Neurology)
Director & HOD, Fortis Memorial Research Institute
Gurugram, Haryana

Abstract

COVID has the world caught by its neck. There has been lot of interest and confusion on modes of spread. As we await the third wave lot has ben learnt about second wave and how covid has affected our world its perhaps the greatest medical emergency experienced in our lifetimes and how covid has affected our world. There are theories and myths about covids and treatments. The review will try to put covid virus its manifestations management in medical and scientific perspective . It will also touch upon the skepticism and value of vaccination . It will then piece together an algorithm for reasonable medical practices for covid management in the context of our country and its people.

Abstracts

Abstract - 1

Impact of COVID-19 on Antimicrobial Resistance

Amit Sharma[1] Sonika Sharma[2]

[1] Medical Officer, District Civil Hospital, Sonipat Email ID: walkone84@gmail.com
[2] Assistant Professor, Department of Zoology, Daulat Ram College, University of Delhi, E mail ID: sonikasharma@dr.du.ac.in

Abstract

Antimicrobial Resistance (AMR) is an adaptive mechanism wherein microbes become resistant to medical treatments and lead to severe disease outcomes and uncontrolled spread of infections. It has been declared a global public health threat by the World Health Organization. The major contributors to the emergence and spread of AMR are indiscriminate, both misuse and overuse of antimicrobials, substandard medicine quality and poor access to Water, Sanitation and Hygeine (WASH) for both humans and animals.AMR leads to significant mortality as well as economic loses and affects humans, animals and environment too. The coronavirus disease (COVID-19) pandemic caused by SARS-CoV-2 is having a global impact and has challenged the existing healthcare facilities. In December 2019, the SARS-CoV-2 outbreak in Wuhan China led to many people manifesting severe acute respiratory distress symptoms (ARDS). This viral infection rapidly spread to many other countries and the World Health Organization (WHO) declared it a pandemic on March 11, 2020. Immune-compromised people suffering from COVID-19 are more likely to suffer from secondary infections. The indiscriminate use of Antibiotics and self-medication practices prevalent in the Indian scenario could be responsible for the higher infection and mortality rates. This review is an attempt to build the birds-eye view of AMR in context to COVID-19 and understand if COVID-19 has contributed to exaggerating the impact of AMR.

Keywords: Antimicrobial Resistance, WASH, COVID-19, Immune-compromised, secondary infections

Abstract - 2

Mechanistic perspective of NETs induced lungs cytotoxicity in sepsis

Anupam Jyoti[1*], Sanni Kumar[2], S. Mehta[3]

[1] Faculty of Applied Sciences and Biotechnology, Shoolini University of Biotechnology and Management Sciences, Bajhol, Solan, Himachal Pradesh 173229.

[2] Amity Institute of Biotechnology, Amity University Rajasthan, Jaipur

[3] Department of Geriatric Medicine, SMS Medical College & Attached Hospitals, J.L.N. Marg, Jaipur, Rajasthan, India

[*] Corresponding author

Email –anupamjyoti03@gmail.com

Abstract

Recent reports from this lab have demonstrated a higher incidence of NETs, nitrosative, as well as oxidative stress, have a direct correlation with the severity of sepsis and organ damage. Though, underlying mechanism of NETs persuaded cell death in sepsis is not inferred entirely. Interaction of inducible nitric oxide synthase (iNOS) with Rac2 in regulating reactive oxygen species (ROS) and reactive nitrogen species (RNS) generation and its implications in microbial killing has been reported. This study was, therefore, undertaken in neutrophils of sepsis patients to investigate the functional importance of iNOS-Rac2 interaction in ROS/ RNS, peroxynitrite generation, NETs generation, and NETs mediated cell death. Overall, 50 control (healthy person) and 100 patients with sepsis were recruited. It was found to be enhanced interaction between iNOS and Rac2 in sepsis neutrophils in comparison with control. This was accompanied by an increased level of superoxide ($O_2^{\cdot-}$), nitric oxide ($NO^{\cdot}$) and peroxynitrite ($ONOO^-$) which were decreased in the presence of NADPH oxidase and NOS inhibitors signifying the role of iNOS-Rac2 interaction. Enhanced NETs release from activated sepsis neutrophils were abrogated in the presence of iNOS and Rac2 inhibitors. NETs from sepsis neutrophils exert a cytotoxic effect on lung epithelial cells (A549) in a concentration-dependent manner. Our findings exhibit the functional role of iNOS-Rac2 interaction in ROS/RNS, peroxynitrite generation, NETs generation, and NETs mediated cell death.

Keywords: iNOS, Rac2, Neutrophils, NETs, Cytotoxicity, Sepsis

Abstract - 3

Immunogenic Properties, and Structure of the SARS-COV-2 Envelope Protein Prediction Using Bioinformatics Approach

Juhi Saxena[*]**, Anupam Jyoti**

Faculty of Applied Sciences and Biotechnology, Shoolini University of Biotechnology and Management Sciences, Bajhol, Solan, Himachal Pradesh 173229

[*] Corresponding author

Email – jina.saxena@gmail.com

Abstract

Severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) causing respiratory illness has been outburst in Wuhan, China in late December 2019 and is associated with high level of infectivity and mortality. The SARS-CoV-2 envelope (E) protein with 75 amino acids play critical role in the viral pathogenesis. The present study was designed to analyze the amino acid sequence, secondary, as well as tertiary structure of SARS-CoV-2 E protein using bioinformatics approach. Amino acid sequences of E protein from 46 SARS-CoV-2 were retrieved from NCBI database followed by sequence alignment. The physio-chemical properties of SARS-CoV-2 E protein were determined using Protparam tool. ABCpred online software was used for the prediction of B cell linear epitope in E protein. We found E protein sequence to be highly conservative, stable, and amphipathic in nature. Furthermore, two potential antigenic epitopes with starting amino acid positions 30 and 48 having ABC prediction score > 0.8 was confirmed. We found SARS-CoV-2 E protein has maximum identity with 5X29 using BLAST, hence selected for the three-dimensional structure determination Swiss modeler and visualized by PyMol. Finally, Ramachandran plot analysis of model using RAMPAGE was performed to predict allowed and disallowed regions for the three-dimensional predicted structure of SARS-CoV-2 E protein. Hence, the present study will be helpful in understanding the current knowledge in vaccine, monoclonal antibody, immunomodulatory agents against SARS-CoV-2.

Keywords: SARS-COV-2, Envelope Protein, Bioinformatics

Abstract - 4

Carbapenem Resistance Trends in pre-COVID and COVID Times in a North Indian Tertiary Care Hospital

Nirupama Chatterjee[1*], Shruti Srivastava[1], Pushpa K Nirwan[1], Ruchi Rati[2] Shivani Sharma and Namita Jaggi[1,2]

[1] Department of Education and Research, 2. Department of Microbiology, Artemis Hospitals, Sector-51 Gurugram -122001, Haryana

* Corresponding Author: Dr. Nirupama Chatterjee, Principal Research Scientist, Department of Education and Research, Artemis Hospitals, Gurugram

E-mail: nirupama.chatterjee@artemishospitals.com Mobile: 9618037209

Abstract

Resistance to carbapenems, one of the last resort antibiotics is of serious concern. Carbapenem resistance is mainly spread through five carbapenemase genes (VIM, IMP, KPC, NDM and OXA-48). In the present study, we screened these five carbapenemases by Polymerase Chain Reaction in multidrug resistant gram negative isolates of *Escherichia coli*, *Klebsiella pneumoniae*, *Psuedomonas aeruginosa* and *Acinetobacter baumanii* during Pre-Covid (August to October 2019) and COVID (January –February 2021) periods. There was no significant difference in age, gender or nationality of the patients harbouring resistant strain in the two study periods. Majority of the resistant strains were isolated from samples of ICU patients. Mortality rates increased in patients having resistant bacteria during the COVID periods (17.8% vs 26%) and patients suffering from COVID-19 and related complications were more likely to have resistant isolates ($p<0.05$). Carbapenem resistance rate was significantly higher in COVID times (27.5% vs 41.0%, $p<0.05$). Of the four organisms, *Klebsiella pneumoniae* and *Psuedomonas aeruginosa* showed a significant increase in resistance rates during the COVID period, $p<0.05$). Amongst the carbapenemases; NDM, OXA-48 and co-expression of NDM and OXA-48 were the most commonly detected. Conjugation assay showed that most NDM genes were plasmid based and NDM-5 was the most common variant in both the study periods. In conclusion, carbapenem resistance rate increased in COVID times. This rise could be attributed to the increase in patients with severe co-morbidities during COVID times as well as to the occurrence of COVID-19 and related complications.

Keywords: carbapenem, resistance, COVID-19, NDM, OXA-48

Abstract - 5

Reverse Vaccinology Based *in silico* Analysis of Epitope Prediction in *cya, lef* and *pag* genes from *Bacillus anthracis* against anthrax infected species: An Immunoinformatics Approach.

Uma Bharathi Indrabalan[1], Kuralayanapalya Puttahonnappa Suresh[1], Sharanagouda S Patil[1], Mallikarjun S Beelagi[1], Praharshit Sharma[1], Chandan Shivamallu[2], Mohan Pappana[3], Raghavendra Amachavad[4*]

[1] ICAR-National Institute of Veterinary Epidemiology and Disease Informatics (NIVEDI), Yelahanka, Bengaluru-560064, India.
[2] Department of Biotechnology and Bioinformatics, Faculty of Life Sciences, JSS Academy of Higher Education & Research, Mysuru 570015, India.
[3] Huck Institutes of the Life Sciences, 205 Wartik Laboratory, The Pennsylvania State University, University Park, State College, PA 16802, USA
[4] Department of Clinical Sciences, Kansas State University, Manhattan, KS 66506-5606, USA
[*] Corresponding author: Raghavendra Amachavad, E-mail: agraghav@vet.k-state.edu

Abstract

Bacillus anthracis is a Gram-positive spore-forming bacteria that causes the zoonotic disease: anthrax, an abrupt illness that disproportionately impacts grazing livestock and wild ruminants, and *B.anthracis* is a bacterium that may be found naturally in soil and affects domestic, wild animals and also humans all over the world. The anthrax's geographical reach despite years of research on anthrax epizootic and epidemics behaviour, till date remains to be elucidated. Existing therapeutics, however, are ineffective in combating this infectious disease, necessitating the development of a better vaccine to halt the pandemic using immunoinformatics approaches, this study intended to predict an efficient epitope for vaccine against the anthrax in animals and humans using the toxin genes such as *cya*, *lef* and *pag* that are positioned at the plasmid pXO1of *B.anthracis* . The B-cell and T-cell (MHC-I and MHC-II) against the BoLA and HLA alleles were obtained from IEDB: immune epitope database. Consequently, it was found that the evaluated epitopes had no allegenicity, high antigenicity and no toxicity so that it would provide an effectual and most rapid technique to estimate peptide synthetic vaccines. Furthermore, this study predicted epitopes with respective molecules that would be an effective target to impede the anthrax. Subsequently, it can be anticipated that the obtained epitopes may serve as a best candidate to recognise appropriate antigen, cellular or humoral immune responses that is time and cost efficient in developing or improving better vaccines and diagnostics against anthrax. This study even benefits the academicians and researchers to find drug targets.

Key words: Anthrax, cya, lef, pag, B-cell and T-cell epitopes.

Abstract - 6

A Long Term Cell Culture and Insect Extracts

***[1]T.N. BANKAR AND PANDIT R.S[2]**

[*1,2] Department of Zoology,Savitribai Phule Pune University,Ganeshkhind Road, Pune-411007, Maharashtra,India.

*[1] Corresponding first author E-mail address: tanujabankar@yahoo.com

[2] Co-author E-mail address:panditrao499@gmail.com

Abstract

Mouse spleen cells are well known to survive only as primary cultures. In order to overcome this limitation, we derived an long term mouse spleen cell line from mouse species. Cell lines have applications in toxicity analysis. Insect venoms are known to cause inflammatory reactions at the site of their bite on human body, which induces an immune response to the insect venom. What happens during such a reaction, needs to be studied in a system outside the body. Cell lines are one of the systems which are helpful in such studies. We have developed a näive cell line which will allow to study the effect of various venoms or toxins synthesized by a variety of insects. Therefore, preliminary testing of whole ant extract on this cell line *in vitro*, was carried out by us. Results obtained from this study, indicate that this derived mouse spleen cell line could possibly serve as a model for evaluating toxicity for a variety of insect extracts *in vitro*.

Key words: Murine, Cell line, Insect extracts, Toxicity, Red ant.

Abstract - 7

COVID-19 Pandemic: Treatment and Management in India

Hemu Choudhary[1]

[1] Associate Professor, Dept of Zoology,Govt Girls College, Magra Punjala, Jodhpur
Email: hchemuchaudhary06@gmail.com
Mobile No. 9414104965

Abstract

COVID-19 is a viral disease, caused by SARS CoV-2. It was started from Wuhan City of China and spread in 210 countries of the world, so declared as a pandemic by WHO. It is a respiratory disease and the best treatment is the prevention by avoiding contact with infected person. Use of face masks, washing hands with regular intervals, use of sanitizer and isolation is the best practices to avoid the disease. The disease affects the whole world in every field like education system socio-cultural and economy aspects etc. The paper shows ways of treatment and management of COVID-19 in India, having a huge (130 Crores) population. Due to best practices and strategies death rates was found low in India as compare with USA and Brazil like developed countries.

Key words: COVID-19, treatment, management, challenges, opportunities.

Abstract - 8

AI Assisted Telehealth and Healthcare Delivery Through Smartphones, A Possible Solution for COVID Like Pandemics - A Scoping Review

Hima Bindu Dubasi[1], Surabhi Pandey[2], Aditi Deshpande[2]

[1] Department of Epidemiology,Public Health Foundation of India, IIPH-H, Bangalore Campus, SIHFW Premises (beside the leprosy hospital), 1st Cross, Magadi Road, Bangalore, Karnataka 560023, India; email: hibinduba@gmail.com

[2] Indian Institute of Public Health, Delhi, Plot No. 47, Sector-44, Gurgaon-122002, Haryana, India email: surabhi.pandey@phfi.org.

Aditi Deshpande, Consultant at Department of Epidemiology, Public Health Foundation of India, IIPH-H, Bangalore Campus, SIHFW Premises (beside the leprosy hospital), 1st Cross, Magadi Road, Bangalore, Karnataka 560023, India: email: aditid1408@gmail.com

Abstract

Background: Artificial Intelligence (AI) aims to develop computer systems, capable of performing tasks usually requiring human intelligence. Almost omnipresent, the applications of AI in the health care industry as well, are galore. With restricted movement and an overwhelmed health care system during COVID-19, a need to understand and develop forms of contactless quality health care delivery is required. Studies have shown that using AI has reduced costs and improved efficiency.

Objective: Through this scoping review, we aim to explore the current evidence on Telehealth and smartphones which use AI in health care as a form of remote health intervention as the world nervously foresees subsequent waves of COVID 19.

Methods: We searched PUBMED and Science Open using MeSH terms and keywords: ‘AI’, ‘Telehealth’, ‘Smartphones’ for the past one year for the most recent studies, which yielded 63 results and 16 studies met the eligibility criteria.

Results: A myriad of health contexts were discussed, 3 specific to COVID 19. The studies were categorised into, AI assisted tele heath and or smartphone use or potential use in diagnosis/screening of diseases (n=4), monitoring and or intervention (n=8), management and or treatment’(n=2), aiding in remote consultations (n=2).

Conclusion: Most of the studies were limited by inadequate data for real world deployment, so the evidence base around this field needs to be strengthened. Our review is a small step towards the prospect of integrating AI in remote health delivery, as India takes a giant stride towards digitalisation.

Key words: Artificial Intelligence; Telehealth; smartphones; COVID-19

Abstract - 9

Determination of Correlation Between the Concentration of Chlorpyrifos and the Efficacy of Immune System in Averting Parasitic Infections

Priya Goel[1]* and Jyotika Kapur-Ghai[2]
[1] Assistant Professor, Deen Dayal Upadhyaya College (University of Delhi)
[2] Professor, Punjab Agricultural University, Ludhiana (Punjab)
Email: priyagoel@ddu.du.ac.in, contact no.9873267400

Abstract

Background: Immune system is the body's primary line of defence against infectious agents, so weakening its response could increase the toll of disease. Besides, one of the leading cause of immunosupression is 'exposure to pesticides'. Injudicious use of pesticides makes even non-target species prone to their toxic effects and prolonged exposure even at low doses reduces resistance to parasite infections. Chlorpyrifos [O, O-diethyl O-(3,5,6-trichloro-2-pyridinyl) phosphorothioate] is the most widely used broad spectrum organophosphate (OP) insecticide in both agricultural and domestic settings. It can suppress the human immune response to invading bacteria, fungi, parasites, and viruses.

Method: The present study was undertaken on humans to determine the impact of chlorpyrifos concentration on susceptibility to parasitic infections, and to check the effect of factors such as age, health and/or gender. Sera from 400 patients suffering from some confirmed infection viz. malaria, colitis, cholera, tuberculosis, typhoid, hepatitis, gastroenteritis, etc. were collected from various hospitals and pathology laboratories. An equal number of control samples were also collected from healthy individuals. All age groups, ranging from <1 to 85 years of both genders were included. Competitive inhibition ELISA was employed to detect the presence of chlorpyrifos in these samples.

Results: A significantly higher number of infected samples (78.8%) were found to have chlorpyrifos accumulated in them as compared to healthy ones (56%). Also, chlorpyrifos was significantly concentrated at higher levels (in the range 40µg – 110mg) in the infected samples whereas control samples showed a relatively lower concentration (in the range 15µg – 41mg). However, age and gender made no significant contribution in predisposing the individuals to parasitic infections.

Conclusion: The present studies confirmed that chlorpyrifos concentration has direct correlation with the incidence of parasitic infections, irrespective of age/sex. In other words, stress in the form of pesticide accumulation causes immunosuppression and makes the body more prone to infections.

Keywords: chlorpyrifos, parasitic infection, age, sex, infectious agent, correlation

Abstract - 10

The Covid 19 Havoc and Clues from Sex Disaggregation of Data in the Indian Population

Divya Bajaj[1], Varunendra Singh Rawat[1], Preeti Bansal[2], Neetu*[1]

Department of Zoology, Hindu College, University of Delhi, Delhi, India[1], Department of Biosciences, Jamia Millia Islamia, Delhi, India[2]
*Corresponding author: neetukukreja@gmail.com

Abstract

The Coronavirus infectious disease (COVID-19) has created a turmoil across the globe, with 219 million confirmed cases and more than 4.5 million deaths. India is among the worst-hit countries, reporting more than 33 million cases and a death toll of ~ 4.41 lakhs. The Global scenario indicates a gender bias with a higher COVID-19 Case fatality rate (CFR) in males as opposed to females. It is suggested biological elements (immune responses) and behavioural risk aspects (like smoking, lifestyle) predispose men to an elevated risk of disease severity and death resulting from COVID-19 infection. However, a few countries like India along with Nepal, Vietnam and Slovenia have reported a reverse trend. Our study aimed to procure sex-disaggregated data in the Indian population by using a google form based online health survey. The questionnaire was framed to analyse parameters like age, gender, occupation, sex, severity of COVID infection based on CT score and requirement of steroids for treatment, need for hospitalisation etc. The responses were evaluated by descriptive statistics by excluding arbitrary correlation. We found that although there was no significant difference in the proportion of males and females contracting the COVID-19 infection, males were at significantly greater risk of severe disease and death than females. The number of deaths were two times in males as compared to females, the death toll, however, was not restricted to a particular age group. We also found that the male patients presented almost fourteen times the odds of requiring intensive care unit (ICU) admission as treatment procedure as compared to females; death toll and ICU treatment reflecting severity of the infection. Availability of Real-time sex disaggregated data with a larger dataset would enable gender-equitable solutions to this pandemic.

Key Words: COVID 19, Sex disaggregation, gender, severity, Case fatality Rate

Abstract - 11

Differentiating Between Dengue Primary and Secondary Cases: An Observational Hospital Based Study From Central India

Ankita Agarwal[1], Deepti Chaurasia[2]

State Virology Laboratory, Department of Microbiology, Gandhi Medical College, Bhopal-462001, Madhya Pradesh, India

*Presenting Author: Dr. Ankita Agarwal , State Virology Laboratory ,Department of Microbiology ,Gandhi Medical College ,Bhopal-462001 ,Madhya Pradesh, India

Email: agarwal.ankita81@gmail.com

Abstract

Dengue virus (DENV) infection can lead to spectrum of clinical illnesses ranging from asymptomatic/mild Dengue fever (DF) to severe forms like Dengue Haemorrhagic fever (DHF) or Dengue shock syndrome (DSS). As compared to primary infection, secondary infection with a heterologous serotype could lead to severe outcomes. In light of DENV endemicity in central India, secondary infections could be common. Due to the limited reports from Central India, present study was carried out to understand the prevalence of primary and secondary infections during 2019 dengue outbreak.

In this study, we tried to differentiate secondary infections from primary infections using clinical and serological parameters (case definitions and IgM/IgG ratio). For this study, DENV IgM positive samples were retrospectively selected and IgG testing was done. We have also performed ROC (Receiver Operating Characteristic) curve analysis for generating IgM/IgG ratio cut-off. Based on case definitions and IgM/IgG ratio, primary and secondary dengue cases were identified.

On the basis of ROC curve analysis, an IgM/IgG ratio cut-off of 1.2 was obtained. As per the case definition and IgM/IgG ratio, high rates of secondary infections were observed. Further, on comparing clinical characteristics between the primary cases and secondary cases, significant differences in haemorrhagic manifestations was observed. This points towards high coincidence between haemorrhagic manifestations and secondary dengue.

Identification of secondary dengue is important and should be included in currently ongoing national dengue surveillance programme. This would reduce the associated morbidity and mortality by implementing disease and vector control strategies.

Abstract - 12

Brucellosis Vaccine Design-directed Epitope Prediction for HLA-A*0201 allele

Praharshit Sharma[1], Kuralayanapalya Puttahonnappa Suresh[1], Sharanagouda S Patil[1], Chandan Shivamallu[2], Uma Bharathi Indrabalan[1], Divakar Hemadri[1], Raghavendra G. Amachawadi[3]

[1] ICAR-National Institute of Veterinary Epidemiology and Disease Informatics (NIVEDI), Yelahanka, Bengaluru – 560064 (Karnataka, India).
[2] Department of Biotechnology and Bioinformatics, Faculty of Life Sciences, JSS Academy of Higher Education and Research, Mysuru – 570015 (Karnataka, India).
[3] Department of Clinical Sciences, Kansas State University, Manhattan, KS 66506-5606 (USA).
Corresponding author*: **E-mail: agraghav@vet.k-state.edu **Phone:** +1-785-532-4356

Abstract

Here, we aim to map Human Leukocyte Antigens (HLA), based on HyperProteoGenome, as a possible solution for T-cell epitope prediction geared toward Brucellosis vaccine-design.

We note a natural corollary of the HyperProteoGenomic (HPG) equation given below,

$$4^{4^{x}} = 20^{20^{1}} = 1.048576 \times 10^{26}$$

PROSITE – motif *for* Small set of sequences of peptides known to bind to the

HLA-A*0201 molecule: $\mathbf{X_1[LMIV]_2X_3X_4X_5X_6X_7X\ X_8\ [MNTV]_9}$

that the Nonamer-motif deduced above is but a relative entropy based subset as given by KLD-equation as follows:-

$$\log_2(20^9) + \log_2(20^1) = \log_4(20^{20})$$

The information content is a measure of the degree of conservation and has a value between **zero** (no conservation; all amino acids are equally probable) and log2(20) = **4.32** (full conservation; only a single amino acid is observed at that position). Our model then addresses the entire specturm of these Extremes by splitting the RHS of HPG right from 20 data structures of 100% LCRs/ CBZs (Low Complexity Regions, or Compositionally Biased Zones) namely **A(20), C(20)...Y(20)** upto **20!** completely complex PROSITE motifs and mine them in actual protein sequences in large Protein sequence databaes such as **UniProt/ Swiss-Prot** and **TrEMBL** using **ScanPROSITE.** A simple relative entropy conservation equation is used for epitope prediction in the context of Brucellosis, specifically targeting HLA-A*0201 allele. Generalization would lead us to an Emerging era of pioneering work in Precision medicine, formulating "Rules" for individuals of a species in so far as to develop Effective vacciness indeed. This approach can be e generalized for T-cell epitope prediction and validated using IEDB, NetCTL 1.2 and IMGT, for robustness of the model.

Keywords: Nonamer-peptides, Relative entropy conservation, Dynamic Programming, Estimated Independent-Counts model, Genetic-coding.

Abstract - 13

Rotavirus A Strains: Phylogenetic Analysis, Molecular Diversity and Screening of B Cell and T Cell Epitopes for Potential Vaccine Design

Pooja Rani Kuri

Research Scholar, Department of Biosciences and Bioengineering, Indian Institute of Technology Guwahati, India
Email: poojaranikuri5@gmail.com, Contact no. 03612582238

Abstract

Rotavirus is a leading cause of severe infantile gastroenteritis worldwide, with about 199,000 childhood deaths in 2015, of which 90% cases occurred in low-income countries. India alone accounts for 22% of the global rotavirus gastroenteritis related deaths among children below 5 years of age. The World Health Organization recommends introducing rotavirus vaccines as a priority in developing countries where high rates of rotavirus gastroenteritis are observed. There are however gaps in molecular data on rotavirus epidemiology in India. We therefore reviewed molecular data on rotavirus A (most common etiological agent of infantile gastroenteritis) isolated from India and also analyzed viral capsid protein genes (vp7, vp4 and vp6) to assess any particular trend with reference to different genotypes by phylogenetic analysis. The capsid proteins vp4 and vp7 were also subjected to antigenic analysis to determine epitopes for potential development of subunit vaccines. Such kind of study is important for monitoring prevalence of circulating strains and to assess the possible efficacy of currently available rotavirus vaccines in controlling rotavirus gastroenteritis in the region, as well as assessing the possible designing of new vaccines.

Keywords: Rotavirus, phylogenetic analysis, antigenic analysis, gastroenteritis

Abstract - 14

Traditional Practices and Their Role in The Development of Immunity and a Comparative Study with the Current Practices

Chandhana Prakash

Daulat Ram College, DU, 4, Patel Marg, Maurice Nagar, Roop Nagar, Delhi, 110007
E-Mail – chandhanaprakash39@gmail.com**; Phone –** 9953665465

Abstract

The COVID-19 pandemic brought about a drastic change in the lifestyle of people. The importance of hygiene came into a lime light and people started becoming more aware about certain hygiene practices. Many preventive strategies including hand hygiene, social distancing, isolation and methods for boosting immunity were encouraged. The multiple traditional practices followed by people all around the world may act as a guide to a hygienic life style and provide several preventive facets in transmission of infections. Apart from these practices even the eating habits that make use of various herbs and spices in our daily lives have proven to contain ingredients that have the ability to boost the immunity. This review aims to look at some worldwide traditional practices with a focus on Indian practices, to try and deduce a scientific logic behind it and to find a connection between these practices and the development of immunity in people. The change in modern practices and eating habits from the traditional ways will also be compared and conclusions on how the changed lifestyle has led to a decrease in immunity in individuals will be made.

Keywords: Infections, Traditional and Cultural Practices, Hygiene, Immunity, Eating Habits

Abstract - 15

Prevalence and genotypic diversity of multi-drug resistant (MDR) *Mycobacterium tuberculosis* circulating among sputum smear positive cases of tuberculosis in Agra region of Uttar Pradesh, North India

Anjali Yadav[1,2], Suman Singh[1], Rakesh Kumar Sharma2, Santosh Kumar[2], Ajay Vir Singh[1], Devendra Singh Chauhan[1]

[1] Department of Microbiology and Molecular Biology, ICMR-National JALMA Institute for Leprosy and Other Mycobacterial Diseases (ICMR), Taj Ganj, Agra- 282 004, India.
[2] Department of Biotechnology & Life Sciences, Managalayatan University, Aligarh
[3] Department of TB and Chest, S.N. Medical College, Agra, Uttar Pradesh, India
Email Id: Anjali Yadav: njali.biochem@gmail.com

Abstract

Uttar Pradesh (UP) is the highest TB burden state in India. But, information about the prevalence and genotypic diversity of MDR-*M.tububerculois* strains circulated in different sub-regions of the UP is limited. Present study was aimed to investigate the prevalence and genotypic diversity of MDR-*M.tuberculosis* strains circulating in Agra region (Agra, Firozabad, Mathura and Manipuri districts) of UP. A total of 450 sputum smear positive samples of suspected TB patients were processed for the isolation of *M.tuberculosis* using Lowenstein-Jensen (LJ) medium. The isolates were characterized using biochemical methods and *M.tuberculosis* isolates were subjected to first line (rifampicin, isoniazid, ethambutol and streptomycin) drug susceptibility testing (DST). Genotypic diversity of the MDR-*M.tuberculosis* strains was studied using spoligotyping method. Out of 450 sputum samples, 302 (67.11%) samples were found positive for the presence of growth on LJ medium. Out of 302 isolates, 300 (99.33%) were identified as *M.tuberculosis.* The DST results were available for 300 *M.tuberculosis* isolates. Among the 300 *M. tuberculosis* isolates, 43(14.33%), 250(83.33%), 219(73.0%), 124(41.33%) and 129(43.0%) were found total sensitive, resistant to rifampicin, isoniazid, ethambutol and streptomycin drugs, respectively. The prevalence of MDR among sputum smear positive samples was found 48.66%. Spoligotyping identified 49 genetic patterns and CAS1_DEL (50.68%) followed by Beijing (10.50%) as pre-dominant spoligotype clades among MDR-*M. tuberculosis* isolates in Agra region of UP. In conclusion, our study reported high proportion of drug resistance TB in study population, and highlights that the MDR-TB is caused by heterogeneous geno-groups of *M.tuberculosis* strains in Agra region of UP, North India.

Key Words: Tuberculosis, Multidrug resistance**,** *Mycobacterium tuberculosis*, Genotypic diversity, Spoligotyping.

Abstract - 16

Mutational Analysis of HHK3 Ortholog- An Important Drug Target in Fungi

Soorya Partap Sasan, Yogita Martoliya, Alok K Mondal
School of life Sciences, Jawaharlal Nehru University, New Delhi *110067* India.
Email: akmondal@mail.jnu.ac.in

Abstract

Fungal infections are a major cause of morbidity and mortality in patient with weak immune system. Presently used clinically approved antifungal drugs have certain limitations like drug resistance, off target toxicity which demands the discovery of new antifungal drug targets. Group III hybrid histidine kinase (HHK3) is a potentially novel antifungal target which is known to act as upstream sensor in HOG/p38 MAPK pathway. HHK3 is conserved in all pathogenic fungus. Characteristic feature of HHK3 is a poly HAMP domain at the N terminal of the protein which regulates its activity. DhNik1 is an important HHK3 orthologue from yeast *Debaryomyces hansenii*. Previous SAXs studies indicate that the poly-HAMP domain imposes a dynamic regulation on the kinase domain in DhNik1. To illuminate this further, we conducted a proline scanning mutagenesis of HAMP 4b domain in the present study. The mutants are classified into distinct groups as revealed from the functional analysis. Furthermore, through random mutagenesis we have identified a cytotoxic mutant of DhNik1p. Nucleotide sequencing showed that the mutant contained a small deletion in HAMP3 and HAMP4b domain. This observed toxic effect is due to the up regulation of HOG pathway that correlates with phosphatase conformation of this protein. Together, these results clearly demonstrates that the upstream poly-HAMP domain imposes distinct active state on kinase domain through conformational changes.

Abstract - 17

Hybrid Histidine Kinase III- A Novel Drug Target In Fungal pathogen causing mucormycosis

Anita Yadav, Alok Kumar Mondal
School of Life Science, JNU, New Delhi
Email ID:alok.imt@gmail.com, yadavanitajnu108@gmail.com

Abstract

Rhizopus delemar is an opportunistic human pathogenic fungi which belongs to the family *Mucoraceae*. It is responsible for aggressive and rapidly progressive fungal infection in immunocompromised patients. The surge in mucormycosis infection in Covid patients undergoing glucocorticoid therapy has brought worldwide attention towards the severity of this infection. It infects the host through angioinvasion and causes systemic illness. Unfortunately, currently available antifungals, which primarily target the cell wall and cell membrane components are less effective towards this infection. Thus, novel and effective pharmacological targets are needed to overcome these constraints. In that direction, Hybrid histidine kinase III (HHKIII) has the potential to be a therapeutic target because it is only present in the fungal system. They are involved in sporulation, Conidiation, pathogenicity, and other physiological activities. Using bioinformatics tools, we have identified four paralogs of (HHKIII) in *R. delemar*. Notably, we observed a significant difference in expression of these four paralogs under distinct stress conditions. In order to understand its involvement in virulence and pathogenicity, we have also cloned a paralogue of group III hybrid histidine kinase. In *Saccharomyces cerevisiae*, it displays complementation with sln1 mutant and acts as a negative regulator of the Hog pathway. To know whether HAMP domains are important for functionality of group III hybrid histidine kinase, HAMP deletion mutants were also formed.

Altogether, our study points towards an important role of this paralog and highlights its relevance as a crucial drug target.

Key Words: Mucormycosis, Hybrid Histidine Kinase, *Rhizopus delemar,* Covid.

Abstract - 18

Comparative Epidemiology of Covid 19 Pandemic with SARS and MERS Epidemics

Aditi Deshpande[1]

Consultant at Department of Epidemiology, Public Health Foundation of India, IIPH-H, Bangalore Campus, SIHFW Premises, 1st Cross, Magadi Road, Bangalore, Karnataka 560023, India; email:aditid1408@gmail.com;+919881320133

Abstract

Background: The 20th century saw the rise of several respiratory disease outbreaks such as SARS, MERS and Covid 19. World has been grappling with the covid-19 pandemic; from lockdowns to quarantine and isolation, viruses to vaccination; from masking to double masking and sanitization.

Aim: The aim of this study was to compare and evaluate the impact and severity of Covid19 to that of SARS, MERS viral outbreaks over time through indicators: Case Incidence, R0 and CFR. This will help gauge the affected countries' case control, treatment and management strategies.

Methodology: The data for the viral outbreaks were collected from Worldometer, WHO and data science community of Kaggle. The epidemiological and statistical analysis was carried out using *R* software, at the country and continent level for epi-indicators: Cases per 100,000, Deaths per 100,000 and Case Fatality Ratio (CFR) to understand and compare above mentioned epidemics.

Conclusion: The CFR for SARS(10%) and MERS(31%) was higher compared to ongoing Covid-19 (2%). Though for better insight on the CFR, we shall estimate at the end of COVID19. The low CFR of Covid19 can be attributed to various factors- pandemic affected all the countries whereas other two epidemics were limited to specific regions; the immunity developed over time; improved management strategies. Further research in this regard is needed. We must focus on vaccination, case control and management strategies to keep the CFR of Covid19 at minimum.

Key Words: Epidemiology; Covid19, SARS, MERS, Case Fatality Ratio

Abstract - 19

COVID-19 and Vitamin D (Co-VID Study): A Meta-Analysis of Randomized Controlled Trials

Seshadri Reddy Varikasuvu [1], Balachandar Thangappazham [2], Hemanth Raj [3]

[1] Department of Biochemistry, All India Institute of Medical Sciences (AIIMS), Deoghar, Jharkhand, India
[2] StepOne NGO, Pegasus Block, Malleswaram West, Bengaluru, Karnataka, India
[3] Department of Medicine, Mount Medical Centre, Tamil Nadu, India
* Corresponding author:
Dr. Seshadri Reddy Varikasuvu,Assistant Professor, Department of Biochemistry
All India Institute of Medical Sciences,AIIMS, Deoghar, Jharkhand-814142, India
Phone: +91 81 0 61 45 001, E-mail: lifeschemistry@gmail.com
https://orcid.org/0000-0002-2230-4676

Abstract

Background: Vitamin D levels have been reported to be associated with COVID-19 susceptibility, severity and mortality events. We performed a meta-analysis of randomized controlled trials (RCTs) to evaluate the use of vitamin D intervention on COVID-19 outcomes.

Methods: Literature search was conducted using PubMed, Cochrane library, and ClinicalTrials.gov databases (latest search on August 5, 2021). We included RCTs reporting the use of vitamin D intervention to control/placebo group in COVID-19. Two independent researchers did literature search, abstracted data, and the risk of bias assessment.

Results: A total of 6 RCTs with 551 COVID-19 patients were included. The overall collective evidence pooling all the outcomes across all RCTs indicated the beneficial use of vitamin D intervention in COVID-19 (relative risk, RR = 0.60, 95% CI 0.40 to 0.92, Z=2.33, p=0.02, I^2 = 48%). However, no statistical significance was observed for individual outcomes of ICU care (RR = 0.11, 95% CI 0.15 to 1.30, Z=1.48, p=0.14, I^2 = 66%) and mortality (RR = 0.78, 95% CI 0.25 to 2.40, Z=0.66, p=0.02, I^2 = 33%), though decreased rates were noted. The rates of RT-CR positivity were significantly decreased in the intervention group as compared to the non-vitamin D groups (RR = 0.46, 95% CI 0.24 to 0.89, Z=2.31, p=0.02, I^2 = 0%).

Conclusion: COVID-19 patients supplemented with vitamin D are more likely to demonstrate fewer rates of ICU admission, mortality events and RT-PCR positivity. Completion of ongoing trials is largely needed to precisely establish the association between vitamin D use and COVID-19 mortality.

Keywords: Cholecalciferol; COVID-19; Randomized controlled trial; SARS-Cov-2; Vitamin D

Abstract - 20

Multiple Serotypic Infections of DENV: A Trend in The Northern West Bengal, India.

Sudipta Kumar Roy, M.Sc. [1.], Bidyut Krishna Goswami, MD[2], Soumen Bhattacharjee[3]*

[1] Cell and Molecular Biology Laboratory, Department of Zoology, University of North Bengal,
[2] Department of Pathology, North Bengal Medical College and Hospital P.O. Sushrutanagar, West Bengal, INDIA,
Email ID: drbkg61@gmail.com
[3] Cell and Molecular Biology Laboratory, Department of Zoology, University of North Bengal, Raja Rammohunpur, P.O. North Bengal University, Siliguri,
* Corresponding Author:
E-mail: soumenb123@rediffmail.com/ soumenb@nbu.ac.in

Abstract

Background and objectives: Dengue has become a major public health concern in the dengue-endemic northern West Bengal, popularly, North Bengal. It has been severely affected by Dengue in the past few years resulting in morbidities, mass hospitalizations, related complications and deaths. Presently, not available, molecular characterization of the circulating endemic dengue virus (DENV) serotypes is of paramount importance as a part of vaccine development. This study undertakes characterization of circulating dengue serotypes/genotypes of the region, and their phylogenetic analyses, based on capsid (C) and (PrM) region.

Methods: Whole blood (EDTA) was collected from 83 acute symptomatic febrile patients (NS1+) from different health centres, along with clinical parameters through framed-questionnaires**.** Total RNA was purified, followed by the complementary DNA (cDNA) preparation. Serotype determination of dengue infection was done by using conventional PCR and phylogenetic tree was constructed implementing the Maximum-likelihood method.

Results: Out of 83 blood samples 17 were positive for dengue infection. DENV3 was the predominant serotype in the single-infection cases; however, concurrent dual, triple and multi-serotypic infections were also recorded through-out the study.

Interpretation and conclusion: Sequence analysis suggested that both of the DENV1 and DENV3 circulating genotypes are in the genotype III group, and are closely related to the Indian clade. To the best of our knowledge, this is the first report on the genetic characterization of circulating DENVs in North Bengal, which may contribute to the study of dengue pathogenesis, its heterogeneous presentation and in vaccine development.

Keywords: C-PrM, DENV3, Dengue outbreak, Multi-serotypic, North Bengal

Abstract - 21

A Bi-Antigen Recombinant Subunit SARS-Cov-2 Vaccine Comprising S1 Subunit and N Protein Expressed In *Pichia Pastoris*: A Low-Cost, Safe And Effective Candidate For Low- And Middle-Income Countries

Ganesh Kumraj[1], Jainendra Jain[1], Syed Ahmed[1], Davender Bhati[1], Sanket Shah[1], Piyali Majumder[1]

[1] Techinvention Lifecare Pvt. Ltd, #1004, The Summit Business Park, Off WEH Metro Station, Andheri Kurla Road, Andheri East, Mumbai 400093. India. **Email:** syed@techinvention.biz

Abstract

SARS-CoV-2 Spike (S) Glycoprotein is directly recognized by the immune system, representative antigen for T-cell response and key target for neutralizing antibodies. S1 subunit of S protein has RBD which binds to host ACE-2 receptors mediating attachment. RBD has multiple dominant neutralizing epitopes and targeted by neutralizing antibodies. NTD within S1 is also a target for neutralizing antibodies. N protein is highly conserved, abundantly expressed during infection and representative antigen for T-cell response. Both S1 and N protein induce stable immune responses and presents the idea of a bi-antigenic recombinant subunit SARS-CoV-2 vaccine. *Pichia pastoris* is the most desirable expression platform in recombinant technology to produce cost-effective product with high yield and easy to scale up process. Furthermore, *Pichia pastoris* is a suitable host for high expression with several post-translational modifications and offers easy technology transfer to developing countries. Therefore, we have developed a bi-antigenic recombinant subunit SARS-CoV-2 vaccine comprising S1 and N protein using *Pichia pastoris* as the platform technology. As SARS-CoV-2 continues to unleash mayhem globally, there is an urgent need to develop accessible and low-cost vaccine for the developing countries. Our technology addresses several challenges in vaccine design by providing economic and effective option for preventing SARS-CoV-2 infections in developing countries. The platform used to develop the technology has the advantage of not requiring dedicated or specialized facility making it an affordable option using existing manufacturing facilities without significant investments. Highly conserved N protein across coronavirus species makes it an attractive target for universal coronavirus vaccine.

Keywords: Vaccines, *Pichia pastoris*, Recombinant, Technology Transfer, SARS-CoV-2

Abstract - 22

Intravesical BCG Immunotherapy for Non-Muscle Invasive Bladder cancer during COVID-19 Pandemic: Mutual Impact and Implications

Vanshika Lumb[1], Preeti Karwal[1]*

[1] Department of Biochemistry, Deshbandhu college, University of Delhi, Delhi-110019, India.

* **Corresponding Author**: Dr. Preeti Karwal, Department of Biochemistry, Deshbandhu College, University of Delhi, India. Tel: +91 – 9711699469, Email: pkarwal@db.du.ac.in

Abstract

Urinary bladder cancer (BC) is the tenth most common malignancy worldwide, with higher incidence in developed nations. The disease is four times more common in men than women, with 90% of cases diagnosed at the age of 55 years and above. An early stage of tumor that invades up to the lamina propria, but not into the smooth muscle of urinary tissue accounts for 75% of all newly diagnosed BCs and is termed as Non-muscle invasive bladder cancer (NMIBC). The most effective treatment for NMIBC since last three decades is its removal by transurethral resection followed by intravesical immunotherapy with *Mycobacterium bovis* Bacillus Calmette-Guerin (BCG). The COVID-19 pandemic situation has negatively impacted disease management as well as patient care for many life-threatening diseases, including BC. In order to adapt the clinical practice during pandemic, certain adjustments have been recommended in BCG therapy regimen of NMIBC by urologists. Interestingly, there are certain reports of possible protective role of BCG against COVID-19 in NMIBC patients undergoing BCG immunotherapy, while others warn of higher cumulative incidence of COVID-19 infection in NMIBC patients receiving BCG instillations. In this study, we plan to conduct an extensive literature review in order to critically analyse the mutual interplay of BCG immunotherapy for NMIBC and COVID-19 incidence and associated risk. It will not only help us draw conclusions regarding bilateral impact of BCG therapy for NMIBC and COVID-19 but also serve as a basis of pragmatic improvisation of guidelines for BCG therapy of NMIBC during COVID-19 health crisis.

Keywords: Bladder Cancer, NMIBC, BCG, COVID-19, Immunotherapy, Intravesical BCG therapy

Abstract - 23

Genome-Wide Screening of Immunodominant T and B cell Epitopes in Spike Glycoprotein of SARS-CoV-2 Emerging Variants Of Concern

Shatadha Spandan[1]

[1] Department of Zoology, Daulat Ram College, University of Delhi, India

Abstract

Since reported first in Wuhan, Spike glycoprotein (S protein) of 2019-nCov has been undergoing several synonymous and non-synonymous mutations. Many of the mRNA, viral vector and protein subunit-based therapeutic COVID-19 vaccines target the S protein of SARS-CoV-2. However, as evidenced from Israel and other nations, many people vaccinated with therapeutic S protein-based vaccines are now susceptible to highly contagious novel SARS-CoV-2 Variants of Concern (VOC). This results due to the escape mechanisms adapted by SARS-CoV-2 VOCs when an individual's 2019-nCov specific antibodies cannot recognize these VOCs. Sequence conservation analysis showed that irrespective of escape mechanisms, D614G like mutations are conserved across VOCs. This strengthens the fact that due to purifying selection, which shapes the evolution of virus populations, even in any future variants of 2019-nCoV, these conserved mutations may remain as they are. A pan-corona virus vaccine aiming to develop immunogenicity and promiscuity against all the existing VOCs and any future variants will aid in this context. This study uses robust immunoinformatics approaches to identify potential human B cell, CD8+, and CD4+ T cell-specific epitopes in context to spike glycoprotein region substituted with all the known synonymous and non-synonymous mutations that constitute the SARS-CoV-2 VOCs (Alpha (B.1.1.7), Beta (B.1.351), Delta (B.1.617.2) and Gamma (P.1)). Usage of these epitopes in a multi-epitope vaccine candidate will aid in combating a higher degree of hospitalization and deaths caused due to the highly severe SARS-CoV-2 VOCs and bring a curb on the pandemic.

Keywords: SARS-CoV-2, Variants of Concern, Pan-corona virus vaccine, Epitopes, T cell, B cell

Abstract - 24

In-Silico Analysis of Ivermectin Drug Off-Target Human Proteins

Simran Walia[1] and Poonam Sharma[1]*

[1] Department of Zoology, Gargi College, University of Delhi, Delhi-49, India
* Associate Professor, Department of Zoology, Gargi College, University of Delhi, India
Email: poonam.sharma@gargi.du.ac.in,
Contact no.: +91-11-46040310

Abstract

COVID-19 is an infectious pandemic caused by the severe acute respiratory syndrome corona virus 2 (SARS-CoV-2). Researchers from all around the world are repurposing medicines that might be beneficial in combating coronavirus, but these come with a slew of side effects and issues. Ivermectin, an antiparasitic drug is approved for Covid-19 patients and is reported to bind with importins (IMPα/β1) and blocking viral replication. It also binds to glycine receptor alpha-3 (GLRA-3) leading to increased membrane permeability to chloride ions causing hyperpolarization of the cell and killing of the parasite. In this study, *in-silico* analysis of off-target proteins of ivermectin was done to understand this drug's disrupting effects on other biological processes in humans. Using databases, ivermectin was found to binding to two off-target protein families GLR and GABA, and five proteins: CHRNA6, VWC2L, HTR3A, TNPO1, and CNGB1 owing to the structural similarities with GLRA-3 and IMPα/β1. GLR receptors proteins function as neurotransmitter-gated ion channels and when blocked leads to muscular rigidity. Excitatory imbalance of GABA receptor family can result in neuronal injury as detected in neurodegenerative disorders. CNGB1 protein plays important role in both visual and olfactory signal transduction, CHRNA6 and HTR3A are neural receptor proteins involved in neurotransmission and VWC2L protein is involved in neurogenesis. By binding to off-target proteins, ivermectin can disrupt signal transmission in the CNS and neuroactive ligand-receptor interactions in the human biological system. Thus, leading to severe side effects like blurred vision, hypotension, visual hallucinations, loss of coordination and balance, depression, and seizures.

Keywords: COVID19, SARS-CoV-2, Ivermectin, GLRA-3, GABA

Abstract - 25

Alcoholism and Hepatocellular Carcinoma

Suman Deshwal[1], Minakshi Vashist[2] and Rajiv Gupta[3]

[1] Research Scholar, Deptt. of Genetics, M.D. University, Rohtak
[2] Professor, Deptt. of Genetics, M.D. University, Rohtak
[3] Sr. Professor and Head, Deptt. of Psychiatry, Pt.B.D.S.University of Health Sciences, Rohtak
Email: sumandeswalgenetics@gmail.com

Abstract

Alcoholism is a condition characterized by alcohol cravings, compulsive and uncontrollable alcohol consumption .It is a very serious global health issue . Alcohol consumption is associated with an increased risk of the Liver cancer. Worldwide epidemiology data of Alcoholic hepatocellular carcinoma suggests that alcohol accounts for around one third of global incident cases of primary liver cancer. Hepatocellular carcinoma is ranked the sixth most common form of cancer globally, and is the third most common cause of cancer mortality. Ethanol is not carcinogenic but has to be viewed as a procarcinogen involved in the development of Alcoholic hepatocellular carcinoma. This process is triggered by Reactive oxygen species including activated molecules derived from ethanol or acetaldehyde metabolism attacking hepatocellular DNA. To prevent Alcoholic hepatocellular carcinoma, individuals with an alcohol problems must early be identified in order to achieve alcohol abuse, because only a long period of abstinence will substantially reduce the risk of Alcoholic hepatocellular carcinoma initiation, short term abstinence contributes not or little to risk reduction. In other words, early abstinence is better than late abstinence.

Keywords: Alcoholism, Hepatocellular carcinoma, Procarcinogen

Abstract - 26

In-silico Study of Phytochemicals for Anticholinesterase Activity as a Potential Drug Target against Alzheimer's Disease

Tushar T Khandagale[1#], Kuldeepkumar Singh[1#], Sangeeta Sinha[1*], Akshita Puri[2*]

[1] Department of Zoology, Nowrosjee Wadia College, Pune, India, Savitribai Phule Pune University, Pune, India
[2] P.G.T.D Zoology, R.T.M Nagpur University, Nagpur, Maharashtra, India
* Corresponding authors
Dr. Sangeeta Sinha - sangeeta.amma@gmail.com
Dr. Akshita Puri Bajaj - akshitapuribajaj@gmail.com
\# Presenting authors:
Tushar T Khandagale- tushar763425@gmail.com
Kuldeepkumar Singh- kuldeep621998@gmail.com

Abstract

Alzheimer's disease (AD) is a neurodegenerative age-linked fatal disease of the central nervous system reported to be increasing at a very high pace across the globe. AD pathology is characterized by down-regulated levels of neurotransmitter acetylcholinesterase in the neocortex and hippocampus and aberrant processing and polymerization of Amyloid Precursor Protein (APP). The neurotransmitter acetylcholinesterase (AchE) and butyrylcholinesterase (BchE) play a central role in the cholinergic functioning of the brain. Presently, there is no clinical treatment or therapy available for AD. However, anticholinesterase drugs are being used to regulate levels of ChE activity. But these synthetic drugs have several side effects like diarrhea, dizziness, drowsiness, fever, hallucinations and trouble breathing. In the present study, *in silico* analysis of anticholinesterase activity, using molecular docking method for 12 plant phytochemicals revealed that three plant based compounds- Quercetin, Cirsimartin and Genkwanin could be potential drug candidates as they showed high binding affinity and interaction with the target proteins AchE and BchE. These phytochemicals may play important role in regulating ChE activity in AD patients and also, they are previously reported to play a key role in the alteration of other AD contributing factors. Thus, present study reports potential drug targets which can be used for the development of drug against AD after experimental validation.

Keywords: Alzheimer's disease; Anticholinesterase activity; Drug development; Molecular docking; Phytochemicals.

Abstract - 27

Bacterial Growth Inhibitory Activity of the Maceratives of Prepupal Stages of Black Soldier Fly (BSF) (*Hermetia illuncens* L.).

Vitthalrao B. Khyade

Shardabai Pawar Mahila Mahavidyalaya, Shardanagar Tal. Baramati Dist. Pune – 413115 India.
vbkhyade.2016@gmail.com

Abstract

The attempt is dealing with of effect of maceratives of prepupal stages of black soldier fly (BSF) (*Hermetia illuncens* L.) in methanol on the inhibition of the growth of selected bacterial species. The bacterial species used for the study include: *Salmonella typhimurium* (L.); *E*scherichia *coli* (L.); *Pseudomonas aeruginosa* (L.); *Bacillus cereus* (L); *Bacillus subtilis* (L); *Streptococcus cremoris* (L); *Streptococcus faecalis* (L); *Staphylococcus aureus* (L); *Klebsiella pneumoniae (L); Salmonella enterica* (L) and *Proteus vulgaris* (L). Various strengths in ppm (mg/Lit) of methanol maceratives of prepupal stages of black soldier fly used in the study include: 50; 100; 150; 200; 250 and 300. The diameter (mm) of growth inhibition zone in the bacterial species in the attempt through the use of standard antibiotic compound (chloramphenicol) was found measured 14.76 mm to 35.78 mm. The use of methanol maceratives of prepupal stages of black soldier fly was reported inhibiting the growth bacterial species in the attempt. The bacterial growth inhibition for the methanol maceratives of prepupal stages of black soldier fly zone was ranging from 7.13 (± 0.27) to 20.55 (± 4.93) mm units. The use of methanol maceratices of prepupal stages of black soldier fly is highlighting the potential challenges towards the efforts on developing therapeutic antibacterial product.

Key Words: Antimicrobial Proteins; *Hermetia.illucens*L.; Bacterial Species; Maceratives.

Abstract - 28

Prevention and Management of the Severe Acute Respiratory Syndrome Coronavirus- 2 (SARS Cov-2) Through Endogenous Nitric Oxide Production During Bhramari Pranayama- A Review

Chitra Chand[a], Dhananjoy Shaw[*]

[a] Research Scholar, Department of Yoga Science, University of Patanjali, Haridwar, Uttarakhand, India, *chitra.chand5@gmail.com, +919971965347*

[*] Head of Department, Department of Physical Education and Sports Sciences, University of Delhi, Delhi, India, *dhananjoyshaw1960@gmail.com, +918373998064, *Corresponding author*

Abstract

SARS CoV-2 is a single stranded positive RNA virus of Coronaviridae family that is highly contagious and has caused over four million deaths and infected 185 million lives worldwide. Similar to other viral infections it triggers the immune response of the body that results in the innate and acquired immune responses in the hosts' body. Nitric oxide (NO) is a gaseous neurotransmitter, mediator and an immunomodulator synthesized by certain cells and tissues of the body that stimulates the innate response of the host towards the viral pathogen. Most of the NO produced in the respiratory tract is synthesized by the paranasal sinuses and its production increases by 15 to 20 times during humming as compared to normal exhalation. The potential role of nitric oxide in the management of the disease was widely studied during SARS CoV pandemic and it was observed that NO reversed pulmonary hypertension and also, improved hypoxia and reduced the stay on intensive support systems thereby, improving the survival rate of the infected patients. Researches have depicted that bhramari pranayama (the humming bee breath), increases endogenous nitric oxide in the respiratory tract and other body parts. Therefore, this review will enlighten the role of bhramari pranayama and other similar chanting during exhalation and how it will positively coordinate the effect on the mechanism of action of SARS-CoV-2 in regard to nitric oxide. The analysis will enhance the knowledge on whether endogenous nitric oxide production through humming bee breath will help in prevention and management of Coronavirus disease.

Keywords: SARS CoV-2, bhramari pranayama, nitric oxide, humming, immunity, coronavirus disease, prevention, viral infection

Abstract - 29

Biological Characteristics of SARS-CoV-2 Variants of Concern (VOC) and their Prevalence across India

Nimita Kant*, Shamashree Samanta, Ishika Panchal, Abhishek Pandey, Lagna Ghatak, Adyasha Rout, Jitendra Kumar Chaudhary*

Department of Zoology, Shivaji College, University of Delhi, New Delhi-110027

* Authors for Correspondence: nimita@shivaji.du.ac.in ; jnujitendra@gmail.com

Abstract

The origin of current pandemic has categorically been traced to SARS-CoV-2 outbreak originally reported from Wuhan, the capital of Central China's Hubei province, in December 2019. Thereafter, it spread globally, causing devastating severe respiratory infections in humans and various other mammals. The illness caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is referred to as coronavirus disease 19 (COVID-19), which is responsible for millions of death worldwide. With the passage of time, the original virus, referred to as severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1 (RefSeq NC_045512), evolved into various variants owing to acquisition of genome-wide mutation. Such genomic alterations, involving point mutation and deletion, led to emergence of several variants, such as Variant of Interest (VOI), Variant of Concern (VOC) and Variant of High Consequences (VOHC), throughout the pandemic. This variant classification scheme was developed by the US government SARS-CoV-2 Interagency Group (SIG), principally aiming at rapid characterization of emerging and evolving variants, and monitoring the impact of potential prophylactic and therapeutic measures, including vaccines, pharmacological intervention, as well as diagnostics. Our comprehensive study entails crucial discussion with regard to multiple SARS-CoV-2 variants; namely Alpha (B.1.1.7 + Q sublineages), Beta (B.1.351 and sublineages, B.1.351.2, B.1.351.3), Gamma (P.1 and P.1 sublineages**)** and Delta (B.617.2 and all AY sublineages), and their properties, such as transmissibility, reduction in antibody-mediated neutralization, virulence, disease severity, vaccine effectiveness, diagnosis, and prevalence across the India. Our preliminary data on VOC, pooled from the Global Initiative on Sharing All Influenza Data (GISAID) (https://www.gisaid.org/hcov19-variants/) on 9 September 2021, shows around 87% prevalence of Delta VOC among the total genome variants sequenced across various Indian States.

Abstract - 30

The effect of ABO blood group and antibody class on susceptibility and severity of COVID-19 infection

Priya Bhardwaj[1], Sunita K. Yadav[2] and Jyoti Taneja*

[1] Department of Zoology, University of Delhi-110007
[2] Daulat Ram College, University of Delhi-110007
* Corresponding author- Daulat Ram College, University of Delhi-110007

Abstract

Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), causing the current COVID-19 pandemic, has led to over 230 million infected cases and 4 million deaths worldwide that cause immense strains on healthcare systems worldwide. Since the COVID-19 outbreak in December 2019, research has been focused on its treatment and preventing the disease spread. Currently, there is no biological biomarker available that can predict the susceptibility and severity of COVID-19 infection. Several studies reported an association between the ABO blood group and susceptibility or resistance to various infectious diseases. In the present study, we have used the cross-sectional survey study data to decipher the relationship between ABO blood group and susceptibility and severity of COVID-19 infection. Further, we have also investigated the potential role of antibody class on the risk of COVID-19 infection. Our results indicated that blood group B individuals had higher susceptibility to acquire COVID-19 infection. In contrast, blood group A was associated with a lower risk of acquiring severe COVID-19 infection. Further, we extended the analysis to study the association of antibodies; anti-A (blood groups B and O) and anti-B (blood groups A and O) with COVID-19 infection. Analysis of antibody classes showed anti-A antibody associated with a high predisposition to acquire COVID-19 infection. The present study indicates that blood group B and anti-A antibodies are associated with proneness to COVID -19 infection and severity however, additional data on COVID-19 infected patients in the different populations are required to validate our findings.

Abstract - 31

Phage Therapy in the Treatment of SARS-COVID-19 Infection

Aashi[1] and Jyoti Taneja[2]

[1] Department of Life Sciences, Daulat Ram College, University of Delhi, Delhi-110007, INDIA, Email: aashimakhija829@gmail.com

[2] Dr. Jyoti Taneja, Department of Zoology, Daulat Ram College, University of Delhi,

Abstract

Since Dec. 2019 Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) has spread at an alarmingly high rate failing healthcare systems, crashing the world's economy, and taking a massive toll on human lives which accounted for a total of 231,003,493 cases and 4,735,234 deaths (as per the United Nations Geoscheme Worldometer's COVID-19 data up to 20 Sept.2021). To date, no known antiviral therapy or vaccine claims to pose zero side effects or no harm. Phages may contribute to antiviral immunity while maintaining the homeostasis of the human microbiota. By inhibiting the activity of NF- Kappa B and Reactive Oxygen Species (ROS) production, phages can counter-regulate the excessive inflammatory reactions responsible for the high mortality rate due to COVID-19. Phagicin, one of the antiviral agents produced as a result of phage replication acts as a barrier for replication of viral DNA while causing no harm to host DNA. Repurposing phage therapy for viral infections can help us get the "magic pill."

Keywords: Phage therapy,antiviral, NF-Kappa B, ROS, phagicin

Abstract - 32

Application of Artificial intelligence and Personalized Machine Learning for Cancer Immunotherapy

Sharma Charu

Daulat Ram College, University of Delhi, New Delhi
charusharma2606@gmail.com

Abstract

Artificial intelligence means the ability of a machine to mimic human intelligent behavior for performing complex tasks with minimal human intervention.

Tumor cells are genetically unstable, compared to normal cells, henceforth, there is a large incidence of mutations. The expression of these mutations can produce tumor-specific antigens called neoantigens. Neoantigens are highly immunogenic and can activate an immune response, as they are not present in normal tissues and are linked to the tumor mutation. Therefore, the identification of these neoantigens can assist in maneuvering the immune system to differentiate between cancer and non-cancer cell types.

AI can be used to identify mutated HLA-I and HLA-II neoantigens and can open gates for personalized vaccines. It can also be used to identify individuals who are crucial to personalized cancer immunotherapy, to select patients for therapy and to predict outcomes of the immunotherapy. This workflow begins with patient observation, using algorithms to screen variables and searching combinations for predicting outcomes. These features of artificial intelligence can prove to be highly useful in cancer immunotherapy and management of the disease, owing to its improving accuracy for diagnosis, refined treatment plans and reducing human resource costs.

The prominent advantage of using AI in medicine remains that it can exploit data extracted from medical images that would not be possible with human analysis. However, one of the main barriers, is the insufficient amount of data available, machine learning can be possible by feeding large amounts of data to train the algorithm.

Keywords: Artificial intelligence, neoantigen, immunotherapy, cancer vaccines, immunopeptidomes

Abstract - 33

Sex difference in immune responses and their impact on the presentation of Corona virus infection

Barasa Rani Kalita, Divya Mehul and Rita Singh

Division of Molecular Endocrinology and Reproduction, Department of Zoology, University of Delhi, Delhi-110007

Abstract

Severe acute respiratory syndrome coronavirus (SARS-CoV-2) is one of the highly pathogenic coronavirus and is the causative agent of coronavirus disease 2019 (COVID-2019). The entry of SARS-CoV-2 virus into the target cell is mediated by binding of its spike protein (S-protein) to angiotensin converting enzyme-2 (ACE-2) receptor which is a transmembrane receptor protein of the renin-angiotensin-aldosterone system. Another important transmembrane protease, serine 2 (TMPRSS2) is also involved in the process of viral entry by priming the S-protein. A significant difference is observed in the susceptibility towards COVID-19 between men and women, men being more susceptible. Women appear to be more immune privileged then men because of the difference in sex hormones. Sex chromosomes associated factors and sex hormones have a modulatory role in the immune responses against SARS-CoV-2 infection. Furthermore, responses to various types of vaccination may also be influenced by the sex of the patient. Sex-based biological mechanisms underlying the differences in immune responses and its association with severity of corona virus infection in populations in different countries substantiate these observations. Therefore, we discuss here the gender-based differences in immune responses generated against various infections.

Keywords: Coronavirus disease 2019, Severe acute respiratory syndrome coronavirus, sex hormones, vaccination.

Abstract - 34

Correlation Between COVID Infection and Patients Suffering from Comorbidities: A Meta-Analysis

Tejendra Kumar and Luni Sharma*

Assistant Professors, Department of Zoology, Maitreyi College, University of Delhi, New Delhi-110021

* Correspondence to: luni@maitreyi.du.ac.in

Abstract

The outbreak of COVID-19 raised concern for individuals suffering from underlying disease as most of the COVID-19 patients were suffering from pre-existing diseases. The published data also suggested that comorbidities increase the severity and mortality of COVID-19 patients. This study aimed to determine an accurate proportion of COVID-19 disease in the morbid and old aged patients. By extracting and analyzing available published clinical data, the present study finds out the correlation of comorbidities and Coronavirus infection. In our results, mainly eight comorbidities have been identified globally that are prevalent for the infection. Specifically, pre-existing disease Hypertension, and obesity patients were more in number among COVID-19 infected patients than diabetes, smoking, cardiovascular disease, chronic kidney disease, cancer, and lung disease. This is contrary to other results where, after hypertension, heart disease, and diabetic patients were more affected by COVID-19 infection. We have also found the prevalence of COVID-19 patients with pre-existing hypertension was most in many regions like Canada, Italy, Switzerland, and America, while obesity was mainly in countries like China and America. These findings will help in making of better policies and overcome the susceptibility percentage factor in old age persons who are suffering from different morbidities.

Keywords: Pre-existing disease, Covid-19, Hypertension, Diabetes, Obesity.

Abstract - 35

Metabolomics and Metagenomics of Gut Microbiota to Rescue Diabetic Patients

Siya Ram*, Ravi Rajwanshi, Neera Kapoor

Discipline of Life Sciences, School of Sciences, Indira Gandhi National Open University, New Delhi, India

Abstract

Diabetes is a serious metabolic disorder spread throughout the world and among all age groups. Recent experiments and clinical studies have shown the possibilities of utilizing the medicinal plant-based antioxidant therapies as a novel approach to rescue diabetic patients. The disease has been associated with a sedentary lifestyle along with a rapidly growing urban lifestyle and industrialization. Researchers have shown that diabetes pathogenesis could be attributed to specific pathogens invading the gut and bile acids released by the microbiota. The methodology of integrating metabolomics and metagenomics knowledge to study gut microbiota can be a beneficial tool to establish a correlation between diabetes and the gut microbiome. The long-term damage, dysfunction, and failure of different organs such as the eyes, kidneys, nerves, heart, and blood vessels, are related to chronic hyperglycemia of diabetes mellitus. Medicinal plants, microbial products, and genetically engineered microbes can be used to cure diabetes. By the introduction of significant numbers of beneficial microbes in the gut for the diabetes prophylaxis, researchers believe that such approach could improve the regulation of blood glucose level which is the main cause for diabetes. Research have shown that diabetes is attributed to high-risk genes and the response of the body to its intestinal microbiota. Global association analyses, among the thousands of profiled microbes, may relate to the future diagnoses of diabetes. The interrelationships between gut microbiota and host metabolism need to be well elucidated to recommend a suitable way of life and wholesome rules.

Keywords: Diabetes, Gut microbiota, Medicinal plants.

Abstract - 36

HIV Infection and Vaccine

RAJNI ARORA

Associate Professor, Zoology Department, Swami Shraddhanand College, Alipur, (University Of Delhi), Delhi-110036
Email: rajniarora@ss.du.ac.in, Phone No. 9873833223

Abstract

The infections by virus are a great threat to our immunity but array of powerful vaccines have successfully protected mankind from the attack of many of them. HIV is a tough enemy of human body as it eludes the immune system by various mechanisms. It attacks immune cells causing a disease which gradually progresses to AIDS in some infections. Despite the success of the ART, which has converted its infection into a manageable chronic condition, it is a major global health problem as 37.7 million people worldwide are HIV infected. ART is a lifelong treatment where a variety of drug options are designed to replace its resistant forms. Vaccine can protect from the stigmatized disease of HIV and also control it in the absence of ART. In stark contrast with the speed with which the Covid-19 vaccines were developed in two years of pandemic, an effective vaccine for HIV is still a challenge after decades of ongoing research. Coincidently, both HIV and SARS-CoV-2 are pandemic causing mRNA viruses, which have spilled from animal source. They mutate and attach to their host cells with their surface spikes. The paper is a review on the status of HIV/AIDS pandemic, unique challenges by the complex structure of virus for the development of conventional vaccines and a hope from the novel game changing mRNA vaccine. After the recent success of mRNA vaccine for Covid-19, it may become a promising tool to defeat HIV also by providing RNA based HIV immunogens to trigger body’s immune response.

Keywords: HIV, AIDS, Vaccine, Pandemic, m RNA vaccine, ART, Immunogen

Abstract - 37

Insights into the Structure and Function of Fatty Acid Pathway Proteins of *Leishmania major* to Identify Potent Anti-Leishmanials

Chetna Dhembla[1], Ravindra D. Makde[3], Swati Saha[1] Monica Sundd[2]* and Suman Kundu[1]*

[1] Department of Biochemistry, University of Delhi South Campus, Benito Juarez Road, New Delhi-110021

[2] National Institute of Immunology, Aruna Asaf Ali Marg, New Delhi-110067

[3] High Pressure and Synchrotron Radiation Physics Division, Bhabha Atomic Research centre, Mumbai- 400085

[4] Department *of Microbiology, University of Delhi South Campus, Benito Juarez Road, New Delhi-110021*

Abstract

Leishmaniases imposes devastating impacts on world's population. The increasing prevalence of drug resistance, necessity for long-term treatment regime, unavailability of functional drugs, the related expenditure, and the growing number of immuno-compromised individuals, due to coinfection of HIV underscores the need for new drugs as well as drug targets.

Genome sequencing has led to the discovery of Type II Fatty acid synthesis pathway in *Leishmania*. An indispensable enzyme of the pathway is 4’ phosphopantetheinyl transferase (PPT) which catalyzes the transfer of 4’-phosphopantetheine arm from Coenzyme A to the conserved serine residue of the Acyl carrier protein. Phosphopantetheinyl transferase from other pathogens viz *M. tuberculosis*, *P. aeroginosa* have been shown to be important for the survival and pathogenecity of the microorganism. Since, *Leishmania* genome encodes a single PPT, it can act as a potential drug target and the understanding of the PPT as well ACP proteins may lead to the design of novel therapeutics against the deadly disease leishmaniasis.

Thus, the present study involves biophysical (Fluorescence, CD Spectroscopy) and biochemical characterization (Native PAGE, C18 reverse phase HPLC, SPR) along with structure determination (X-ray crystallography and NMR) of ACP of the type II fatty acid pathway of *Leishmania*. To speed up the search of a novel inhibitor the study also focuses on exploring the current drug repurposing strategies by screening small molecule chemical libraries as well as synthesized compounds against the *L. donovani* promastigotes, axenic amastigotes and intramacrophagic stages of the parasite followed by calculation of the IC_{50} values and determining the cytotoxic effects of the molecules. We also aim to take forward these inhibitors to animal models of Leishmaniasis.

Abstract - 38

Isolation and Characterization of *Cronobacter Sakazakii* from Dairy Products

Shruti Sharma and Alka Prakash

Cell Biotechnology Lab, Department of Zoology, Faculty of Science,
Dayalbagh Educational Institute, (Deemed University) Agra-282110
E-mail: drshrutisharma6@gmail.com

Abstract

Cronobacter sakazakii is a ubiquitous microbe that has been isolated from a wide range of food products like milk powder, herbs, spices, cheese products, meat, and vegetables but its origin is still obscure. It has also been isolated from a number of environmental and clinical samples like soil, dust, water and blood and CSF. It is a gram-negative, motile, non- spore forming, rod shaped bacterium and belongs to the family Enterobacteriaceae. Some strains of *C. sakazakii* have been reported to survive in a desiccated state for more than two years. *C. sakazakii* causes septicemia, meningitis and necrotizing enterocolitis in infants and immunocompromised individuals. ICMS (International Commission of Microbiological Specifications for foods) has given a status of “severely hazardous bacteria” to *C. sakazakii* in 2002. In the current study this bacterium has been isolated from milk and milk products and the effect of various stresses has been studied on the bacterium. Some antibiotics and probiotics were used as control for these isolates among these Cefotaxime, Ciplofloxacin, Ofloxacin and Co-trimoxazole were found to be most effective against all tested isolates.

Abstract - 39

Lifestyle and Cancer Risk

Shramana Guchhait[1], Ojaswita Pant[2], Gunja[3], and Jyoti Taneja[4]

[1] Daulat Ram College, University of Delhi, 4, Patel Marg, Maurice Nagar, Roop Nagar, Delhi, 110007, Email - shramanaguchhait884@gmail.com

[2] Miranda House, University of Delhi, GC Narang Road, University Enclave, New Delhi, Delhi - 110007, Email - ojaswitapant1999@gmail.com

[3] GD Goenka University, Gate No 3: GD Goenka educational city, Sohna - Gurgaon Rd, Sohna, Haryana - 122103, Email- Gunjakumari9902@gmail.com

[4] Department of Zoology, Daulat Ram College, University of Delhi, 4, Patel Marg, Maurice Nagar, Roop Nagar, Delhi, 110007, Email - jyotitaneja@dr.du.ac.in,

Abstract

Cancer is caused by the unwanted division of the abnormal cells which further metastasizes by invading the nearby blood vessels. According to the global cancer statistics of 2020 published by the American Chemical Society, around 19.3 million cases related to cancer were registered, and approximately 10 million deaths occurred. These figures are expected to witness a 47% rise, to almost 28.4 million cases in 2040. As reported by WHO in 2018, one in ten Indians will develop cancer during their lifetime and one in fifteen will die of cancer. This trend is highly influenced by the social, economical, and demographic changes in the lifestyle around the world. Genetic inheritance leads to only about 5-10% of all cancer cases, while about 90-95% contribution to the increased mortality rate is due to environmental and lifestyle changes like tobacco smoking, obesity, physical inactivity, environmental risks, sexual and reproductive health, unhealthy diet, commonly used household chemicals and cosmetics, and alcohol consumption. We plan to do a comprehensive review of previous research studies from the period of 2016-2020 and study how certain lifestyle changes contribute to the rise in cancer cases in recent times.

Key Words: Cancer, lifestyle, smoking, obesity, physical inactivity

Abstract - 40

Post COVID Infections

Vaishali Pant[1] and Jyoti Taneja[2]

Life sciences, Daulat Ram College, University of Delhi, Email: vaishalipant0008@gmail.com
Department of Zoology, Daulat Ram College, University of Delhi

Abstract

Introduction: Covid 19 has become a global health pandemic since late November 2019. In a few patients who have been infected with SARS-CoV-2, it has been reported that the virus has new recurring, or symptoms, four or more weeks after infection. Post-COVID conditions have been reported in patients who had mild or asymptomatic conditions or shown acute illness during the infection.

Aim of the research: The aim of the study is to know more about the underlying cause of Post COVID infections, and the variation in percentage of individuals being infected in comparison to the general population.

Methodology: An analysis of various reports and reviews was carried out and data was collected which was used to investigate this domain.

Result: Researchers are still in the process of understanding the various Post covid conditions. To this date, the commonly reported conditions include: fatigue, dyspnea, chest pain, joint pain and exhaustion. According to the studies carried out in Italy, 87.4% patients had heavy persistence of at least one symptom, especially dyspnea and fatigue. When compared with the general population, the individuals discharged from hospitals after Covid 19 showed an increase in the rates of multiorgan dysfunction.

Conclusion: Fatigue and anhedonia were prevalent and commonly reported in patients recovering from Covid 19. Due to the prolonged stay in the Intensive care units (ICU), many people developed ICU-acquired weakness which led to a disturbance in their socio-occupational functioning. In several patients diagnosed with Covid 19, incidences of viral pneumonia have been reported. Rehabilitative facilities involving motor and pulmonary rehabilitation treatment must be provided to patients after Covid 19 to prevent post covid syndrome, in which long-term chronic fatigue is associated with post-exertional neuroimmune exhaustion.

Keywords: Covid 19, Post Covid, fatigue, anhedonia, pandemic

Abstract - 41

Oncolytic Virus Mediated Cancer Therapy

Anchita Roy

Dept. Of Biotechnology, University of Bhuvneshwar.

Abstract

Cancer is basically uncontrollable growth of any organ or tissue of the body . They invade their boundary and spread to other organs ,which is called metastasis. Oncolytic viruses represent a new class of therapeutic agents to promote anti tumor responses through a dual mechanism one is selectively killing of tumor cells and other is induction of systemic anti tumor immunity.

Oncolytic engineered virus will infect only cancer cells and stimulate reversing inhibition of adoptive immunity by blocking T cell checkpoint pathways or it lyse tumor cells and from their antigenic molecule adaptive immunity will stimulate against tumor cells ,also stimulate dendritic cell ,NK Cell like innate immune cells.

In this technique there are some positive as well as negative points but how we will be able to use this technique and what should be the protocol for the therapy I wanted to show those points via my presentation.

Abstract - 42

Skin and Soft Tissue Infections

Khushi Goel[1] and Jyoti Taneja[2]

[1]Daulat Ram College, University of Delhi, Patel Marg, Maurice Nagar, Delhi, India-110007
Email ID - khgoel217@gmail.com
[2] Department of Zoology, Daulat Ram College, University of Delhi, Patel Marg, Maurice Nagar, Delhi, India-110007 Email ID - jyotitaneja.dr.du.ac.in

Abstract

The skin is colonized by a diverse collection of microorganisms which, for the most part, peacefully coexist with their hosts. Skin and soft tissue infections (SSTIs) encompass a variety of conditions, account for a large percentage of infections requiring hospitalization, and are associated with substantial morbidity. In immunocompromised hosts, SSTIs can be caused by diverse microorganisms-most commonly bacteria, but also fungi, viruses, mycobacteria, and protozoa. The diagnosis of SSTIs can be a huge challenge because the symptoms often masquerade as other clinical syndromes or can be a manifestation of systemic disease.

The variations in clinical presentations of SSTIs in different patients, account for a challenging definitive diagnosis of disease. Clinical dermatological assessment should be performed to identify the pathogens, which will lead to appropriate treatment. Etiology including cultures of lesions and blood, biopsy with histology, specific microbiological analysis with special stains, molecular techniques, and antigen-detection methodologies are some of the strategies that can be adopted to diagnose the disease.

In the study, we have done an interdisciplinary review of essential principles of the diagnosis and therapy of SSTIs, reflecting present knowledge supported by evidence-based medicine.

Keywords: skin and soft tissue infections - SSTIs - diagnosis - therapy, immunocompetent patients.

Abstract - 43

Saving Mankind Affecting Marine Life! Covid Dilemma

Anita Garg Mangla [1]*, Neeru Dhamija [1]*, Prerna Lal [2], Bhawana Gaur [2]

[1] Assistant professor, Department of Biochemistry, Daulat Ram College, University of Delhi, Delhi 110007, India

[2] Student, Department of Biochemistry, Daulat Ram College, University of Delhi, Delhi 110007, India

* Corresponding Authors: anitamangla@dr.du.ac.in, 0091-9811088789, Department of Biochemistry, Daulat Ram College, University of Delhi, Delhi 110007, India
neerudhamija@dr.du.ac.in, 0091-9871631316, Department of Biochemistry, Daulat Ram College, University of Delhi, Delhi 110007, India

Abstract

Covid-19 is a highly contagious viral illness caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and was first reported in Wuhan, China on December'2019. It has emerged as one of the most consequential global health crisis since the era of the influenza pandemic 1918 and had a catastrophic effect on the world's demographics resulting in more than 4.75 million deaths worldwide, and was declared as a global pandemic by WHO on March 11th, 2020. Globally covid-19 for has affected not only human lives, economies and government but also other organisms food chain living on land, air and water. This global spread of virus resulted in overwhelming usage of plastics: single use mask, shields gloves, personal protective coveralls, sanitizer bottles to name a few. It did have a positive impact on marine life during the lockdown, but later on when there was a massive outbreak of the disease, about 80% of the marine debris consisted of micro and macro plastics. As per WHO estimates, every month the world needs 76 million plastic examination masks, 89 million plastic medical masks and 1.6 million plastic protective goggles. The year long efforts to reduce its usage and manage its disposal are drastically getting reversed due to its high demand in this pandemic era. As per current estimates about 75% of covid-19 plastic will become waste, clogging the landfills and floating in seas. Not only the surge in plastic waste has become a big problem but at the same time it has been witnessed that recycling plastic has become more expensive than making new plastic. Data suggests about 3.4 billion one time use masks/ face shields are discarded daily, globally. The paper focuses on not only addressing the plastic surge and careless ways of its disposal but also the changes that need to be implemented at the grass root level for coping with the problem.

Key Words: Covid-19, Plastic, Disposal, Marine

Abstract - 44

Building Natural Immunity with Nature Cure by Focusing on Gut Dysbiosis – A Meta-analysis

Sinha Pritam [1], Taneja Jyoti[2], Misra Monica[3], Gambhir Geetu[4] Jetly Sunita[5]*

[1] Swami Vivekananda Anusandhana Samanthana,Bengaluru, Karnataka
[2] Zoology Department, Daulat Ram College, University of Delhi-110007
[3] Department of Zoology, Acharya Narendra Dev College, University of Delhi-110019
[4] Department of Chemistry, Acharya Narendra Dev College, University of Delhi-110019
[5] Department of Biomedical Sciences, Acharya Narendra Dev College, University of Delhi-110019
* Corresponding Author: Dr. Sunita Jetly, Associate Professor, Acharya Narendra Dev College University of Delhi, Delhi-110019, India, Phone: +91 9312922180; E-mail: sunitajetly@andc.du.ac.in

Abstract

In light of recent emerging evidence based Scientific research under Human Gut microbiome project, Gut Dysbiosis has been identified as fundamental root cause of infectious as well as chronic illnesses like Diabetes, Hypertension and Cancer. Gut Dysbiosis is a situation wherein our self-healing mechanism fails to eliminate toxins accumulation in Gastrointestinal tract which results as uncontrolled growth of pathogenic microorganisms. The human intestinal microbiota is made up of trillions of microorganisms that are primarily considered to be non-pathogenic and balances pathogenic microorganisms naturally. However, alterations in the microbiota can result from exposure to various environmental factors, including diet, toxins in chemically grown food, pesticides, antibiotics and medicines. Gut Dysbiosis typically occurs when the microorganisms in gastrointestinal tract become unbalanced and results into infectious diseases or chronic illness. In fact, Disease symptoms are an intelligent alarm mechanism to get rid of toxins and pathogenic bacterial viral load caused due to Gut-Dysbiosis. Nature Cure has great disease preventive and curative aspects by application of scientific evidence-based protocol which includes fruits and raw vegetables based dietary interventions and intermittent fasting to accelerate elimination of toxins from gastrointestinal tract. As per meta-analysis of recent scientific research, it is evident that beneficial microorganisms like Bifidobact as pre-biotic in fruits and vegetables and Lactobacillus in fermented food can rejuvenate gut microbiota and ultimately cure any infectious pathogenic bacterial diseases as well as chronic diseases. Most importantly, Rejuvenation of gut microbiota could also be protocol for Covid as Gut-Dysbiosis has been a common factor in symptomatic Covid cases. Our paper aims to provide meta-analysis of Gut-dysbiosis as the basis of infectious and chronic illness together with gut rejuvenation through dietary intervention.

Abstract - 45

Maternal Microbial Transmission and Its Effect on Fetal Immune Development: A Review

Khushi Khandelwal[1] and Dr. Sushma Bhardwaj[2*]

[1] Department of Life Science, Daulat Ram College, University of Delhi,
E mail ID: khandelwalkhushi122@gmail.com

[2*]Corresponding Author: Department of Zoology, Daulat Ram College, University of Delhi, E mail ID: sushmabhardwaj@dr.du.ac.in

Abstract

The abstract reviews the maternal microbial transmission and how it affects the fetal colonization, immunity and evolutionary development. Bacterial transmission from mother to fetus is a regular occurrence in the animal kingdom. Studies show that factors such as diet, medications, genetic predispositions and environmental stress shapes the maternal microbiome, affecting the fetal immune signaling and prenatal and postnatal bacterial colonization. Shared microbiota strains were observed between mother and fetus, suggesting vertical transmission of microbiota, externally or internally via maternal gut, vagina, in utero and breastfeeding. The mode of child delivery also affects the species associated with fetal microbiota and its immunity. Infants born naturally via maternal vagina have microbiota similar to vaginal bacterial community while those born via cesarean have microbes found on maternal skin surfaces. Reports suggests that cesarean born infants have high chances of obesity, asthma, allergic rhinitis, depicting that vaginal-fetal microbes are unique and crucial. Bacterial colonization of neonatal gut plays a significant role in fetal neurodevelopment. Alteration in maternal microbial population due to environmental factors such as stress or diseases such as obesity affects the fetal microbiome and may lead to diabetes. Route of microbiome transmission from mother to infant is via breastfeeding has also been studied extensively. Transmission of microbes like lactic acid bacteria, during breastfeeding helps the infant to grow, develop resistance against infections, allergies and asthma. This review is a meta-analysis on maternal microbial transmission and suggests that maternal immune and microbiome ultimately affects the immunity and health of infant. Additional studies are required to further understand the role of maternal microbiome transmission in fetal immune response.

Keywords: Maternal microbiota, bacterial transmission, fetal microbiome, fetal immune system

Abstract - 46

Knowledge, Attitude and Responses of COVID-19 Vaccination in India

Priya Bhardwaj[1], Sunita Jetly, Geetika Arora, Kumar Naidu, Daman Saluja, Sunita Yadav and Jyoti Taneja*

[1] Department of Zoology, University of Delhi-110007

* Corresponding Author- Daulat Ram College, University of Delhi-110007; Email ID - jyoti4arora@gmail.com

Abstract

Background: Widespread COVID-19 vaccination is crucial to break the transmission cycle and to end the global pandemic. Several studies have investigated COVID-19 vaccination attitude and responses among healthcare workers in India, however there is a paucity of data that assess knowledge, attitude and responses of COVID-19 vaccination among the general population in India.

Methods: An online and offline survey was conducted in the month of May to August among Indians aged 18 years and above to find out the knowledge, attitude, practice, and responses of COVID-19 vaccination.

Results: A total of 2051 individuals participated in the survey. The overall acceptance and hesitancy rate were found 92.8% and 7.2% respectively. Hesitancy was high among the young aged individuals 18-40 years and academician (56.6%). News channel was the most trusted source among COVID-19 vaccination programs. The most common concerns regarding vaccine hesitancy were vaccine's side effects (48.2%), and risk due to low immunity (55%). In addition, individuals in the vaccine acceptance group also had concerns regarding the side effects, long term safety and efficacy (64%) and an external factor like unavailability of vaccine (12.5%).

Conclusions: The results indicated the high prevalence of COVID-19 vaccine acceptance among Indians. Despite the high acceptance rate, it is important to promote evidence-based communication, mass media campaigns, and vaccine education policy initiatives across India for building trust in vaccine safety.

Keywords: Knowledge, Hesitancy, acceptance, Attitude, COVID-19

Abstract - 47

Association of Gender, Age and Comorbidities with COVID-19 Infection in India

Sunita K. Yadav[1], Priya Bhardwaj[2], Jyoti Taneja*[1]

[1] Zoology Department, Daulat Ram College, University of Delhi-110007; E-mail ID (Dr. Sunita K. Yadav): sunitayadav@dr.du.ac.in; E-mail ID (Dr. Jyoti Taneja): jyotitaneja@dr.du.ac.in

[2] Department of Zoology, University of Delhi-110007; E-mail ID: priyabhrdwaj@gmail.com

* Corresponding author

Abstract

Objectives: COVID-19, a novel pandemic disease, has been responsible for a huge number of morbidity and mortality in the world. Several reports have concluded that males, old people and individuals suffering from an underlying preclinical conditions are at a greater risk of COVID-19 infection. However, due to scarcity of data on the association of gender, age and comorbidities with COVID-19 in the Indian population, the present study was carried out to comprehend the relation amongst these parameters in Indian population.

Methods: A cross-sectional population survey using a questionnaire-based form that included questions on demographic characteristics, COVID-19 infection and any pre-underlying conditions (n=1146) was carried out.

Results: The results showed that number of COVID-19 cases in 2021 were twice (n=406) as compared to 2020 (n=187). The COVID-19 infection was higher in male patients (58.6%) than the female patients (41.3%). The patients suffering from a comorbid condition, such as diabetes, obesity, and hypertension, are more probable to suffer from a moderate or severe form of COVID-19 (50.6%) than non-comorbid patients (36.5%). Obesity/overweight (n=69) was identified as the most predominant comorbid condition in COVID-19 patients, trailed by diabetes (n=35), thyroid (n=19) and hypertension (n=11). In severe cases of COVID-19, ~85% of patients were found to have an underlying preclinical condition, while only ~15% were non-comorbid patients.

Conclusion: Males are more prone to COVID-19 infection than females, and severity of COVID-19 infection was higher in old people. Individuals with a comorbid condition were more susceptible to COVID-19 infection and can lead to aggravated infection.

Keywords: COVID-19, comorbidity, age, gender, obesity, diabetes, hypertension

Abstract - 48

Computer Aided Screening of Potential Inhibitors of SinI, a Vital Regulatory Protein Involved in Biofilm Formation by *Bacillus Subtilis*, Towards Discovery and Development of Novel Anti-Biofilm Therapeutics

Usha Kantiwal and Dr. Janmejay Pandey*
Department of Biotechnology, School of Life Sciences, Central University of Rajasthan, NH-8, Bandarsindri, District-Ajmer, PIN-305817 Rajasthan, INDIA.
E-mail ID: *2016phdbt02@curaj.ac.in*, janmejay@curaj.ac.in
Mobile Number: 9166322600, 9950765936

Abstract

Introduction- Biofilms are organized structure of microbial cells encased within a self-created polymeric matrix adhered to a surface. Biofilms have been recognized for a vital role in antimicrobial resistance and chronic microbial infections. Biofilms also protect resident microbial cells from host immune response, disinfectants, and harsh chemicals etc. Consequently, diseases caused by biofilm forming microorganisms are exceedingly difficult to treat with use of conventional antimicrobial therapeutics. Therefore, there is a pressing requirement for development of anti-biofilm agents to fix infections related with biofilms. Biofilm inhibition can be accomplished by utilization of inhibitors against structural components- proteins, eDNA and extracellular polysaccharides of extracellular lattice as well as signaling proteins that are associated with biofilm. Here we present results obtained with 'Computer aided screening of potential small molecule inhibitors of SinI, a vital regulatory protein involved in biofilm formation by *Bacillus subtilis*.

Materials and Methods- Virtual screening of FDA-approved drugs was done with the crystal structure of SinI. Top 12 complexes having high score of MMGBSA dg bind and docking score were used for Molecular Dynamics simulations of 10ns.

Results- After Molecular Dynamics simulations of 10 ns, Molecule A and Molecule B showed the maximum stability as a complex with SinI protein as the target molecule.

Conclusion- These two molecules can be tested *in-vitro* for their antibiofilm role in the biofilm formation of *Bacillus subtilis*.

Keywords- Chronic microbial infections, Biofilms, antimicrobial resistance, molecular docking, molecular dynamics

Abstract - 49

“Awareness About Human Brucellosis in Healthcare Professional in India”

Jinal Patel

Department of Microbiology, Pramukh swami medical College, Bhaikaka University Karamsad, Anand, Gujarat-388325, India. Email: jinalmlt@gmail.com.

Abstract

Introduction: Human brucellosis is a widespread zoonosis of serious public health consequences. The infection is transmitted from animal to human through direct contact with infected animals or consumption of infected, unpasteurized animal milk. Being a disease with wide and non-specific clinical manifestations, a case of brucellosis can be detected only if the treating health care professional is aware of the disease and keeps a high rate of suspicion when dealing with suspected cases. We conducted a survey to find the extent of awareness about Human brucellosis in healthcare professionals in Gujarat, India.

Aim: To study the Awareness about Human brucellosis in healthcare professional in India.

Methodology: An online survey was conducted after approval from Institutional Research Ethics committee through Google form. The survey questionnaire had a list of skills and faculty were asked to share their perceptions and practices on Likert scale about teaching, learning and assessment of microbiology skills. Few open ended questions were also asked. A cross-sectional study was conducted among healthcare professionals from December 2020 to May 2021 using a self-administrated questionnaire. This study included healthcare professionals including AYUSH practicing in Gujarat. A validated questionnaire consisting of 23 items was administered to assess the knowledge of professionals toward suspecting, diagnosing, preventing, and managing of a case of brucellosis. Both physical and Google forms were used to collect data. Data were analyzed using Statistical Package for the Social Sciences (SPSS) program, IBM version 22.

Result: Sixty-nine healthcare professionals responded to the questionnaire. The findings of the study showed overall good awareness about brucellosis with a higher rate of knowledge in allopathic healthcare professionals and nurses in comparison to AYUSH doctors. Nearly 50% of respondents did not know the treatment as well as the preventive potential of human brucellosis.

Conclusion: The current study finding suggests a need for creating more awareness in the healthcare professional, particularly AYUSH practitioners about brucellosis for better management and prevention.

Keywords: Brucellosis, Awareness, Healthcare professionals.

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