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INTERNATIONAL VACCINES CONGRESS

OCTOBER 18-19, 2021

Website: https://vaccinescongress.com/

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IVC 2021

BOOK OF ABSTRACTS

INTERNATIONAL

VACCINES CONGRESS

OCTOBER 18-19, 2021

Theme:

Current challenges and advancements in vaccines research

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About MAGNUS GROUP

Magnus Group (MG) is initiated to meet a need and to pursue collective goals of the scientific community specifically focusing in the field of Sciences, Engineering and technology to endorse exchanging of the ideas & knowledge which facilitate the collaboration between the scientists, academicians and researchers of same field or interdisciplinary research. Magnus group is proficient in organizing conferences, meetings, seminars and workshops with the ingenious and peerless speakers throughout the world providing you and your organization with broad range of networking opportunities to globalize your research and create your own identity. Our conference and workshops can be well titled as 'ocean of knowledge' where you can sail your boat and pick the pearls, leading the way for innovative research and strategies empowering the strength by overwhelming the complications associated with in the respective fields.

Participation from 90 different countries and 1090 different Universities have contributed to the success of our conferences. Our first International Conference was organized on Oncology and Radiology (ICOR) in Dubai, UAE. Our conferences usually run for 2-3 days completely covering Keynote & Oral sessions along with workshops and poster presentations. Our organization runs promptly with dedicated and proficient employees' managing different conferences throughout the world, without compromising service and quality.

About IVC 2021

Magnus Group with gratification and privilege announcing its "International Vaccines Congress"(IVC 2021), an Online Event scheduled during October 18-19, 2021 with the theme "Current challenges and advancements in vaccines research." The main aim of IVC-2021 is to provide interaction between health care professionals, Pharma industries, R&D department, Young Researchers, Ph.D. scholars, and other experts in the areas of Infectious Diseases and Vaccines around the world to share about their research studies and new innovations in the field. You can increase your professional skills and discuss the practical challenges encountered and the solutions adopted.

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KEYNOTE FORUM

DAY 1

INTERNATIONAL

VACCINES CONGRESS

OCT 18-19, 2021

Hao Song
Australian Institute for Bioengineering and Nanotechnology, Australia

Nature inspired nanoparticle-based DNA vaccine

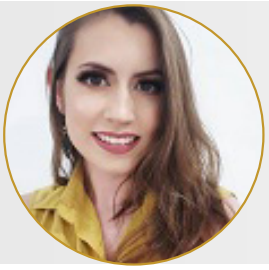
Recent advances in nanotechnology has greatly boosted the development of drug delivery systems for therapeutic and vaccine applications, in particular the great success in nanoparticle-based mRNA vaccines for COVID-19. To be noted, rational design and fabrication of safe and efficient nano-carries is the key to lead a successful technology development. It is noteworthy that the delivery performance could be possibly maximized by custom-designed nano-carriers considering the configuration and surface textures of both cargo biomolecules and target cell/environment. Here, we showcase our recent progress on the development of silica based advanced delivery platform. Through a biomimetic approach, silica nanoparticles with an intrinsic spiky surface are fabricated and characterized by the unique tool of electron tomography. We demonstrate that control over delicate nanotopography of silica nanoparticles as plasmid DNA vectors has significant impact on the transfection efficacy. A designer spiky of silica nanoparticles acts as hooks to entangle the DNA loops and protect the gene molecules sheltered in the spiky layer against nuclease degradation. Further in vivo demonstrations present enhanced immune responses mediated by spiky silica nanoparticle-mediated DNA vaccines, showing superior performance than the commercial product of *in vivo* JET-PEI. From bench to market, this spiky nanoparticle based delivery platform is on the industrial translation toward novel nanoparticle-based vaccine technology.

Audience Take Away:

- A novel nanoparticle-based gene delivery platform that can be easily adopted.
- New understanding in the impact of nanoparticles surface nanotopography on plasmid DNA binding, cellular delivery, transfection and vaccine performance.
- A patterned technology that may attract the commercial interest for the development of cancer or COVID vaccine.

Biography:

Dr. Hao Song obtained his PhD degree in 2018 from Australian Institute for Bioengineering and Nanotechnology, the University of Queensland, followed by postdoc research training at the same institute. In 2021, he was promoted as an ARC DECRA & NHMRC Emerging Leadership Fellow. Dr Song has published over 50 paper including JACS, Adv Mater, Angew Chem Int Ed, Adv Sci, etc. He is the Associate Editor for Frontiers in Drug Delivery. He has attracted over AUD$1.8 million of funding as chief investigator, and promoted his technology translation in collaborations with several industrial partners.



Patricia Canteri de Souza
State University of Londrina, Londrina, Brazil

Production and biological characterization of egg yolk antibodies (IgY) against Ftr1 iron permease of *Candida albicans*

Iron is essential for the functionality of biological processes, however, excess iron is toxic. In humans, due to its toxicity, this metal is found coupled to proteins, such as transferrin, which transports iron to tissues, and ferritin, an intracellular storage molecule of this metal. During an infection, microorganisms obtain iron from the host to survive. *Candida albicans*, one of the major pathogens responsible for severe fungal diseases, contains a transmembrane protein, iron Ftr1 high-affinity permease, which uses to get iron from ferritin, transferrin, and iron chelators synthesized by other organisms. In the search for new mechanisms to contain fungal multiplication, antibodies are applicable since it is possible to produce specific antibodies against a microbial structure. In this context, the work objective was to produce and perform the biological characterization of egg yolk antibodies (IgY) against the Ftr1 iron permease of *C. albicans*. A peptide derived from Ftr1 was synthesized and used to immunize laying hens seven times. Eggs from pre-immunized chickens and post-3rd, 5th, and 7th immunizations were collected. IgY antibodies were extracted from egg yolks by the ammonium sulfate precipitation technique. Subsequently, they were purified by molecular exclusion chromatography using Sephadex G-100 resin. The samples containing proteins or peptides were analyzed by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) at 10%. After this step, the samples were concentrated by filtration using a 50 kDa cut-off ultra centrifugal filter. Then, an avidity enzyme-linked immunosorbent assay (ELISA) was performed to establish the binding strength of the antigen with the antibodies, using urea as a chaotropic agent. To determine the antifungal effect of immunoglobulins extracted after the 7th immunization, *in vivo* test was performed on larvae of the moth *Galleria mellonella*, an alternative model of systemic infection. Regarding the results, the production, extraction, and purification occurred successfully, being possible to observe the presence of bands corresponding to the heavy (65 kDa) and light (25 kDa) IgY chains in the electrophoresis gel. Besides, after purification, contaminants (38 kDa) were removed. The immunoglobulin was reactive to the antigen and the avidity was considered low for pre-immunization antibodies, moderate for antibodies extracted post-3rd and 5th immunizations, and high after the 7th immunization. Concerning the challenge in the larvae, at 96 h after the beginning of the experiment, the survival of larvae treated with 80 mg/kg of anti-Fr1 IgY was 90%. In contrast, all larvae that did not receive treatment died ($p < 0.0001$). Meanwhile, only 16% of the larvae that received 80 mg/kg of pre-immunized IgY survived, and there was no difference between this group and the untreated group ($p = 0.2359$). This work showed that an antibody produced against *C. albicans* Ftr1 was able to increase the survival of *G. mellonella* larvae infected with the yeast.

Audience Take Away:

- In our work, we show an example of the applicability of antibodies as potential immunotherapeutic for the treatment of fungal infections.
- We have shown that avian IgY antibodies can be used for this purpose to replace the IgG antibodies of mammals, in an attempt to reduce the pain and suffering of animals, since the extraction of antibodies from the blood is not necessary.
- Given the variety of methods for extraction and purification of IgY antibodies (derived from egg yolk), the protocols we use were very efficient and can be explored by other researchers.

- Our work shows other researchers the importance of carrying out heavy doses during the immunization of birds to produce antibodies with high avidity to antigens.

Biography:

Dr. Patricia Canteri de Souza graduated in Biological Sciences in 2013 from the State University of Londrina. She finished her master's degree in 2016 and her doctorate in 2021, both in Microbiology and studied at the same institution. She has experience in the areas of Medical Mycology and Immunology, working with: (I) evaluation of compounds with antimicrobial activity, (II) production of egg yolk antibodies (IgY) as possible immunotherapeutic agents for the treatment of candidiasis, (III) use of insects as models of fungal infections. She has experience as a professor of Microbiology and Immunology of the Dentistry course at Faculty Gamaliel.

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SPEAKERS DAY 1

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Heather Mathie*, Barbara Shih, Anirudh Patir, Irene McGuinnes, Lindsay Waddell, Anna Raper, Prakash Ramachandran, Marianna Beltran-Sierra, Neil Henderson, Tom Freeman, Ivan Morrison, Jayne Hope

Roslin Institute, University of Edinburgh, UK

Characterising the Dendritic cell response to BCG using a bovine afferent lymphatic cannulation model and single-cell RNA-Seq

Vaccination is a key component in the control of animal pathogens that impact the livestock industry. However, deployable, efficacious vaccines remain unavailable for many prevalent diseases, particularly those requiring cell-mediated immunity, such as bovine tuberculosis (TB). In addition, the current 'vaccinate and challenge' approach offers little insight into why a candidate vaccine may fail. BCG is a live-attenuated form of Mycobacterium bovis, the causative agent of bovine TB, and is known to induce a strong Th-1 response associated with protective immunity. This project aimed to identify protective signatures associated with cell-mediated immunity in afferent lymphatic DC (ALDC) trafficking from BCG vaccination sites to the lymph node. To achieve this, we utilised a bovine afferent lymphatic cannulation model and collected pseudo-afferent lymph both pre- and 24h post- BCG vaccination, allowing us to perform analysis directly ex-vivo. ALDC were analysed by flow cytometry, single cell and bulk RNA-sequencing. We found three major populations of ALDC draining from the vaccination site: CD172a+ve DC, CD172a-ve DC, and Langerhans Cells. These major populations were divided into 10 sub-populations which exhibited differential gene expression in response to BCG, indicating that individual populations may have differing roles in response to mycobacteria. Pseudo-afferent lymph was also exposed to BCG *in vitro*, with the aim of using cultured ALDC as a novel way to screen vaccine candidates prior to animal studies.

Irina Zyrianova
Federal Science Center For Animal Husbandry, Russian Federation

Bovine leukemia virus *tax* gene/Tax protein and *pre-miRNA* genes' polymorphism and its relation to Enzootic Bovine Leukosis

Objectives: The aim of this study is the investigation of the polymorphism of the *tax* gene/Tax protein and *pre-miRs-B* (*pre-miRNA* genes of Bovine leukemia virus (BLV)) polymorphism and its relation to Enzootic Bovine Leukosis.

Methods: Peripheral blood samples of 2 to 5 years old female Holstein cattle (farming in Moscow region, Russia) have been used. They have been tested for proviral DNA host genome insertion by PCR (BLV-positive or BLV-negative) and for the presence of antibodies to gp51 BLV antigen by AGID (BLV-seropositive or BLV-seronegative). All samples have been divided into two groups: the group of 16 BLV-seropositive and proviral BLV-positive samples (further: BLV-positive) and another group of 26 BLV-seronegative and proviral BLV-negative samples (further: BLV-negative). WBCs of the samples have been counted on the Abacus Junior Vet 5 Automatic Hematology Analyzer (Diatron, Austria). The BLV-positive samples group has been used for further investigation of the *tax* gene/Tax protein and *pre-miR-B* genes' polymorphism. DNA fragments of *tax* and *pre-miR-B* genes have been amplified and further cloned and sequenced. Five or six clones for each of the BLV-positive samples have been sequenced by Sanger's method. The t-test (http://www.graphpad.com/quickcalcs/) and ANOVA test (GraphPad Prism V.7.04 (1992–2017 GraphPad Software, Inc.)) have been made for statistical testing of the results.

Results: Several alleles of the tax gene and pre-miR-B genes have been received as proof of its polymorphism. Some of them have a highly significant association with an increase and others – with a decreased number of the WBCs in BLV-infected cows. The specific *pre-miR-B* alleles can be responsible for the increased number of WBCs in BLV-infected cows. The specific *tax* alleles (and corresponded Tax protein variants) can be responsible for the decreased number of the WBCs in BLV-infected cows, which could be considered the feature of the aleukemic form of BLV infection. They could be named the aleukemic tax alleles.

Audience Take Away:

- This study has been shown the *tax* gene/Tax protein and *pre-miRs-B* polymorphism and its significant association with the high or low WBC count.
- The polymorphism of *pre-miRs-B* genes could be a key for investigating a precise mechanism of BLV pathogenicity.
- The aleukemic *tax* alleles (and corresponded Tax protein variants) can be used to create a test system for searching BLV aleukemic strains to minimize the clinical losses in cattle because of BLV infection.

Biography:

Dr. Irina Zyrianova studied Cytology and Genetics at the Tomsk State University, Tomsk, Russia, and graduated with MS in 1985. She then studied Chemistry at the Moscow State University and finished with Ph.D. in molecular biology in 1993. After three years of postdoctoral fellowship (1996-1999) supervised by Dr. Sheila MacIntyre at the University of Reading, School of Animal and Microbial Sciences, Reading, the UK, she was one year Exchange Visitor at The University of Miami, School of Medicine, Miami, Fl, USA. After that, she returned to Moscow, Russia, and worked in the different Research Institutions: Institute of Engineering Immunology (Lyubuchany, Chekhov district, Moscow region), Institute of Bioorganic Chemistry, and Institute of Molecular Genetics (Russian Academy of Sciences). She works in Institute for Innovative Biotechnologies in Animal Husbandry (The branch of the Federal Science Center for Animal Husbandry named after Academy Member L.K. Ernst). She has published six research articles in SCIE journals.

Afshona Anoyatbekova
Federal Scientific Center, Russia

Identification of Hobi-like pestivirus as a contaminant of the vaccine against peste des petits ruminants

Introduction and objective: Along with the success of developing biological products of new generation the traditional vaccines, as well as hyperimmune sera, remain as the main means of preventing viral diseases in animals. However, there is a potential threat of the dissemination of emergent infections in a case of insufficient control in the production of animal origin products. It has been already confirmed almost all around the world that pestiviruses are frequent contaminants of live modified vaccines and fetal serum, which induce infection in the organism of animals. Hobi- like virus or Pestivirus H is one of the 11 main viral species of the genus Pestivirus in the Flaviviridae family. This virus was first identified in 2004 in a batch of bovine fetal serum. This research presents the results of the detection of the Hobi-like pestivirus in the virus vaccine against PPRV used for the vaccination of small ruminants in some farms of the Republic of Tajikistan.

Materials and methods: The studies were carried out in the laboratory of virology of the FSC VIEV. Serum samples of sheep and goats with symptoms of respiratory and reproductive failure from some regions of Republic of Tajikistan were tested by AGID. The vaccine strain of PPRV and strain "Oregon C24V" of BVDV was used as the control antigens. The total RNA was extracted by the commercial kit Syntol (Moscow, Russia) according to the manufacturer's protocol. RT-PCR for the identification of N and F genes of PPRV and NS3 genes of BVDV was performed in accordance with the recommendations of the OIE Terrestrial Manual, 2013. Viruses were sequenced and phylogenetic analysis carried out using MEGA 7.0.

Results: It has been obtained a positive result when PPRV vaccine strain was used as an antigen. A precipitation line formed between the well with the PPR vaccine and the well with the field serum indicated the presence of antibodies to the PPR virus. In some cases, when examining blood serum samples from sheep and goats with a commercial virus vaccine against PPR, double precipitation lines were observed. In this stage of the study, it has been assumed that the vaccine against PPR contained two viruses. Consequently, we had tested the commercial vaccine used in the Republic of Tajikistan for the presence of contamination. The results of RT-PCR had shown that in addition to the PPR virus, the vaccine contains the genome of bovine viral diarrhea virus (BVDV). When sequencing the amplification products, it was determined that the detected virus belongs to the BVDV genotype 3 or the so-called Hobi-like pestivirus. The sequences of detected virus were deposited to GenBank under accession number KX900607.

Audience Take Away:

The priority in the development of national programs for the prevention of diseases in livestock is specific prevention. In a number of countries, vaccination is an integral part for many economically significant viral infections controlling. Currently, the prevention of viral infections is carried out mainly with the use of live and inactivated vaccines. The main stage in the manufacturing of cultural antiviral vaccines is the cultivation of the virus strain. Consequently, it is very important to pay attention: To the problem of the vaccine contamination with Pestiviruses, as it is known that the application of contaminated vaccine may lead to cause the outbreaks in the herds. In addition it is very necessary for the laboratories to exclude the

contamination of fetal serum, trypsin and cell cultures with pestiviruses. Blood serum, used in the growth medium for culturing cells should be free not only from the bovine viral diarrhea virus but also from antibodies to this pathogen. Furthermore, the biological products have to be free from any bacterial, fungal and mucoplasma contamination.

Biography:

Dr. Afshona Anoyatbekova studied at the Veterinary faculty of Tajik Agrarian University, Dushanbe Tajikistan in 2008-2011. Then she had transferred to the Faculty of Veterinary Medicine of Moscow State Academy of Veterinary medicine and Biotechnology (MVA by K.I. Skryabin, Moscow, Russia) in 2011 and graduated it in 2013. December 2013 she started working as a junior researcher at the Laboratory of Virology in FSC VIEV in the research group of Professor Yurov Konstantin Pavlovich. In 2014 simultaneously studied at the graduate school and graduated it in 2017. She received her Phd degree in 2018 at the same institution. After one year, she was promoted to a senior researcher of the Virology Laboratory and currently is working there. She has published more than 11 research articles in journals indexed in the Scopus, Web of Science and Russian Higher Attestation Commission. She has presented her studies results in different international conferences. She is married and has got two children.

Carlo Iavarone, Subeena Sood, Majed Matar, John Henderson, Jessica Kim, Alanna Smith, Jeff Sparks, Jennifer Rice, Jospeh Rogers, Khursheed Anwer*

Celsion Corporation, USA

Immunogenicity of DNA vaccines based on multicistronic vectors and synthetic DNA delivery systems

Nucleic acid-based vaccines represent an attractive alternative to live attenuated and subunit-based vaccines due to their capacity to trigger both humoral and cellular immunity and potential for low-cost and shortened production processes. The fast-track approval and the worldwide vaccination programs for Covid-19 pandemic underscores the efficacy and safety of these novel class of vaccines. DNA and RNA vaccines have been recognized to provide an efficient protection without significant safety risk. Despite the recent successes in Covid-19 vaccines there is strong rationale to continue the investigations of other vaccine strategies to address the need for emergence of new variants (Covid-19), uncontrolled outbreak (flu), the demand for infectious diseases with an unmet need (CMV, RSV), and the requirement for diseases demanding diversified immune response (malaria). Our DNA-based vaccine approach encompasses molecular elements that are designed to improve the breadth of immune response by targeting multiple antigens of a pathogen or multiple mutants of the same antigen, improve the intrinsic adjuvanticity of the vaccine as needed by co-expressing a potent molecular adjuvant particularly against pathogens where conventional vaccines are poorly immunogenic, promote uptake and chemical adjuvanticity of the DNA vaccine with the use of synthetic delivery system, prolong vaccine shelf-life and stability at working temperatures, and utilize an existing cost-effective and scalable process that can be rapidly functional in case of a new outbreak or an evolving existing pandemic. To that end, we have initially produced a family of DNA vaccine vectors expressing one or more of SARS-CoV-2 surface antigens as a proof-of-concept target, verified vector composition, and demonstrated expression of the encoded genes. We have also developed an intramuscular vaccine formulation based on a covalently modified co-polymer that yields high levels of a reporter gene expression within 24 hours after treatment, a critical time window for immune activation, followed by durable expression potentially conducive to B- and T-cell responses. Immunization of Balb-C mice with a plasmid expressing the Spike protein of SARS-CoV-2, resulted in the production of IgG antibodies with evidence of viral neutralization and cytotoxic T-cell response specific to the antigen. Parallel in vivo studies are in progress to optimize vector and antigen design, improve the delivery system, explore alternative route of administration, identify the optimal vaccine dose and regimen. The current data and results from the ongoing studies will be presented at the conference.

Audience Take Away:

- Use of DNA-based vaccines to generate immune responses against a pathogen
- Vaccine composition comprising a DNA vector and formulations based on synthetic DNA delivery systems
- Provides information on the design and testing DNA vaccines in preclinical models

Biography:

Dr. Anwer is Executive Vice President & Chief Science Officer at Celsion Corporation since June 2014. Prior to Celsion Corporation, Dr. Anwer served as President and Chief Science Officer of EGEN, Inc. from 2009. Dr. Anwer has over 25 years of experience in the discovery and development of gene-based therapeutics from bench to bedside. He is the inventor on over 100 U.S. and international patents, recipient of NIH and FDA funding, and has authored about fifty peer reviewed scientific publications including original research articles. Dr. Anwer received his Ph.D. from Ohio University and MBA from University of Alabama.

Alessia Quatela*, Adam M. Gilmore, Linda H. Kidder
Horiba Scientific, France

Fluorescence A-TEEM method for vaccines characterization

We will present several examples to highlight the capabilities of the fluorescence A-TEEM method, a novel approach which combines UV/Vis with fluorescence EEM spectroscopy. The benefit of this approach is the ability to provide robust and rapid spectroscopic characterization of vaccine components and vaccine formulations, samples that are extremely challenging to traditional spectroscopies, such as Raman and NIR. The Coronavirus pandemic applied historic pressure on vaccine development and production, collapsing development timelines from years to months, with many firsts in formulation and production. Requirements for product quality still had to be met though, highlighting the need for rapid analytical techniques to characterize vaccines from R&D to formulation development, and through manufacturing to final QA/QC. Spectroscopic techniques are known to be rapid and are therefore used extensively for PAT and QA/QC testing. However, the "go-to" techniques such as Raman and NIR often do not work for vaccines, as they struggle with low protein concentrations typical of these formulations. The fluorescence A-TEEM method is a unique alternative, combines high sensitivity and specificity, with limits of detection to 0.015 ug/mL, and data acquisition times typically under 60 seconds. As the method combines two well established techniques (UV/Vis and fluorescence), the technique can be validated by following the relevant USP chapters, <853> and <857>. We will present results from an A-TEEM study on four closely related combination vaccine formulations, Solo-Jec brand canine vaccines from Boehringer Ingelheim VetMedica. A-TEEM was able to accurately differentiate between the four formulations, even when they differed by only a single coronavirus component. To ensure repeatability, calibration data (two separate samples for each formulation) were collected, and reproducibility was assessed with a third unique set of validation samples, collected on a different instrument by a different operator. The A-TEEM is able to identify and validate "unknown" samples with 100% certainty. In addition to vaccine formulations, we will present AAV characterization studies, where the A-TEEM was able to rapidly (<90sec) differentiate biotinylated AAV samples that are complexed with streptavidin-dye conjugates from uncomplexed AAVs.

Audience Take Away:

- We'll describe how the A-TEEM method works by combining UV/Vis and Fluorescence EEMs spectroscopy. The audience will learn how this unique combination overcomes the limitations of each technique used on its own. We will show how A-TEEM can be used for vaccine QA/QC, demonstrating repeatability and reproducibility, conformance with USP validation requirements, speed and sensitivity, and low limits of detection. The A-TEEM has shown promise for the rapid characterization of AAVs.

Biography:

Alessia Quatela, Ph.D. in Physics, spent her postdoctoral experiences in Paris at the "École Normale Superiore" (ENS) to work on an innovative electro-optical microscope for trans-membrane action potential measurements and then at the "Institut Curie" characterizing adhesion forces exerted by the filopodia. She participated as a Research Fellow to the construction and development of a femtosecond broadband stimulated Raman setup at the Department of Physics of the University of Rome "Sapienza". In charge of the spectroscopy laboratory at the Centre for Hybrid and Organic Solar Energy (CHOSE) in Rome, she is now Product Specialist for the Fluorescence Analytical products at HORIBA France SAS.

Huang Wei Ling
Medical Acupuncture And Pain Management Clinic, Brazil

Is the mandatory implementation of a passport for COVID-19 vaccine reduce the transmission or Not?

Introduction: In this theme the author will discuss various explanations that was used or not to implement this kind of rules in Europe and in many countries nowadays.

Purpose: To demonstrate that using only this type of measures to control the spread of the virus, will not be reducinf the incidence of he infecton because the author is demonstrating that the type of population that we have nowadays are not immune competent but immune deficient in energy , that will compromise the formation of antibodies for SARS-CoV-2 after receiving the vaccines and also, there are other variants and strains that only one vaccine cannot prevent all forms of SARS-CoV-2. Also, there are studies showing that persons that are fully vaccinating can spread virus even if assymptomactic due to maitaing virus in the nose and in the throat.

Methods: In this study,the author is showing the studies that we have nowadays reagarding this theme and also, said by many specialists in the area.

Results: In these studies, they are waiting for the B and T cells responses after the vaccination. In another talk from Antony Falci, he is also saying that there is no evidence that the vaccine can control the wide spread of the virus. And there will be increase in the formation of auto-immune disease in the near future, according to some studies , due to this massive vaccine implementation.

Conclusion: The conclusion of this study is that the implementation of universe vaccination is not based on studies very well done and are based on studies that have no conclusion yet. According to the author, the vaccination will not control the widespread of the SARS-CoV-2 infection due to the fact that persons full vaccinated can spread virus to other even if assymptomactic and the majority of the population nowadays are with immune supressed, induced by the chronic exposition to electrtomanectic waves and affecting our energy and immune system, leading to less respónse to vaccines nowadays. The use of other forms of measurements to increase the immune system of the entire population nowadays, such as the use of highly dilluted medications such as homeopathies, increasing the viotal energy of the population , that is very low nowadays, is the major importance, to treat the cause of the problem and not just treating the symptoms, that is the SARS-CoV-2 infection.

Biography:

Huang Wei Ling, born in Taiwan, raised and graduated in medicine in Brazil, specialist in infectious and parasitic diseases, a General Practitioner and Parenteral and Enteral Medical Nutrition Therapist. Once in charge of the Hospital Infection Control Service of the City of Franca's General Hospital, she was responsible for the control of all prescribed antimicrobial medication and received an award for the best paper presented at the Brazilian Hospital Infection Control Congress in 1998. Since 1997, she works with the approach and treatment of all chronic diseases in a holistic way, with treatment guided through the teachings of Traditional Chinese Medicine and Hippocrates. Researcher in the University of São Paulo, in the Ophthalmology department from 2012 to 2013.Author of the theory Constitutional Homeopathy of the Five Elements Based on Traditional Chinese Medicine. Author of more than 100 publications about treatment of variety of diseases rebalancing the internal energy using Hippocrates thoughts.

Huang Wei Ling
Medical Acupuncture And Pain Management Clinic, Brazil

Why do patients still have potential to transmit Covid-19 despite receiving vaccination?

Introduction: This process is not very easy to explain in the eyes of Western medicine and the author will explain it from the perspective of traditional Chinese medicine, following the commandments of Hippocrates, father of medicine. In an article written by the author entitled Is *SARS-CoV-2 Strong or Our Body Is Weak?* it shows that more than 97% of patients have low *Zheng-Qi,* which is the energy that protects the individual's body against the invasion of external pathogenic factors. In another article written by the author *entitled Energy Alterations and Chakras' Energy Deficiencies and Propensity to SARS-CoV-2 Infection*, she demonstrates that more than 90% of her patients studied between 2015 and 2020 are without energy in the five massive internal organs , which are responsible for maintaining our health, and that this energy deficiency is responsible for the formation of infectious and non-infectious diseases today. In another article written by the author, entitled What have behind in all kinds of infections that we need to know?, the author says that what all bacterial, viral and fungal infections have in common, is the deficiency of energy in the chakras and formation of internal Heat. The purpose of this study is that, the author wants to show that most people are considered immunedefiient , due to the energy deficiency pattern , generating in this way, internal Heat formation, this being the predominant factor for colonization and infection by bacteria and viruses.

Method: the author uses many articles written by her explaining how to treat community and nosocomial infections withouyt need to use any antibiotics or antiviral medications.

Results: because she knows that If we replenish the energy of these patients in order to reduce the formation of internal Heat, there would no longer be viral colonization in the nasal cavity of these vaccinated individuals, because currently, even if they are immunized, the underlying cause of immunodeficiency was not treated, which is low state os energy, due to the electromagnetic radiation generated by the modernization of communication.

Conclusion: to reduce virus colonization even after vaccination for COVID-19, individuals need to improve their energy state, which is weakened, to reduce the production of internal Heat, responsible for the adherence of bacteria and viruses in individuals with these infections and which, according to the author's experience, who is a specialist in infectious diseases, but treats most community and hospital diseases without using antimicrobials, she uses the methods of older medicines, such as Chinese medicine and thus manages to treat most of the infections by resistant bacteria and viruses, only drawing internal Heat and rebalancing the internal energies of *Yin, Yang, Qi* and Blood.

Biography:

Huang Wei Ling, born in Taiwan, raised and graduated in medicine in Brazil, specialist in infectious and parasitic diseases, a General Practitioner and Parenteral and Enteral Medical Nutrition Therapist. Once in charge of the Hospital Infection Control Service of the City of Franca's General Hospital, she was responsible for the control of all prescribed antimicrobial medication and received an award for the best paper presented at the Brazilian Hospital Infection Control Congress in 1998. Since 1997, she works with the approach and treatment of all chronic diseases in a holistic way, with treatment guided through the teachings of Traditional Chinese Medicine and Hippocrates. Researcher in the University of São Paulo, in the Ophthalmology department from 2012 to 2013.Author of the theory Constitutional Homeopathy of the Five Elements Based on Traditional Chinese Medicine. Author of more than 100 publications about treatment of variety of diseases rebalancing the internal energy using Hippocrates thoughts.

Luiza Guilherme*, Edilberto Postol, Luiz Carlos Sá-Rocha, Roney Orismar Sampaio, Lea Maria Ferreira Demarchi, Raquel Elaine de Alencar, Karen Kohler, Samar S Freschi, Simone Santos, Maria Cristina Donadio Abduch, Jorge Kalil

University of São Paulo, Brazil

Vaccine against S. pyogenes

StreptInCor, a candidate vaccine against S. pyogenes is based on protective 55 amino acids residues of C-terminal portion of the M protein. Experimental assays have demonstrated that the StreptInCor peptide induces high titers of opsonic and neutralizing and protective antibodies in outbred immunized mice. Using HLA class II transgenic mice, it was possible to evaluate the immunogenicity and safety of the StreptInCor vaccine epitope for a period of one year. Specific and non-auto reactive antibodies were produced as well as no autoimmune or pathological reactions were observed in the heart or other organs of these animals. We also performed several studies in mini-pigs in order to evaluate the immune response and safety by submitting these animals to echocardiogram examination before immunization and after the four doses treatment. No alterations were observed. In addition, both repeated intramuscular-dose toxicity tests (28 days) with four doses and echocardiography procedure in mini pigs after 28 days were performed. No harmful effects to the tissues and organs studied were observed indicating that the vaccine is safe. StreptInCor vaccine also induces regulatory T cells (Treg) that strongly indicate that the vaccine peptide may have therapeutic potential to control both inflammatory and autoimmune response in RF/RHD patients.

Alibek Adil
Infection Diseases-Resident, Kazakhstan

COVID-19 vaccines contraindications

There is no doubt that vaccines are the most effective solution against the global challenges that pandemic brought to the world. In addition, thousands of studies all around the web are publishing the succeed results and social media is spreading them rapidly. Nevertheless, there are some noticed cases about people whose general condition turned into worse after the first or even second dose of vaccines. During my personal practical experience in admission department and infectious diseases department of several city hospitals I worked, there are observed cases about patients who had complications with their general condition after they were vaccinated with vaccines such as Sputnik-V, Hayat-vax, Sino-Vac and others. This study is aimed to appeal for a careful attention of society to vaccines with people with chronic and acute infection diseases, or people with first registered personal complications after vaccination and people of elder ages. Also, for an additional information, some clinical cases and patients' histories of diseases will be shown as an example to expand the understandings and widen the view of contraindications and actual side effects which might be already known but underestimated properly or some instances that could be marked as new or rare. It was noticed that during the survey many patients with complications reported they were not informed about possible side effects that may happen after vaccination and were not asked if they have or not other chronic diseases already. So, it is quite clear there is a need of common general list of questions that should be taken as a strict rule by medical personnel. Despite the fact it is not the first year of pandemic, there is still part of people who is not informed well or informed incorrectly which means it is a call for Health Department to increase the methods of spreading the knowledge in all modern and simple ways for public.

Audience Take Away:

- This study is focusing on observation the presence the chronic diseases of patients before the get vaccinated
- Marking the top chronic and acute diseases as potential contraindication for vaccination
- Recommendations about surveillance on clinical condition of already vaccinated patients with chronic diseases.

Biography:

Dr. Adil studied General Medicine and Therapy at Kazakh National Medical University (KazNMU), city of Almaty, Kazakhstan and graduated as MD in 2019. He then joined to study Public Health in Central-South University, city of Changsha, China. Came back to Almaty for winter holidays in January 2020 and could not back cause of closed borders with China after pandemic. Started working as a therapist in City Hospital №4 in Almaty as a therapist in therapy department, transit department and admission department. After 6 months he then studies at Infection Disease department at Kazakh-Russian Medical University (KRMU). Having a practice at one of the biggest city Hospital of Infection Diseases which is currently accepting patients with severe forms of COVID-19.

Idania Marrero*, Eduardo Barranco, Greta Kcomt Del Rio, Samantha Satyavrata, Bonaventure Orizu, Stephanie Ramos, Matthew Morrow, Jill Castner, Kim Kraynyak, Kathleen Walker, Kate Broderick, Laurent Humeau, Joseph Kim and Jean Boyer

Inovio Pharmaceuticals Inc., USA

INO-4500, a DNA-based LASV vaccine, induces robust T cell responses and long-term memory antigen-specific T cells.

Lassa fever (LF) is an acute viral haemorrhagic disease caused by Lassa virus (LASV), which is endemic in Western Africa and is associated with high rates of infection and mortality. Currently, there are limited treatment options and no licensed vaccines to protect against LASV infection. Previously, we reported on a DNA vaccine, INO-4500, encoding the LASV (Josiah strain) glycoprotein precursor (LASV GPC) gene, that elicits protective immunity and completely protects guinea pigs and non-human primates against viremia, illness, and death after Lassa virus exposure. Here, we present T cell responses after vaccination with INO-4500 from a randomized, placebo-controlled phase 1 LASV vaccine trial in healthy adults. Two doses of 1 mg of INO-4500 were administered by intradermal injection followed by electroporation using CELLECTRA® 2000 device at day 0 and week 4. The cellular immune response was assessed at day 0 and weeks 6, 12, 24 and 48 following vaccination. INO-4500 elicited a strong T cell response against overlapping LASV peptide pools as measured by IFN -ELISpot compared to placebo controls. Using flow cytometry, we examined specific LASV reactive T cells after stimulation with LASV peptides and analysed their cytokine profile. Significantly higher frequencies of polyfunctional CD4+ and CD8+ T cells, producing IL-2, IFN and TNFα, were observed at week 6 and 12 following vaccination. Also, activation-induced LASV-specific IRF4+CD137+-CD4+ and -CD8+ T cells were significantly expanded at week 6 but were detectable up to 48 weeks after vaccination, suggesting induction of long- term memory antigen-specific T cells. This is supported by a significant increase of IL-2, IFN , TNFα, IL-6, IP-10 and MIG in the supernatant of cultured cells stimulated with LASV peptides at different time points post-vaccination as detected using Legendplex. These results revealed that INO-4500 LASV-GPC DNA vaccine induce robust T cell responses, which are critical for protection against LF. The activation and persistence of LASV-specific T cells supports the potential of INO-4500 to protect against LASV.

Audience Take Away:

- INO-4500, a LASV DNA vaccine, induce a potent T cell immune response against LASV-specific peptides within 4-6 weeks of administration that persist for long-term.
- Strong T cell immune response against LASV appears to be the key to protection from infection.
- INO-4500 paired with intradermal electroporation is a promising vaccine for both routine prophylaxis and outbreak.

Biography:

Dr. Marrero studied Medicine at the Medical University of Havana, where she also obtained her MS in Immunology. She joined the Immunology Laboratory at the Heart Institute, University of São Paulo (USP), Brazil. She received her PhD in Immunology at the Institute of Biomedical Sciences, USP. She joined first as Postdoctoral and later as Senior Scientist to the TPIMS in San Diego. Later, she joined as Assistant Project Scientist to the University of California San Diego, and more recently, she joined as Scientist to Inovio Pharmaceuticals Inc., San Diego. She has published several research articles in peer review journals.

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Gaurav Joshi*, Carsen Roach, Rohan S Ingrole, Akhilesh K Shakya, Bart E Tarbet and Harvinder Singh Gill

Texas Tech University, USA

Development of universal influenza vaccine using M2e conjugated PLGA nanoparticle.

To prevent next flu pandemics and to reduce the burden of seasonal flu infections, there is an urgent need to develop vaccines that are broadly protective against different influenza strains. In this regard we investigated polymeric nanoparticles as antigen carriers of a highly conserved epitope, the extracellular domain of M2 membrane protein (M2e) of the influenza type A virus, and compared immunogenicity from simple adsorption versus the chemical conjugations of M2e on to polymeric nanoparticles. We synthesized two types of nanoparticles from similar molecular weight polymers: i) PmNPs: nanoparticles made of poly (lactic-co-glycolic acid)–polyethylene glycol with maleimide linker, ii) and PNPs: nanoparticles made of methoxy-polyethylene glycol-poly (lactic-co-glycolic acid). PmNPs and PNPs were characterized by transmission electron microscopy and dynamic light scattering. We conjugated M2e on the surface of PmNPs, via maleimide-thiol rxn, whereas for PNPs, M2e was physically adsorbed at the same dose. We were immunized mice via intramuscular or intranasal routes on day 0 and 21 using M2e conjugated PmNPs or PNPs with soluble form of CpG as an adjuvant. Anti-M2e-specific IgG, IgG1 and IgG2a responses were determined in serum samples and lungs lavage after day 42 by ELISA. Cellular immune response was determined through cytokine analysis from splenocytes restimulation. Mice were challenged after day 42 with 3xLD50 of various strain of influenza virus and survival and weight loss were monitored daily. We synthesized PmNPs and PNPs of the comparable size (~100 nm). We found that covalently attached M2e at PmNPs with CpG had a more significant immune response and protection with challenge than from physically adsorbed M2e on PNPs. The intramuscular route was identified to be significantly better than the intranasal route in terms of anti-M2e immunoglobulin G (IgG), IgG1 and IgG2a, cellular immune response and protection with challenge. We found full protection in PmNP-M2e with CpG immunized mice against challenged influenza viruses such as A/California/04/2009 (H1N1pdm), A/Victoria/3/75 (H3N2) and A/PR/8/34 (H1N1). We equally found reduced lungs virus titers and histopathological signs at day 5 after challenge in PmNPs-M2e with CpG immunized mice in comparison to other groups. Based on these data, we are successfully demonstrated that the use of PmNPs-M2e with CpG formulation could lead to the development of a universal influenza vaccine.

Audience Take Away:

- Academic audience can learn pre-clinical development process of making universal flu vaccine using M2e as conserve influenza antigen and PLGA nanoparticle as antigen carrier.
- Govt. healthcare audience can learn that how we can rectify the problem of taking every year flu vaccine because this is an universal flu vaccine people need only once a time and they would be protected for lifelong time. Which can also reduce the burden of cost, pain and time.
- Industry audience can use this information for commercialization of this vaccine because all vaccine components are synthetic therefore vaccine could be scalable rapidly in industry.

Biography:

Dr. Gaurav Joshi studied Biotechnology at the Banaras Hindu University, India and graduated as MS in 2010. He next joined the research group of Dr. Manmohan parida at the Virology department, Defence research and development establishment, India. He received his PhD degree in 2015 at the same institution in Biological science in the area of novel antiviral drugs against 2009 pandemic H1N1 influenza virus . Since 2016, he joined as postdoctoral research associate in Texas Tech University under the supervision of Prof. Harvinder Singh Gill in the area of development of universal influenza vaccine.

Domenico Merante
Global Clinical Development, Switzerland

Focus on vaccine safety: The clinical relevance to keep focusing on the close monitoring and safety surveillance of Covid-19 available and forthcoming vaccines. Can all the available and future safety clinical data be conveyed in one global safety database

History teaches us all about the course of past pandemics and the importance of the use of effective and safe vaccines to contribute to prevent diffuse bacterial and viral infections. But vaccines have also generated ethical controversies over the years. It is important to learn from the past and to make sure the efficacy and the safety of the available and future vaccines is continuously and carefully monitored.

There is an urgent need today to merge all serious and non-serious adverse events post COVID-19 vaccine administrations generated on a national and continental level, in order to globally assess the safety profile of these vaccines, so they can be conveyed in one only global clinical safety database. This harmonized and coordinated effort would allow generating a global clinical safety report to be continuously assessed and monitored by an independent global panel of safety experts across the world. The approach is of highest clinical relevance to figure out any potential safety signal emerging from all adverse events around the world post COVID-19 vaccinations. The approach would allow to eventually recalibrating, if deemed necessary, the clinical positioning and the labelling of the approved vaccines, which are currently utilized for preventing COVID-19 infection.

This abstract aims to generate awareness on this topic and to invite all involved regulatory authorities to collate all the adverse events arisen from every single country and to promptly disclose in one global report the available information related to the serious and non-serious side effects occurred post-COVID-19 vaccinations. This is of clinically high relevance, particularly to the whole world community. It is extremely important to carefully evaluate and not to downplay any emerging safety signal from the real world data, even if this was assessed as 'minimal'.

Due to the accelerated timing to develop and to produce the approved COVID-19 vaccines by several regulatory agencies, also by considering the limited information from the available clinical studies at the time of their approval, i.e. because of the studies sample size; the limited number of patients/subgroups; the study durations, the absence at that time of the latest variants of the virus etc. based on prediction of more vaccines to become available, the clinical relevance to urgently identify vaccine-specific subgroups of people at higher risk to develop specific side effects, especially those most serious ones, all this is of high clinical importance. The approach could help to better understand the use of the existing vaccines and the most eligible populations needed to be vaccinated and to complete the full course of each vaccination. This is also relevant in light of future vaccination recalls and a full global vaccination campaign necessary to tackle the ongoing pandemic'.

Audience Take Away:

- Through this work the audience will be able to learn about keeping the high focus on vaccine safety during this and all future pandemics;
- The presented topic will increase awareness on vaccine safety of the available and forthcoming COVID-19 vaccines. The

tangible benefits relate to the importance of safety reporting of all the adverse events, including those events of minimally defined clinical relevance. This is of vital importance for the full acknowledgement of the safety of all available Covid-19 vaccines.

- To continuously monitor the vaccine safety vigilance and to adjust the benefit/risk profile of any approved and administered vaccine utilized during and after this Covid-19 pandemic is relevant alongside the benefits to identify those patients groups at higher safety risk and the need to adjust the benefit/risk profile of all vaccines on an ongoing basis.

Biography:

Dr Domenico Merante graduated in Medicine and specialized in diabetes and endocrinology at the University of Pisa/Italy in 1988 and 1993, respectively. His focus is on neuropathic pain and diabetic wound treatment. His experience includes positions as medical officer of the Italian Navy (3 years) and emergency doctor in the NHS/Italy (12 years). With 25 years of drug global clinical development experience (phase 1-3), Dr Merante has worked in pain, antibiotics, type 1/2 diabetes, painful diabetic neuropathy, severe hypertension and endocrine area. To date Dr Merante has 103 publications as main or co-author among full papers, abstracts and oral presentations.

Azadeh Zahmatkesh*, Reza Gholizadeh
Razi Vaccine and Serum Research Institute, Iran

Endosomal TLRs may have no important effect on higher transmissibility of SARS-CoV-2 alpha and delta variants

Toll-like receptors (TLRs) are essential for activation of innate immunity and initiation of adaptive immune response. They have been associated with several respiratory diseases, but information on the relation of TLRs with SARS-CoV-2 still needs to be completed. Endosomal TLRs can detect viral or bacterial nucleic acids and have an important role in initiation of immune responses against the pathogens. TLR7/8 can detect consecutive uridine-containing single-stranded RNA of the viral genome. TLR9 binds CpG signaling motifs in bacterial and viral DNA molecules, and is found to be highly expressed in peripheral blood mononuclear cells after infection with SARS-CoV. Also, the SARS-CoV genome has higher numbers of TLR9 signaling motifs than some other respiratory diseases viruses. It was shown that SARS-CoV-2 genome has more TLR7/8-detectable motifs than SARS-CoV genome, representing a higher probability to interact with TLR7/8. This was linked to the potential ability of SARS-CoV-2 to induce pro-inflammatory responses in severe lung injury cases. Since it was shown that alpha and delta variants are associated with higher transmission rates, in this study, we performed a bioinformatic analysis on the interaction of endosomal TLRs and SARS-CoV-2 wild type, alpha and delta variants. We used Sequence Searcher software for searching TLR7/TLR8 RNA motifs, and TLR9 CpG motif in the SARS-CoV-2 genome of Wuhan reference sequence and alpha and delta variants. Data analysis showed that the overall number of genomic motifs detectable by TLR7/8/9 in SARS-CoV-2 alpha and delta variants was lower than in SARS-CoV-2 wild type sequence. This suggests that the endosomal TLRs may have no important effect on higher transmissibility of SARS-CoV-2 alpha and delta variants. Also, lower detectable motifs in delta than alpha variant, indicated a potential lower binding affinity to endosomal TLRs compared with alpha. As a conclusion, higher transmission rates reported for alpha and delta variants may not be due to the genomic mutations that alter the number of TLR7/8/9-detectable motifs.

Audience Take Away:

- The audience will find about the possible effect of different mutations in the SARS-CoV-2 genome on its affinity to endosomal TLRs.
- The study shows that the reason of higher transmission rate of alpha and delta variants is better to be detected in relation to receptors other than the endosomal receptors.
- This study sheds light on future in vitro investigations on the interactions of endosomal TLRs and SARS-CoV-2 genome.

Biography:

Azadeh Zahmatkesh studied Genetics and Animal Breeding at Isfahan University of Technology, Iran and graduated as PhD in 2015. She currently works as an assistant professor at the Department of Anaerobic Bacterial Vaccines Research and Production, Razi Vaccine and Serum Research Institute, Iran. Her research interests include molecular biology and genetics, immunology and vaccine production, and she has 19 published scientific papers in these fields.

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Julia Bespyatykh* and Egor Shitikov
Center of Molecular Medicine and Diagnostic, Federal Research and Clinical Centre of Physical, Chemical Medicine, Moscow, Russia

Aureolic acid group of agents as potential antituberculosis drugs

Mycobacterium tuberculosis is one of the most dangerous pathogens. Bacterial resistance to antituberculosis drugs grows each year, but searching for new drugs is a long process. Testing for available drugs to find active against mycobacteria may be a good alternative. In the presented study, we used the fast-growing and nonpathogenic *Mycobacterium smegmatis* to investigate the effect of aureolic acid group antibiotics.

In this work, *M. smegmatis* mc2 155 strain was used. To antibacterial activity analysis, Olivomycin A, Mithramycin A, Chromomycin A3, BRACO-19, and TMPyP4 (all from Sigma-Aldrich, Missouri, USA) (Supplementary Materials Figure S1) were added to the cultures, at a final concentration of 10 μM. As a positive control, Kanamycin was used at a final concentration of 20 μM. Negative control samples were treated with the same volume of DMSO (a solvent for all chemicals above). G4 motifs in the genomes of *M. tuberculosis* and *M. smegmatis* were analyzed, and the ability of the aureolic acid group drugs to stabilize G4 motifs was tested. For scanning electron microscopy (SEM), fixed cells examined using a scanning electron microscopy multipurpose analytical complex Merlin (Carl Zeiss, Germany). Transcriptomic analysis was conducted on Illumina HiSeq 2500.

We presumed that antibiotics of this group may be potential G4 ligands. However, this was not confirmed in our analyses. Our data demonstrate antimycobacterial activity of Olivomycin A. We showed that it significantly inhibits the growth of *M. smegmatis*, the closest relative of *M. tuberculosis*. Transcriptomic analysis revealed a decrease in the transcription of several essential genes and an active cell response on the stress. Mycobacterial cells cultivated in the presence of sublethal doses of antibiotic (0.5 μM) were elongated and formed conglomerates not typical for control cells. Transcriptomic analysis documented increased expression of *MSMEG_3743/soj* and *MSMEG_4228/ftsW*, involved in cell division. Therefore, drugs may affect cell division, possibly disrupting the function of the Z-ring and the formation of a septum. Additionally, a decrease in the transcription level of several indispensable genes, such as nitrate reductase subunits (*MSMEG_5137/narI* and *MSMEG_5139/narX*) and MSMEG_3205/hisD was shown. We concluded that the mechanism of action of aureolic acid and its related compounds may be similar to that bedaquiline and disturb the NAD+/NADH balance in the cell. All of this allowed us to conclude that aureolic acid derivatives can be considered as potential antituberculosis drugs.

Audience Take Away:

- Improve understanding of the molecular characteristics of the formation of resistance in mycobacteria
- Develop new anti-tuberculosis drugs
- Adapt known drugs for new treatment regimens

Biography:

Dr. Julia Bespyatykh is currently a Head of Center of Molecular Medicine and Diagnostic and Head of Laboratory of molecular medicine in the Federal Research and Clinical Centre of Physical-Chemical Medicine, Moscow, Russia. In 2016 she defended the Ph.D. thesis in biochemistry. She has been involved in the development of biochips for the typing of mycobacteria. She's current research interests mainly focus on the mechanisms of drug resistance and pathogenicity factors of Mycobacterium tuberculosis, using different OMICs methods, a description of the population structure of the pathogen. She has published more than 30 research articles in SCI(E) journals.

Lamiae Grimaldi-Bensouda*, Yann Hamon, Philippe Attias, Tom Duchemin, Albert Buchard, Lucien Abenhaim, Yola Moride

Department of Pharmacology, Hospital Group Paris-Saclay, Assistance Publique-Hôpitaux de Paris; UFR des Sciences de la Santé, University Paris-Saclay, Paris, France.

Vaccination and acute flare-ups in rheumatoid arthritis: A nationwide case- crossover study using the French SNDS health care databases

Rheumatoid arthritis (RA) is one of the most common chronic inflammatory autoimmune disease. Patients with RA have a significant increased risk of serious infection following treatment with disease- modifying antirheumatic drugs, and clinical guidelines strongly recommend pneumococcal and influenzae vaccines; recurring allegations on their association with disease incidence are raised. The role of vaccination on the occurrence of flare-ups of the disease is not fully known. Associations with vaccines have been reported, such as those against tetanus, hepatitis B, and influenza, but causality has not been confirmed. This study aimed the association between vaccination and the occurrence of acute flare-ups in patients diagnosed with RA.

A case-crossover study was conducted within a cohort of SLE. All patients with a diagnosis of RA were identified between 1st Jan. 2008 and 31st Dec. 2018 in a nationwide linked health care database covering 97% of the French population. A RA flare-up was defined as either a new pharmacy dispensing claim for high-dose corticosteroid or a hospitalization with a RA-related primary discharge diagnosis (ICD-10 codes). Vaccine exposure in the 2 months prior to the date of flare-up (risk window) was compared to prior exposure in up to 4 control time windows per patient (each of 2 months). GEE models were used to account for the occurrence of multiple flare-ups within an individual, adjusting for health care utilisation. Stratification by type of flare-up (first flare-up in incident patients or any flare-up in prevalent patients) and by type of vaccine (bacterial or viral) was conducted.

A total of 223,612 patients with RA were identified. The mean age of patients at study entry was 56.1 years [SD:14.8] and 72.6% were females. A total of 799,634 acute RA flare-ups were identified over the study period, among which 79,417 (9.9%) were first episodes in incident RA patients. Overall, 81.9% RA patients were vaccinated at least once during the study period, distributed as follows (non-mutually exclusive): vaccine combinations (46.1%), flu (53.0%), pneumococcus (41.7%), hepatitis B (2.4%), tetanus (5.9%) and others (<1%). In patients with prevalent flare-ups, 57,218 (7.49%) vaccinations occurred during the risk window compared to 168,234 (7.11%) occurring in the control windows (odds ratio (OR): 1.13; 95% confidence interval (CI): [1.12-1.14]). The OR for viral vaccines was OR=1.19 [1.18 - 1.21]), for bacterial vaccines OR=0.96 [0.94 – 0.98] and for combinations: OR= 0.93 [0.91-0.96]. Findings were similar for incident flare-ups.

From this large-scale study, we observed a small association between vaccination and flare-ups in RA patients. Further research is needed to confirm this association notably the role of circulating viral epidemics and disease activity on vaccination and flare-ups.

Audience Take Away:

- Infections represent a major cause of morbidity and mortality in auto-immune disease like RA. These patients are widely vaccinated to prevent infection.
- A small but significant association between vaccination and flare-ups was found in RA patients.
- Further research is needed to discuss the benefit-risk of vaccination in RA patients.

Biography:

Lamiae Grimaldi-Bensouda is a professor of clinical pharmacology at Paris Saclay-University and an honorary associate professor of epidemiology at the London School of Hygiene & Tropical Medicine and a member of the INSERM Research Team on Pharmacoepidemiology of infectious disorders. She conducted more than 50 studies on vaccines and drug effectiveness and risks in multiple disorders, including autoimmune diseases and RA.

Maryam Touhidinia*, Fatemeh Sefid
Department of Biology, Faculty of Science, Yazd University, Yazd, Iran

Design of a multi-epitope vaccine using immunoinformatics approach

Immunoinformatics plays a key role in vaccine design and antibody production. In the past, antibody design and vaccine development are expensive and time-consuming. Nowadays, advances in the field of bioinformatics have provided practical tools that can be used to lessen the time and cost of vaccine and antibody design. The Immunoinformatics approach allows the identification of the immunogenic epitopes from the pathogen genomes. Also, the ideal and immunogenic parts could be developed as potential vaccine candidates to trigger protective immune responses in the hosts.

In our studies, are identified the potential and immunogenic epitopes of a selected protein by bioinformatics tools. Then, these are selected based on allergenicity, antigenicity, and solubility features. And we use linkers and adjuvants to structure the epitope vaccines. Then, the 3D structure of the protein was predicted, and its affinity to different HLA, TLR was investigated by molecular docking. These methods have been performed with a wide range of bioinformatics tools to design vaccines against Covid19, Acinetobacter Baumannii, and Neisseria meningitidis. The design technique of these vaccines will be clearly mentioned in the lecture.

Audience Take Away:

The audience will be able to use from:

- In silico method to vaccine design
- Strong and important points in this method
- Useful softwares in this way

Bioinformatics and the prediction of critical criteria in the vaccine design process reduce error and time in the design process that students and professors should better include this topic in the laboratory work process and use it.

Biography:

Maryam obtained a B.Sc. degree in Cellular and Molecular Biology from Yazd University in 2014. Then, she studied Masters of Molecular Genetics at the University of Yazd. He is now pursuing his research at the Department of Biology, Yazd University. Her special research interests focus on Bioinformatics, Microbiology, Structural Biology, Molecular Biology, and Biotechnology especially their application in recombinant vaccine research. In addition, her master's project was 'Isolation, cloning, expression of antigenic region of CarO gene from Acinetobacter baumannii'. Her recently project is the Design a multi-epitope vaccine against COVID-19. She is also an enthusiastic fan and an as new researcher in the field of monoclonal antibody design and drug design for different types of cancer and Covid19. She has published more than 20 research articles in journals and international congresses.

Ghadir Fakhri Al-Jayyousi*, Mohamed Abdelhady Mabrouk Sherbash, Lamees Abdullah Mohammed Ali, Asmaa El-Heneidy, Nour Waleed Zuhair Alhussaini, Manar Elsheikh Abdelrahman Elhassan and Maisa Ayman Nazzal

Department of Public Health, College of Health Sciences, QU Health, Qatar University, Doha P.O. Box 2713, Qatar;

Factors influencing public attitudes towards COVID-19 vaccination: A scoping review informed by the Socio-Ecological model

Major hindrances to getting a COVID-19 vaccine include vaccine hesitancy, skepticism, refusal, and anti-vaccine movements. Several studies have been conducted on attitudes of the public towards COVID-19 vaccines and the potential influencing factors. The purpose of this scoping review is to summarize the data available on the various factors influencing public attitudes towards COVID-19 vaccination. This scoping review was conducted according to the Preferred Reporting Items for Systematic Reviews and Meta-Analyses extension for Scoping Reviews (PRISMA-ScR) Statement. PubMed, Embase, Web of Science, and Cochrane Central were searched without restrictions to reclaim all publications on the factors that shape individuals' attitudes towards COVID-19 vaccines from 1 January 2020 to 15 February 2021. Fifty studies were included. The scoping review revealed that the factors influencing public attitudes towards COVID-19 vaccines were embedded within the different levels of the socio-ecological model. These factors included the sociodemographic characteristics of the individuals, individual factors, social and organizational factors. In addition, certain characteristics of COVID-19 vaccines themselves influenced public attitudes towards accepting the vaccines. Understanding various population needs and the factors shaping public attitudes towards the vaccines would support planning for evidence-based multilevel interventions in order to enhance global vaccine uptake.

Audience Take Away:

- Understand various population needs and the multilevel factors shaping public attitudes towards the COVID-19 vaccine
- Learn about evidence for interventions to enhance vaccine uptake.
- Understand gaps in research that explores factors influencing public attitudes towards the COVID-19 vaccine.

Biography:

Ghadir Fakhri Al-Jayyousi is an Assistant Professor of Health Education and Promotion in the Department of Public Health, College of Health Sciences at Qatar University. Dr. Al-Jayyousi earned her Ph.D. in Health Education from Kansas State University, USA. She had MS in Community Health from the University of Arkansas at Fayetteville, USA and BSc in Medical and Biological Analysis from the University of Jordan. Her research focuses on social determinants of health, including sociocultural and environmental factors that influence health behaviors, interdisciplinary research, family and health, women's health, and public health practice. Another area of research interest is diabetes education.

Sanjeeb Kumar Mishra*, Subrat kumar Pradhan, Sanghamitra Pati, Bimal Krushna Panda, Debdutta Bhattacharya, Sumanta Kumar Sahu, Jaya Singh Kshatri

Principal Investigator, Tutor, Department Of Community Medicine, VIMSAR, Burla.

Anti SARS Cov 2 antibodies among vaccinated healthcare workers: Repeated cross-sectional study in VIMSAR, Burla

Background – Since the day the Novel SARS Cov has been detected and the ensuing pandemic the search or a cure or prevention has been the only target of the medical fraternity. As the second wave racked havoc Vaccine seemed the only viable option to stop this global surge. WHO & subsequently Government of India have issued emergency use authorization to 2 vaccines. Our study is aimed at estimating the seroconversion rates and to identify predictors of antibody titres in vaccinated healthcare workers in VIMSAR, Burla.

Methods – This is a part of the ongoing repeated cross-sectional study. Participants were enrolled well above the Sample size (322) to increase precision. Two rounds of survey were conducted & is being reported. Serum IgG antibodies against spike protein of SARS-CoV-2 was estimated using Elecsys® Anti-SARS-CoV-2S is an immunoassay by ECLIA based Cobas e411 analyzer. Univariate and multivariate regression were used in statistical analysis.

Results - Our results show 95.1 % and 99.5% of the vaccinated individuals have developed anti spike protein antibodies after the 1st and 2nd dose respectively. Previous Covid infection was Significantly Correlated with antibody production and age was negatively correlated. No difference was reported for sex, occupation, diabetes.

Conclusion. Our interim analysis report is coherent with the available literature and research regarding high efficacy of Covid vaccine as far as seroconversion is concerned.

Keywords – SARS CoV 2, Covishield, Vaccine, Seroconversion, ECLIA, Regression.

Audience Take Away:

- Seroconvesion rate after Administraion of Covid Vaccines.
- Predictors of Antibody titres post Covid Vaccination.

Biography:

Dr. Sanjeeb Kumar Mishra completed MBBS from VSS Medical College & Hospital in 2012. There after he worked as a Medical Officer of Primary health center in Left wing extremist dominated area for 5 years. Then he joined his Masters program in Community Medicine in VIMSAR on july 2017. Completed the course in July 2020 and joined as a Tutor. He has been trained in Infodemic Management by WHO & CDC, on implementation research by WHO-TDR, on Disaster risk reduction by UNDRR. He has been selected for NCD Fellowship by ICMR-NIE in July 2021.

Damini Singh*, Sonal Gupta, Rakesh Bhatnagar
Environmental Pollution Analysis Lab, India

Micro encapsulations of outer membrane proteins of Brucella Spp. - Highly potent vaccines against brucellosis

Brucellosis is a zoonotic bacterial infection of pandemic potential – caused by Brucella species. Lack of vaccines against human brucellosis despite continuous research has led us to address this issue using several selectively chosen antigens pertaining to Brucella spp. We have been utilizing different marketed adjuvants e.g. Aluminium hydroxide, MF-59 etc. Simultaneously, we have been developing nano-encapsulations of various antigens namely – rL7/L12, rOmp25 and rOmp28 etc.

Poly-lactide-co-glycolide (PLGA) has been one pf the most successful with all the antigens mentioned above in eliciting a good humoral immune response as well as causing a huge reduction in the organs' bacterial load especially liver and spleen. Additionally, we have been using nano-liposomes which were similar in their efficiacy aspects but had much inferior stability upon storage.

Post-immunization, several parameters e.g. IgG antibody levels, cytokines – their levels, and bacterial load in the organs and all the antigens being highly immunodominant produced significantly high antibody titers apart from ensuing varied cytokine release patterns.

To summarise, Omps were found to spike apical immune responses as well as maximal protective efficacy. Thus, Omps hold a huge promise as prophylactics of future use. More research is aimed to be conducted to understand the immune memory pertaining to these antigenic formulations.

Biography:

I have finished my Doctoral studies from Jawaharlal Nehru University, New Delhi, India - this was focussed at the Development of a Brucella Vaccine suitable for humans. Biodegradable Nano and microparticles encapsulated with conserved as well as immunodominant antigens of Brucella spp. An extension study in this context, helped me to receive a "Young scientist award" by Department of Health Research, Government of India. Further, for post-doctoral research, I had joined "W.M.Keck Centre for Transgene research" at University of NotreDame, Indiana, U.S.A wherein the research was mainly aimed at studying the Group A Streptococci, it's virulenece in mice - wild type as well as knock outs of various blood proteins. Currently, I am working as Scientist at Environmental Pollution Analysis Lab - inculdes protocols' optimization and preparation of materials for trainings, workshops etc as well as preparation of research projects.

Mohammad Jalil Zorriehzahra*, Mina Ziarati , Fatemeh Hassantabar
Department of Information and Scientific Communication, Iranian Fisheries Science Research Institute (IFSRI), Agricultural Research, Education and Extension Organization (AREEO), Tehran, Iran

Introduce of most important aquatic vaccines in aquaculture and marine fish

This fact is well known that the appearance and development of all fish disease process could be the result of the interaction between three parameters such as pathogen, host, and environment. Therefore, only multidisciplinary studies involving knowledge of the characteristics of the potential pathogenic microorganisms for fish, aspects of the biology of the fish hosts, as well as a better understanding of the environmental factors affecting them, will allow the application of adequate measures to prevent and control the main infectious diseases limiting the production of freshwater and marine fishes. Vaccination is becoming an increasingly important part of aquaculture, since it is considered a cost effective method of controlling different threatening diseases. Also, it was alternated for Antibiotic application in some developed countries and it could be positive aspect to decreasing antibiotic resistance in some familiar pathogens in the environment and aquatic ecosystems. The term vaccination strategy has been defined to include the decision as to which diseases to vaccinate against, as well as the vaccine type, vaccination method, the timing of vaccination and the use of revaccination. In this lecture most important aquatic vaccines such as Bacterins, Live attenuated vaccines, killed vaccine and DNA vaccines would be discussed for some important fish bacterial and viral diseases. Also, monovalent and polyvalent and route and strategy of administration fish vaccines would be talked. Meanwhile, economic aspects related to fish vaccination, potential costs and benefits could be discussed.

Keywords: Fish vaccination, vaccine, Aquaculture, Marine Fish

Audience Take Away:

- Discussion about most important fish vaccines through their advantages and disadvantages
- Talking about effectiveness, protection, safety and efficacy of the Fish Vaccines
- Explanation of disadvantages and side effects of produced different fish vaccines.
- Presentation of some solution ways for probably problems about fish vaccines.

Biography:

Dr. Mohammad Jalil Zorriehzahra studied Aquatic animal Health and Diseases at the UPM University, Malaysia with Virology specialization and graduated as DVM in 1987 in Tehran University. He has worked as member of the Iran National Viral Diseases Strategic Network since 2017. He obtained the position of an Associate Professor at the (IFSRI) in 2015. He has published more than 100 research articles in ISI and ISC journals as well as 10 technical books and more than 50 Research Projects in (IFSRI). Also, he applied two research projects about COVID-19 in Iran Health Ministry.

Yacob Mathai
Marma Health Centre,India

Fever is not a symptom in covid-19. None of the diseases require fever as its symptom

All treatments for fever are based on the belief that fits is the result of 41 degrees Celsius temperature and it damages cells of the brain and body. At the same time, there is no evidence-based tests or concrete diagnosing methods to the belief that fits and brain damage is the result of pyrexia [1]. Necessary ingredients to destroy brain cells and fits cannot be seen in fever. In pyrexia or absence of fever, a fainted patient fell on the floor with unconscious state and destroy cells of the brain, and necessary ingredients to become conscious are the same. When disease increases essential blood circulation and energy level also decreases. The vertical height between the heart and brain is more than one foot. When the disease becomes severe, the ability to pump the blood to the brain decreases. As a result of this brain cells are damaged. so the patient might be paralyzed or may even die. In pyrexia or absence of fever, when blood flow to the brain decreases and fits are formed. There is no other way than this to increase blood circulation to the brain. It is a sensible and discreet action of the brain to protect the life or organ. Recovery from Fits. The patient becomes conscious before the time to get decreasing the temperature of fever. When the fainted patient lie on the floor, the vertical height between the heart and brain is decreased, blood circulation increased to the brain. Self-checking methods. When the fainted patient lie on the floor, The patient can stand straight and lie on bed alternatively. Then the patient can experience himself the intensity of blood circulation. The patient can experience when he stands his blood circulation decreases and when lying on the bed the blood circulation decreases. Besides that, he can also experience increased blood circulation when lie on the bed raise the foot higher than the head.

Biography:

A practicing physician in the field of healthcare in the state of Kerala in India for the last 30 years and very much interested in basic research. My interest is spread across the fever, inflammation and back pain. I am a writer. I already printed and published nine books on these subjects. I wrote hundreds of articles in various magazines.After scientific studies, we have developed 8000 affirmative cross checking questions. It can explain all queries related to fever

Mahya Sadat Lajevardi*, Tahereh Taheri, Elham Gholami, Yousef Mortazavi, Negar Seyed, Sima Rafati

Department of Immunotherapy and Leishmania Vaccine Research, Pasteur Institute of Iran, Tehran, Iran

Immunoinformatics and structural analysis for multi-protein vaccine design

To generate more effective subunit vaccines against complex organisms like Leishmania parasites, we need to fuse several immunogenic proteins together. However, the critical issue is that which arrangement of the constituting components should be selected as the favored combination for vaccine design. These days, RNA and protein structure analysis techniques together with immunoinformatics are the handiest approaches available for selecting among the appropriate combinations. To advantage this approach, all possible combinations are designed and analyzed at mRNA and protein levels. At the mRNA level, the full sizes of the transcripts are estimated based on the used expression vector. Then, the secondary structures of mRNAs are predicted by specific web servers. At the protein level, the 3D structures of all combinations are modeled by online platforms. Then, the predicted 3D models are refined and validated by different parameters. Eventually, validated models are superimposed to the original individual proteins to find out structural identity, the higher the similarity the better the reliability of candidate combination. On the other hand, the combined structures are also further analyzed for junctional epitopes by immunoinformatics. This approach was used to combine two immunogenic salivary proteins (PpSP15 from Ph. papatasi and PsSP9 from Ph. sergenti) together to develop an effective vaccine against cutaneous leishmaniasis. The best combination as the vaccine candidate was selected based on mRNA and protein stability results besides peptide analysis and will be presented as an example model for a multi-protein vaccine design.

Biography:

Mahya obtained a BSc degree in audiology in 2011(Tehran University of Medical Science) and her master's degree in medical biotechnology in 2015 (Zanjan Medical School). As a PhD student she is working on a vaccination strategy against cutaneous leishmaniasis in the department of Immunotherapy and Leishmania Vaccine Research at Pasteur Institute of Iran. Her research interests are immunoinformatics, Structural Biology, vaccine design and development. She is really enthusiastic to learn data science for drug and vaccine design against different diseases. She has published 7 research articles in journals and international congresses and has two under submission in high impact journal.

Muhammad Naveed Anwar
Chinese Academy of Agricultural Sciences (CAAS), Pakistan

Phenotypic and genotypic comparison of a live-attenuated genotype I Japanese Encephalitis virus SD12-F120 strain with its virulent parental SD12 strain in vitro in vivo

Japanese encephalitis (JE) is a vector-borne zoonotic viral disease caused by (Japanese encephalitis virus, JEV). Vaccination is the most effective way to control JE in both humans and pigs. However, JEV genotype shift that the dominant genotype III (GIII) has been replaced by genotype I (GI) raised concerns about the effectiveness of GIII-derived vaccines against the GI strain infection. Indeed, GIII-derived vaccine showed a reduced protection against GI strain challenge, suggesting a potential need of development of GI-derived vaccine. In this study, a comparative analysis of the phenotypic and genotypic properties of an attenuated GI strain (SD12-F120) and its virulent parental strain (SD12) was performed.To characterize the attenuated GI strain SD12-F120, the phenotypic and genotypic characteristics of SD12-F120 with its virulent parental SD12 strain were compared in vitro and in vivo. SD12-F120 formed smaller plaque on BHK-21 cells and showed the reduced replication in mouse primary neuron cells and mouse brains as compared with SD12. Mice inoculated with SD12-F120 up to 105 PFU via either intraperitoneal or intracerebral route showed no clinical signs of JEV infection, indicating highly attenuated phenotype in terms of both neuroinvasiveness and neurovirulence. Immunization of mice with SD12-F120 provided a complete protection against SD12 challenge. Comparison of genome variations between SD12-F120 and SD12 revealed that SD12-F120 harbored 29 nucleotide variations, of which 20 were considered silent nucleotide mutations, while 9 resulted in eight amino acid substitutions: two in E, one in NS1, two in NS3, one in NS4B and two in NS5 proteins. Comparison of the amino acid variations of SD12-F120 vs SD12 pair with those from other four isogenic pairs of the attenuated and their virulent parental strains revealed that the numbers and positions of amino acid variations were different from each other. Out of the five pairs, the variations at E138 and E176 positions of E protein were identified in four and three pairs, respectively. The remained amino acid variations were almost unique to their respective strain pairs, suggesting that the genetic changes acquired during the attenuation process were likely to be strain specific and that the mechanisms associated with JEV attenuation/virulence were complicated. The SD12-F120 was obtained by serial passage of its virulent parental SD12 strain on BHK-21 cells, which was not appropriated for vaccine production. Therefore, SD12-F120 was further passaged on Vero cells for 20 passages and a Vero cell-adapted strain SD12-F120VC was obtained. SD12-F120VC had an increased in virus titers compared to early passages, showing an adaptation to Vero cells. The plaque morphology of SD12-F120VC was same as that of SD12-F120. The animal experiments showed that SD12-F120VC had attenuation phenotype in suckling mice. Vaccination of mice with SD12-F120VC completely protected vaccinated mice against challenge with SD12 strain, but failed to provide the vaccinated mice complete protection against the challenge of GIII N28 strain. The neutralizing antibodies titer of immunized mice against SD12-F120VC and SD12 was higher than that of heterologous N28 strain. SD12-F120VC harbored 6 amino acid substitutions in prM protein, of which 5 were present in the pr domain of prM. These amino acid substitutions may be involved in the adaptation of SD12-F120 to Vero cells. Overall, the phenotypic and genotypic characteristics of SD12-F120 with its virulent parental SD12 strain were compared in vitro and in vivo, and the protection of the attenuated strains was determined in mice. The outcome would be useful for development of GI-derived vaccine.

Biography:

My name is Muhammad Naveed Anwar I belong to Pakistan. I have finished my Ph.D. in Preventive Veterinary Science (Microbiology) from the Chinese Academy of Agricultural Sciences (CAAS), Beijing, China in August 2020. My doctoral thesis title was "Characterization of Live-Attenuated genotype 1 strain of Japanese encephalitis virus." Moreover, I have also worked on several relevant projects which include: A Novel recombinant VLP vaccine displaying B and T cells epitopes of JEV; adaptation of Live-Attenuated JEV vaccine to Vero cells in association with mutations to structural proteins. I have published my Ph.D. research work in "Viruses" and "Virus research" journals and my current VLP vaccine paper has been published in "Vaccines". My main research interest is in virology, immunology, and virus-host interaction. I am an innovative, goal-oriented person who possesses a good analytical approach. Currently, I am finding a post-doc position where I would relish my past experience for the benefit of a fruitful outcome.

Mohammad Jalil Zorriehzahra*, Fatemeh Hassantabar, Mina Ziarati
Department of Information and Scientific Communication, Iranian Fisheries Science Research Institute (IFSRI), Agricultural Research, Education and Extension Organization (AREEO), Tehran, Iran

Comparison of several developed new Vaccines against COVID-19

During recent years we have witnessed numerous occurrences of viral infectious diseases such as Ebola, MERS, SARS, and recently COVID-19 with a drastic negative effect on human health. Following the outbreak of the COVID-19 pandemic, it has been declared a public health emergency of international concern by the World Health Organization. The causative agent of this infection would be able to transmit via contact with contaminated secretions of infected people, or close contact with a cough or sneeze. Prompt development and comprehensive investigations about the production of an efficacious vaccine against the SARS-CoV-2 have been performed in some countries, but rigorous studies are required to determine the safety and potency of candidate vaccines. SARS-CoV-2 vaccines are being developed using several different platforms. Some of these are traditional approaches, such as an inactivated virus or live attenuated virus platforms, some are newer approaches, such as recombinant proteins and vector vaccines, and some have never been previously employed in a licensed vaccine, such as RNA and DNA vaccines. Also, following availability and widespread uptake of SARS-CoV-2 vaccines, efficacy issues that were not addressed in clinical trials will need to be evaluated, including the duration of protection and the potential need for additional doses, effectiveness in subpopulations not included in trials, and impact on community transmission. Also, in my country some new vaccines were produced as a new effective vaccine by several Research Institutes as first time in Iran. In this lecture, some COVID-19 vaccines will be discussed for effectiveness, safety, protection and efficacy in sensitive and high risk population.

Keywords: COVID-19, vaccine, protection, Iran,

Audience Take Away:

- Comparison of most important COVID-19 vaccines through their advantages and disadvantages
- Discussion about effectiveness, safety, protection and efficacy of the mentioned Vaccines
- Explanation of disadvantages and side effects of produced different vaccines.
- Presentation of some solution ways for probably problems about COVID-19 vaccines.

Biography:

Dr. Mohammad Jalil Zorriehzahra studied Aquatic Animal Health and Diseases at the UPM University, Malaysia with Virology specialization and graduated as DVM in 1987 in Tehran University. He has worked as member of the Iran National Viral Diseases Strategic Network since 2017. He obtained the position of an Associate Professor at the (IFSRI) in 2015. He has published more than 100 research articles in ISI and ISC journals as well as 10 technical books and more than 50 Research Projects in (IFSRI). Also, he applied two research projects about COVID-19 in Iran Health Ministry.

Yacob Mathai
Marma Health Centre, India

Will fever cure if we treat the cause of disease or the cause of fever?

The physicians are talking about the treatment of fever indifferently. They are talking about not to treat fever but for the underlying cause of fever. At the same time when people have a fever, they instruct to reduce fever urgently. The cause of fever and cause of disease both are different. The physicians misunderstand the cause of disease as cause of fever. If we remove the cause of disease the fever never cures. If we remove the cause of fever, it can be immediately cured. The basic cause of fever is increased severe inflammation and decreased blood circulation. If we remove the cause of disease, the disease will not be cured.If a worm eats the stem and leaf of a plant, we can kill the worm with pesticides, then the destroyed part of the plant will not recover completely. Likewise, we can kill some kind of bacteria with antibiotics. But the problems made by bacteria will not be resolved.The actual treatment to cause of fever.The actual treatment to fever is to increase blood circulation. Two ways to increase blood circulation. 1. Never allow body temperature to lose 2. Apply heat from outside to the body. When the temperature produced by the body due to fever and heat which we applied on the body combines together, the blood circulation increases.

Then the body will stop to produce heat to increase blood circulation. And the body will get extra heat from outside without any usage of energy.

How can we prove that the cause of fever and cause of disease both are different?

"If we ask any type of question-related to fever by assuming that the cause of fever and cause of disease both are different, we will get a clear answer. If we avoid or evade from this definition, we will never get a proper answer to even a single question

If we do any type of treatment by assuming that the cause of fever and cause of disease both are different, the body will accept the cause of fever, at the same time body will resist whatever treatment to decrease temperature and blood circulation.No further evidence is required to prove the cause of fever and cause of disease both are different.

Biography:

A practicing physician in the field of healthcare in the state of Kerala in India for the last 31years and very much interested in basic research. My interest is spread across the fever, inflammation and back pain. I am a writer. I already printed and published nine books on these subjects. I wrote hundreds of articles in various magazines. After scientific studies, we have developed 8000 affirmative cross checking questions. It can explain all queries related to fever

Ismail Hossain
Department of Quality Assurance, Assistant Manager, Globe biotech ltd,Dhaka, Bangladesh

Covid 19 vaccine its present situation in the whole world

First of all I would like to discuss about the global pandemic covid 19 outbreak across the Whole World & how much impact on human after spreading this virus globally.Most of the peoples has been said its (virus) originated from china ,Wuhan state.whatever this virus was increasingly day by day then time. Million of peoples were died by this killer virus across the whole world as well till present time.From that time many scientist were worried about this outbreak ,they Search new innovation how to get rid of the whole world .At last they partially successful to invention new vaccine .Drug regularity authority has approved emergency Authorization to give on human clinical trial .like pfizer &moderna vaccine is found highly efficacy rate until now other than various vaccine. We are also inoculated this.At last we pray to almighty Allah to get rid of each of the part of the world free from this killer virus.

Audience Take Away:

- Public Awarness
- As our country like Bangladesh ,we have already made this vaccine named “bangovax” that is mRNA VACCINE .How to start this work I would like to explain it.I hope it will be better beneficial to the audience

Biography:

Ismail hossain from Bangladesh. He completed Bachelor degree in pharmacy in 2010 from The university of Asia pacific, Dhaka ,Bangladesh. After passing his Pharmacy degree he joined globe pharmaceutical ltd (globe biotech) as a Quality assurance officer & expert in QC instrument &regularity Department like different types of analytical job & deals with different types of drugs (OTC,ANTIBIOTICS,VACCCINE &ETC).

Jennifer E Gerber*, Rupali J Limaye, Andrea Sutherland, Janesse Brewer, Madeleine Blunt, Taylor Holroyd, Gail Geller, Bruce Carleton, Jeff Kahn, Daniel A Salmon

Department of International Health, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD United States of America; RTI International, Washington DC, United States of America

Vaccine hesitancy and influenza vaccine uptake among children and adults: A cross sectional survey

Background: Vaccine coverage is lower for influenza than for other vaccines, varying by age, race/ethnicity, and region. Vaccine safety concerns are common despite a lack of epidemiological evidence. We characterized vaccine hesitancy and identified associations with influenza vaccination.

Methods: Respondents ≥18 years old were recruited from a non-probability-based Internet panel survey (N=1,925). We measured sociodemographic characteristics, vaccine confidence, influenza vaccination history (2018-2019 and 2019-2020), trust in pharmaceutical companies and public health authorities, and perceived vaccine reaction history. The association between variables hypothesized to be associated with vaccine hesitancy and influenza vaccination was estimated with Taylor-linearized variance estimation for tabulations and Poisson regression for unadjusted and adjusted prevalence ratios. Backwards stepwise regression identified parsimonious, adjusted models ($p<0.05$).

Results: The weighted study population was 50.6% female, 61.8% White, non-Hispanic. 62.9% had a child <18 years old, and 47.1% had a high school education or less. High vaccine hesitancy was greatest among parents of young children (45.4% vs. 27.6% parents of teenagers vs. 37.7% adults without minor children). Awareness of federal vaccine safety oversight was low across age groups. In adjusted models of all age groups, higher education and use of complementary/alternative medicine (CAM) were associated with higher vaccination prevalence. Vaccination prevalence was lower among those with high vaccine hesitancy.

Discussion: We identified common vaccine misconceptions associated with vaccine hesitancy. CAM use and higher education were associated with vaccination across age groups. Vaccine hesitancy differed by parental age, which may have influenced results. Results are subject to selection and social desirability biases, though quotas were used to enroll a sample representative of sociodemographic distribution of the U.S.

Conclusions: Age and education-level appropriate, targeted communications are needed. Future research should investigate how to reach sociodemographic minorities, less likely to use CAM or be vaccinated, and whether raising public awareness of federal vaccine safety oversight improves confidence.

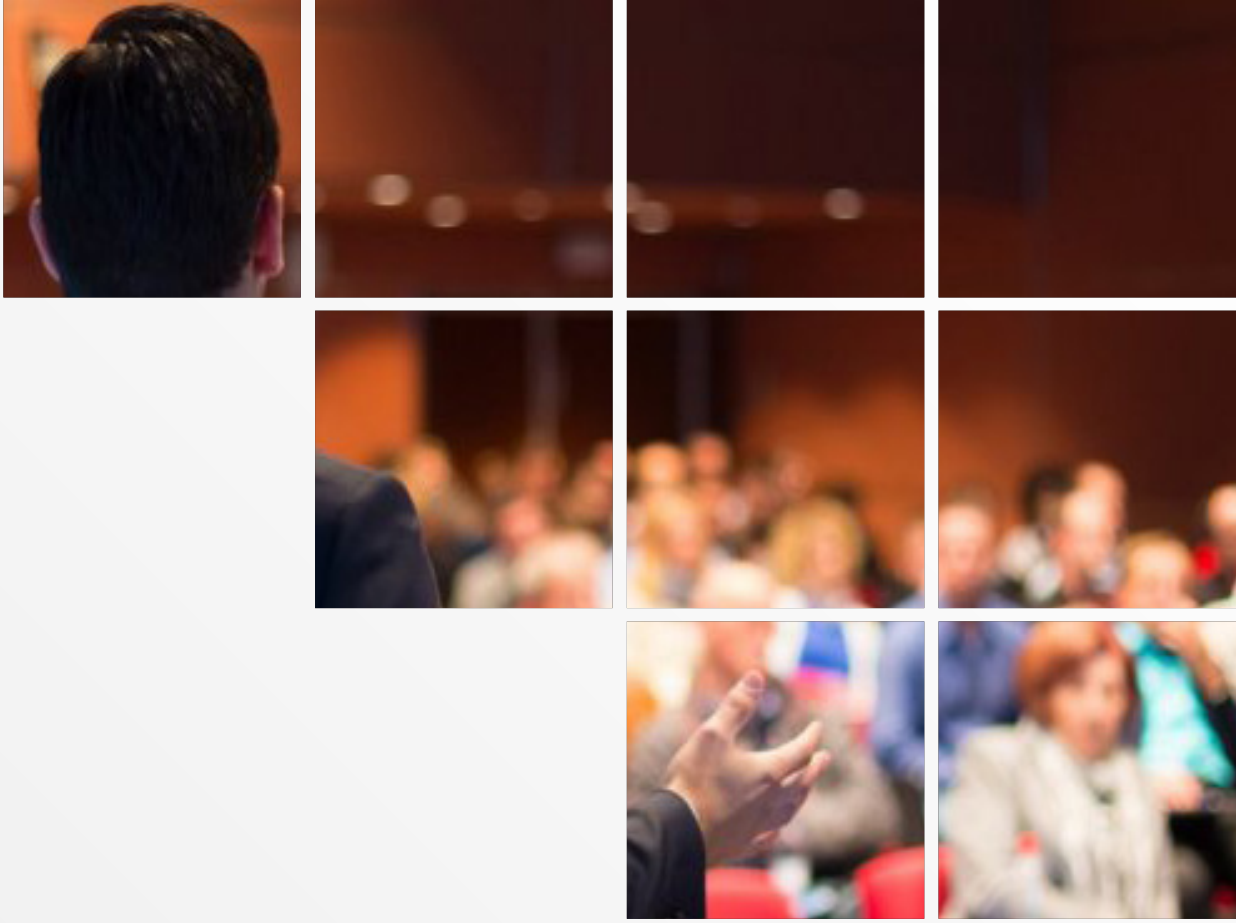
Audience Take Away:

- We will describe common vaccine misconceptions associated with vaccine hesitancy
- Factors associated with vaccine hesitancy and influenza vaccine acceptance in the U.S. will be presented.
- Detailed methods will be shared on how vaccine hesitancy was measured by parity and age group.
- Our findings may provide insights about how to address vaccine hesitancy more broadly, including for COVID- 19 vaccines.

Biography:

Jennifer E. Gerber is an epidemiologist and vaccine subject matter expert in RTI's Survey Research Division. She is experienced at implementing surveys and multisite cohort studies involving biospecimen collection during the H1N1 and COVID-19 pandemics and collecting data from special populations, including racial/ethnic minorities and pregnant women. Dr. Gerber earned her PhD in Global Disease Epidemiology and Control (2020) and a Certificate in Vaccine Science and Policy (2018) from Johns Hopkins Bloomberg School of Public Health. She earned her MSc in Epidemiology from the London School of Hygiene and Tropical Medicine (2013).

PARTICIPANTS LIST



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