conferenceseries.com
896th Conference

9th International

Virology Congress and Expo

March 13-14, 2017 London, UK

Scientific Tracks & Abstracts

Day I

Sessions

Virology | Virology and Other Emerging Viruses | Clinical Virology

Session Chair
Juana Díez
Pompeu Fabra University, Spain

Session Introduction

Title: **Host-directed broad-spectrum antiviral drugs**
Juana Díez, Pompeu Fabra University, Spain

Title: **The role of bacteria and yeast in the process of AIDS: an evolutionary point of view**
Vladimír Zajac, Cancer Research Institute, Slovakia

Title: **Human Viruses, bacteria and cancers**
Luigi Santacroce, University of Bari, Italy

Title: **New therapeutic method and treatment for HIV and HBsAg diagnosed positive patients of both sexes with severe forms of HPV infection (genital warts) with emphasis on vaginal, anal and cervical localization**
Igor Jeremic, Polyclinic Jeremic, Serbia

Juana Díez, Virol Mycol 2017, 6:1(Suppl)
http://dx.doi.org/10.4172/2161-0517.C1.017

Host-directed broad-spectrum antiviral drugs

Juana Díez
Pompeu Fabra University, Spain

Viruses completely depend on cellular factors to multiply. In spite of their unique coding features, different viruses have been shown to depend on some common host factors. Consequently, it should be possible to develop broad-spectrum antivirals by targeting them. In the presentation, the author will give an overview of the concept of host-targeting, broad-spectrum antiviral drugs and our work on natural products. The author will specially focus on metabolites isolated from myxobacteria, one of the top producers of natural products with host-targeting properties.

Biography

Juana Díez is a Professor of Microbiology and Head of the Molecular Virology Laboratory in the Department of Experimental and Health Sciences (University Pompeu Fabra, Barcelona, Spain). She obtained her PhD on Virus-Cell Coevolution (University Autónoma of Madrid) and moved to the Institute of Molecular Virology (Madison, USA) for her Post-doctorate to study host factors supporting positive-strand viral RNA replication. The main focus of her group is to decipher key host-virus interactions and to use this knowledge for development of broad-spectrum antivirals.

juana.diez@upf.edu

Notes:

Vladimir Zajac, Virol Mycol 2017, 6:1(Suppl)
http://dx.doi.org/10.4172/2161-0517.C1.017

The role of bacteria and yeast in the process of AIDS: an evolutionary point of view

Vladimir Zajac
Cancer Research Institute, Slovakia

There is increasing evidence, pointing out that GIT and other mucosal tissue are the main places of HIV infection and CD4+T cells loss but and not the blood. These findings go along with the new studies about the role of bacterial translocation in the gut as central driver of AIDS pathogenesis. We have identified HIV-like sequences and HIV-like proteins in bacteria and yeast in a cohort of 80 HIV positive patients from Slovakia, USA, Kenya and Cambodia. DNA testing of bacteria and yeasts: a) From intestinal tract of American and Slovak HIV-positive patients; b) From respiratory tract of Cambodian and Kenyan HIV-positive children has detected sequences 90% homologous with the corresponding sequences of HIV-1. Using monoclonal antibodies (MAB) against HIV-1 antigens p17, p24, gp41 and p55 we have identified HIV-like proteins in bacterial extracts of most tested patients. HIV-like protein of size 95 kDa was detected by MAB against gp120 only in Candida species of Cambodian and Kenyan samples. Specific properties of patient's microbiota by co-cultivation with HL-60 cells and reducing the viral load in AIDS patients after administration of probiotics E. coli Nissle 1917 were detected. Based on these results it can be hypothetically explained that bacteria and yeasts serve as a natural host of HIV sequences since the beginning of mankind. Thanks to countless epidemics, individuals carrying the pathogenic microbes with HIV sequences largely extinct. This tremendous longtime sanitary process - continued until the 18th century, took place mainly in Europe, consequently in USA, GB colonies, partially in Asia and North Africa. However, administration of antibiotics, drugs and anal intercourse induced intestinal dysbiosis and pathogenic bacteria were re-propagated. When pathogenic microbes bearing HIV sequences moved to the majority, penetrated from the intestinal tract into the blood, invaded the lymphocyte, infected/lysed them, the process of immunodeficiency might start. Presented hypothesis answers to many unanswered questions like the origin of HIV, connection of AIDS with TBC in Africa, absence of gold standard in Africa, the presence of HIV reservoirs after antiretroviral therapy, the rarity of complete viral particles detection in the material from AIDS patients, and detection of HIV sequences and the HIV-like proteins. According to our results there is a strong objection against dogma that HIV was transmitted to humans from apes in Africa about 35-50 years ago on the route of accidental contacts. Based on our results we submit proposals for an explanation of one of the most serious problems concerning this disease, which is a large-scale HIV positive in Africa on the basis of evolutionary process.

Biography

Vladimir Zajac has completed his PhD in 1982 from the Cancer Research Institute of Slovak Academy of Sciences in Bratislava (Slovakia), where he worked as the Head of Department of Cancer Genetics from 1996 to 2010. He joined the Medical Faculty of the Comenius University as an Associate Professor of Genetics in 2007. He has published 69 papers mostly in reputed journals and he was editor of the book "*Bacteria, viruses and parasites in AIDS process*" (InTech, 2011).

vladimir.zajac@savba.sk

Notes:

Luigi Santacroce, Virol Mycol 2017, 6:1(Suppl)
http://dx.doi.org/10.4172/2161-0517.C1.017

Human Viruses, bacteria and cancers

Luigi Santacroce
University of Bari, Italy

Actually, several studies have established a relationship between microorganisms and chronic conditions such as atherosclerosis, neurologic disorders, cancer, and obesity. The link between microorganisms and increasing numbers of diseases never before envisioned as having microbial etiology opens fascinating scientific, medical, and public health perspectives. Apart from bacteria as *Helicobacter pylori*, experimental and epidemiologic data show a causative role for viruses, particularly in cervical and liver cancer, than viruses must be thought of as one of the most important risk factor for cancer development in humans. As a consequence, today we can be certain that many cancers have aetiologies with infectious agents as necessary factors. Several DNA tumor viruses encode viral oncoproteins that can directly transform the cells. In vitro tests (i.e., using the NIH/3T3 cell stocks) allowed to clarify that the nonviral tumors have endogenous activated oncogenes. Generally, tumor viruses, after the infection of their host, determine mild disease conditions or no, or cause non-neoplastic diseases (e.g., HBV). This natural condition is just one of the reasons why it is so difficult to identify the viral agents as causal factors for human cancers. HPV is one of the most recent virus focused as responsible for cancers other than cervical. The clinical scenarios of HPV infection depend from the site of the lesion and the virus serotype. In fact, HPV DNA was detected in 100% of cervical carcinomas, 40% in tumors of the penis, as well as vulvar and vaginal, in 90% in anal carcinomas, 12% in oropharyngeal carcinomas and 3% of cancers of the mouth. Viruses may contribute to the development of human tumors both indirectly, inducing immunosuppression or modifying the host cell genome without persistence of viral DNA, and directly inducing oncoproteins or by altering the expression of host cell proteins at the site of viral DNA integration.

Biography

Luigi Santacroce is working in the Dept. of Medical Basic Sciences in Neuroscience and Sensory Organs, Policlinico Hospital, University of Bari, Italy and is currently researching on neurologic disorders, cancer, and obesity. He is author/co-author of more than 20 papers in reputed journals.

luigi.santacroce@uniba.it

Notes:

Igor Jeremic, Virol Mycol 2017, 6:1(Suppl)
http://dx.doi.org/10.4172/2161-0517.C1.017

New therapeutic method and treatment for HIV and HBsAg diagnosed positive patients of both sexes with severe forms of HPV infection (genital warts) with emphasis on vaginal, anal and cervical localization

Igor Jeremic
Polyclinic Jeremic, Serbia

Problem Statement: HPV infection is the epidemic of modern times. High occurrence of HPV infection as well as genital warts is greatly influenced by a very easy way of infection transmission. It takes only one unprotected sex intercourse (without a condom) and the infection is transferred. With immune compromised patients and patients on immune suppressive therapy (chemotherapy and corticosteroids) incubation period is extremely short. It takes only 45 days for the severe clinical forms of genital warts to appear. Mixed HPV infections (70% of the low and high-risk types) coupled with weak immune system impose additional responsibility to the doctors in therapeutic approach.

Methods: The study includes 100 patients of both sexes between 15 and 50 years of age, HIV and HBsAg positive patients , patients on immune suppressive and chemo therapy, with medium and severe forms of genital warts on all parts anogenital region, with stress on the cervix, vagina, anus and intra-anal localization. Everything above represents a big therapeutic challenge because of the following facts: The sensitivity of anogenital region on forced trauma; Inaccessible area for intervention are intra-anal, vaginal or cervical warts; High vascularization-vagina-cervix-hemorrhoids' ranges. 4. Receptivity to infection - bacterial flora (vagina and colon); Weak immune status; and the risk of professional exposure.

Results: During 12 years of my work with 4 MHZ radio wave therapy, I developed my own special technique so called radio wave vaporization. Radio wave therapy is bloodless technique that protects the local immunity of patients and prevents professional exposure. My technique involves melting of genital warts on the mucous membranes of anogenital region which as a result has a completely bloodless operating field and the accuracy in complete elimination of all forms of genital warts in just one treatment. With the exception of only 20% of patients, when we are dealing with really heavy forms of infections and in Buschke Lowenstein form, it takes two interventions. The intervention is performed in local anesthesia (cream). The duration of the intervention is 5 min to 30 minutes. Patients need not be hospitalized. Thanks to the new technique and specially designed extensions the lateral damage to healthy tissue is less than 10 microns. Minimum lateral damage and minimal bleeding do not affect local immunity, which represents the therapeutic key to a quick recovery without accompanying bacterial infections that often follow with HIV infected patients, with recidive percentage below 3%.

Conclusion: My new technique and approach using 4 MHz radio wave frequencies system make it a very efficient, safe, painless and bloodless method with a maximum therapeutic and esthetic effect. It has the lowest so far known recurrence rates (below 3%) in severe forms of genital warts and with patients with poor immune status. The ease of performing intervention in local anesthesia (cream) makes it the therapy of first choice to protect doctors from a professional exposure to HIV and hepatitis. Returning to everyday life activities including sexual activity regardless of clinical severity is possible after 5 weeks of intervention.

Biography

Igor Jeremic has completed his Medical Doctor degree at the Faculty of Medicine in Belgrade in 1999 and Specialization in Obstetrics & Gynecology in 2006 with the highest grade 10 at the Medical Faculty in Belgrade. He has also completed specialization in Radio Wave Dermatosurgery in New York in 2008. In 2010, he was appointed as a Licensed Educator of radio wave surgery for Europe: Turkey and Russia in the field of gynecology and dermatosurgery by an expert team of doctors in New York. He is the Founder and the Owner of "Polyclinic Jeremic" the Educational Center of radio wave surgery for Europe.

jerigor@yahoo.com

Notes:

Sessions

Modern Virology | Agriculture and Plant Virology | Recent Advances in Viral Therapy

Session Chair
Samira Khiar
Institute Pasteur, France

Session Introduction

Title: **Therapeutic intervention of Hantavirus disease**
Mohammad Mir, Western University of Health Sciences, USA

Title: **Advances in methods used to study structure and function of viruses**
Elena V Orlova, University of London, UK

Title: **Identification of a small molecule that primes the type I interferon response to cytosolic DNA**
Samira Khiar, Institute Pasteur, France

Title: **Aspects in *Tobamovirus* management**
Aviv Dombrovsky, Agricultural Research Organization (ARO), Israel

Title: **Molecular characterization of Foot and mouth disease virus serotypes circulating in Bangladesh for the development of inactivated trivalent vaccine**
M Bahanur Rahman, Bangladesh Agricultural University, Bangladesh

Title: **Deep sequencing of RNAs from vigna mungo plants showing crinkle symptoms reveals the multiple virus infection**
Mir Asif Iquebal, ICAR-Indian Agricultural Statistics Research Institute, India

Mohammad Mir, Virol Mycol 2017, 6:1(Suppl)
http://dx.doi.org/10.4172/2161-0517.C1.017

Therapeutic intervention of Hantavirus disease

Mohammad Mir
Western University of Health Sciences, USA

Hantaviruses, members of the Bunyaviridae family cause severe illness in humans with high Mortality rates. There is no cure for Hantavirus disease at present. An evolutionarily conserved Sequence at the 5' terminus of hantaviral genomic RNA plays an important role in viral transcription initiation and packaging of the viral genome into viral nucleocapsids. Interaction of viral nucleocapsid protein (N) with this conserved sequence facilitates mRNA translation by a unique N-mediated translation strategy. Whereas this evolutionarily conserved sequence Facilitates virus replication with the assistance of N in eukaryotic hosts having multifaceted Antiviral defence, we demonstrate its interaction with N presents a novel target for therapeutic Intervention of hantavirus disease. Using a high throughput screening approach, we identified Three lead inhibitors that bind and induce structural perturbations in N. The inhibitors interrupt NRNA interaction and abrogate both viral genomic RNA synthesis and N-mediated translation strategy without affecting the canonical translation machinery of the host cell. The inhibitors are well tolerated by cells and inhibit hantavirus replication with the same potency as ribavirin, a Commercially available antiviral. We report the identification of a unique chemical scaffold that Disrupts a critical RNA-protein interaction in Hantaviruses and holds promise for the development Of the first anti-hantaviral therapeutic with broad spectrum antiviral activity.

Biography

Mohammad Mir is working As an Associate Professor-Virology, College of Veterinary Medicine in the Western University of Health Sciences, Pomona, California and I am a multidisciplinary virologist interested in molecular mechanism of virus replication and therapeutic intervention of viral diseases. I am enthusiastic to train next generation of virologists with a background in veterinary sciences at the College of veterinary medicine, Western University of Health Sciences. The veterinarians with research experiences in cutting edge virology will serve as specialized lead work force in the frontier areas of infectious disease.

mmir@westernu.edu

Notes:

Elena V Orlova, Virol Mycol 2017, 6:1(Suppl)
http://dx.doi.org/10.4172/2161-0517.C1.017

Advances in methods used to study structure and function of viruses

Elena V Orlova
University of London, UK

Viruses are biomolecular nanomachines designed to infect cell hosts with high efficiency and specificity. Therefore, they are intrinsically flexible and naturally exist in multiple conformations that can be visualized at nearly native conditions by modern structural methods, such as Cryo-electron microscopy (EM). Advances of the last decade in technology and software development led to the revelation of structural variations in complexes and improvements in a resolution of EM structures. Structural analysis based on single-particle methods suggests several approaches for the separation of conformational states and therefore disclosure of the functioning mechanisms of complexes. Revelation of the virus activity through structural analysis requires the examination of large datasets, sophisticated programs, and significant computing power. Hybrid approaches based on combination of X-ray, NMR, SAXS, and structurally driven mutagenesis are essential for understanding the function of biological complexes. We will demonstrate successful applications of these methods in structural studies of bacteriophages. Phages are viruses of bacteria; their genome is packaged in stable and rigid capsids which shield it from the extracellular environment. Our current understanding of phage function has been advanced by the emergence of a number of phage structures over the past decade. The similarity of their structural components indicates that phages have a common ancestor and share a common morphogenetic pathway. In our study we have determined structures of the bacteriophage Spp1 capsids at nearly atomic resolution. These structures have allowed us to trace an extensive network of contacts between capsid proteins and suggest a mechanism of the phage maturation.

Biography

Elena V Orlova received her BSc and MSc in Physics from Moscow Institute of Physics and Technology. She has done her PhD degree in Physics and Mathematics from the Institute of Crystallography in Moscow. After several years at the Institute of Crystallography in Moscow, she has worked in the laboratories of Professor W Chiu (USA) and Professor M van Heel (Berlin/London). Currently, she is a Professor at Birkbeck College (University of London). Her research interests are in structural analysis of biomacromolecular complexes using Cryo-electron microscopy and image processing. Her group has analyzed a range of different bio complexes: Viral Assemblies, Helicases and Secretion Systems.

e.orlova@mail.cryst.bbk.ac.uk

Notes:

Samira Khiar, Virol Mycol 2017, 6:1(Suppl)
http://dx.doi.org/10.4172/2161-0517.C1.017

Identification of a small molecule that primes the type I interferon response to cytosolic DNA

Samira Khiar
Institut Pasteur, France

The type I interferon response plays a pivotal role in host defense against infectious agents and tumors, and promising therapeutic approaches rely on small molecules designed to boost this system. To identify such compounds, we developed a high-throughput screening assay based on HEK-293 cells expressing luciferase under the control of interferon-stimulated response elements (ISRE). An original library of 10,000 synthetic compounds was screened, and we identified a series of 1H-benzimidazole-4-carboxamide compounds inducing the ISRE promoter sequence, specific cellular Interferon-Stimulated Genes (ISGs), and the phosphorylation of Interferon Regulatory Factor (IRF) 3. ISRE induction by ChX710, a prototypical member of this chemical series, was dependent on the adaptor MAVS and IRF1, but was IRF3 independent. Although it was unable to trigger type I IFN secretion per se, ChX710 efficiently primed cellular response to transfected plasmid DNA as assessed by potent synergistic effects on IFN- secretion and ISG expression levels. This cellular response was dependent on STING, a key adaptor involved in the sensing of cytosolic DNA and immune activation by various pathogens, stress signals and tumorigenesis. Our results demonstrate that cellular response to cytosolic DNA can be boosted with a small molecule, and potential applications in antimicrobial and cancer therapies are discussed.

Biography

Samira Khiar is working in the Viral Genomics and Vaccination Unit Institut Pasteur de Paris , France and is currently researching on against infectious agents and tumors she is author/co-author of more than 20 papers in reputed journals.

samira.khiar@pasteur.fr

Notes:

Aviv Dombrovsky, Virol Mycol 2017, 6:1(Suppl)
http://dx.doi.org/10.4172/2161-0517.C1.017

Aspects in *Tobamovirus* management

Aviv Dombrovsky
Agricultural Research Organization (ARO), Israel

In the recent decade, a new outbreak of old and new *Tobamovirus* occurred worldwide. The disease caused by the cucumber green mottle mosaic virus (CGMMV) in cucurbits melon watermelon and cucumber was reported in Israel, North-Europe, Canada, USA, Australia and the Far-east. Recently, the *Tobamovirus* tomato mottle mosaic virus (ToMMV) was discovered in tomato grown in Central America. In the Middle East; in Jordan and Israel, a new *Tobamovirus* isolate infects tomato plants harboring Tm-22 resistance genes putatively named tomato brown rugose fruit virus (TBRFV). The epidemiology and strategies for the *Tobamovirus* management were studied and developed in our national initiative project for CGMMV coordinated by our lab. Growers in large-scale fields adopted the outcome of this extensive study. The experience with CGMMV management was rapidly applied also for the new *Tobamovirus* disease management in tomatoes grown trellised in protected structures (greenhouses, walk-in tunnels, etc.).

Biography

Aviv Dombrovsky has completed his PhD from Hebrew University of Jerusalem, Faculty of Agriculture, Food and Environmental Quality Sciences, Rehovot, Israel and Post-doctoral studies from INRA/CNRS Sophia Antipolis-Agrobiotech, France. He is a Plant Virologist Researcher in the Department of Plant Pathology and Weed Science Agricultural Research Organization (ARO)- Volcani Center. He is the Scientific Manager of Central and North Arava Research and Development Center, Israel. He has published more than 30 papers in reputed journals and has been serving as an Editorial Board Member of *Phytoparasitica Journal*.

aviv@volcani.agri.gov.il

Notes:

M Bahanur Rahman, Virol Mycol 2017, 6:1(Suppl)
http://dx.doi.org/10.4172/2161-0517.C1.017

Molecular characterization of foot and mouth disease virus serotypes circulating in Bangladesh for the development of inactivated trivalent vaccine

M Bahanur Rahman
Bangladesh Agricultural University, Bangladesh

Total 15 samples were collected from cattle infected with FMD, of which 85 (56.29%) was adapted in BHK-21 cell. Viral RNA was extracted from virus infected BH-21 cell culture fluid using RNA extraction kit (Promega®, USA) and used for amplification of *VP1* gene with specific primers by RT-PCR for FMD virus serotyping, of which, 31 (43.67%), 26 (36.62%), 10 (14.08%) were positive for serotype A, O, Asia 1, respectively and 4 (5.63%) for mixed. Partial sequencing of *VP1* gene was performed two from each serotypes and comparison conducted using the BLAST search and 92-99%, 92-100% and 96-98% homology were found with some FMD virus serotypes O, A and Asia-1 isolates of Bangladesh, India, Pakistan, Nepal and Bhutan, respectively. Isolates of this study belonged to PanAsia-02 sub-lineage of ME-SA topotype (serotype O), genotype VII (18) of ASIA topotype (serotype A) and Lineage C (serotype Asia-1), respectively. BAU FMD Vac-1 and -2 developed from isolated FMD virus and antibody titers were determined in sero-negative calves by ELISA and SNT and compared with commercially available FMD vaccines. Vaccines were administered in single and booster dose order; of which BAU FMD Vac-1 produced better immune response than other vaccines including BAU FMD Vac-2. Highest antibody titers were found in all vaccines at 60 dpv, and after 60 dpv the antibody titers gradually decline. Protective immunity persists up to 5 months (single dose) and 6 months (booster dose) in case of BAU FMD Vac-1. On the other hand in case of with BAU FMD Vac-2, Raksha® and Aftovaxpur® protective immunity persisted only 4 months (single dose) and 5 months (booster dose). Efficacy test of BAU FMD Vac-1 and 2 vaccines were carried out in guinea pigs and found 100% potent against FMD virus serotypes O, A and Asia-1.

Biography

M Bahanur Rahman has completed his PhD from Kyoto University, Japan and Post-doctoral studies from Changing University, Molecular Genetics Laboratory, Department of Microbiology and Immunology, Taiwan and Proteomics Lab of Max Planck Institute for Developmental Biology, Tübingen, Germany. He is a Professor of Microbiology, Department of Microbiology and Hygiene, Bangladesh Agricultural University, Mymensingh, Bangladesh. He is also working as a Senior Regional Vaccine Consultant, Department of Livestock Services (DLS), Government of Bangladesh. He has published more than 65 papers in reputed journals and has been serving as an Editorial Board Member of *Bangladesh Journal of Microbiology, Microbes and Health and Journal of Environmental Science and Natural Resources*.

bahanurr@gmail.com

Notes:

Mir Asif Iquebal, Virol Mycol 2017, 6:1(Suppl)
http://dx.doi.org/10.4172/2161-0517.C1.017

Deep sequencing of RNAs from *vigna mungo* plants showing crinkle symptoms reveals the multiple virus infection

Mir Asif Iquebal
ICAR-Indian Agricultural Statistics Research Institute, India

Blackgram (*Vigna mungo*) is one of the important pulse crops grown in Indian sub-continent. It is also known as urdbean. The symptoms of crinkle disease include enlargement, puckering and crinkling of leaves. The disease is known from decades and has been reported to be transmitted by mechanical as well by many types of insects. Though in the literature, there are evidences that this disease is caused by a virus and named as Urdbean leaf crinkle virus (ULCV), however, still the genome of the virus has not been characterized. The present study was aimed to find out the virus (es) involved in crinkle disease of urdbean. Four urdbean samples showing crinkle disease were collected from field and they were sap inoculated separately on urbean plants. The RNA from field infected (n=4), sap inoculated (n=4) and healthy samples (n=1) extracted and were used to prepare three libraries (1-Pooled RNA from field infected samples, 2-Pooled RNA from sap inoculated samples and 3-RNA from healthy sample) for next generation sequencing (NGS). After removing reads pertaining to plant sample, assembly and mapping was done. We found 1161 contigs from sap inoculated sample and 1865 contigs from field infected sample. Cap3 was used to assemble the small contigs into complete sequence. Genome Annotation Transfer Utility (GATU) was used for annotation of viral genomes by using a closely related genome as a reference. Most of the sequences were obtained from Retrovirus-related Pol poly from transposon followed by Cowpea mild mottle virus (CpMMV), Tobamovirus multiplication, Mungbean yellow mosaic India virus (MYMIV) and Peanut bud necrosis virus (PBNV). Three viruses (CpMMV, MYMIV and PBNV) has already been reported infecting many legume crops including urdbean, however, the sequences of retrovirus-related Pol poly transposon and Tobamovirus multiplication are being reported for the first time. There role in urdbean crinkle disease needs to be investigated.

Biography

Mir Asif Iquebal has completed his PhD at the age of 28 years from ICAR-Indian Agricultural Research Institute, New Delhi. Trained on Computational Biology at Iowa State University, Ames, USA. Currently, he is working as Scientist (Senior Scale) at ICAR-Indian Agricultural Statistics Research Institute, New Delhi, a premier agricultural research organization. He has published more than 40 research papers in reputed National and International journals.

ma.iquebal@icar.gov.in

Notes:

conferenceseries.com
896th Conference

9th International

Virology Congress and Expo

March 13-14, 2017 London, UK

Scientific Tracks & Abstracts

Day 2

Clinical and Diagnostic Virology | Virology and AIDS | Plant Virology | Viral Hepatitis

Session Chair
Anil Kumar
University of Missouri, USA

Session Introduction

Title: **Cofilin is a clinical marker of HIV-mediated CD4 T cell dysfunction**
Yuntao Wu, George Mason University, USA

Title: **HIV-1 gp120 and Methamphetamine-Mediated toxicity in the brain**
Anil Kumar, University of Missouri, USA

Title: **The opposing faces of interferons**
Catherine H Schein, University of Texas, USA

Title: **LSDV100 and LSDV101 lumpy skin disease virus-specific PCR and real-time PCR for rapid diagnosis and vaccine quality control**
Ausama A Yousif, Cairo University, Egypt

Title: **Serological detection and genetic characterization of *Pepino mosaic virus* in Moroccan tomatoes**
Amal Souiri, University of Hassan II Casablanca, Morocco

Title: **The role of cellular lipid droplets in rotavirus replication: Compounds disturbing lipid droplet homeostasis decrease rotavirus replication**
Ulrich Desselberger, University of Cambridge, UK

Title: **Emerging and re-emerging diseases: African swine fever in Ukraine**
Oksana F Blotska, University of Ukraine, Ukraine

Title: **Study on the noninvasive markers of liver fibrosis and inflammation in chronic hepatitis B patients**
Weifeng Liang, Zhejiang University, China

Yuntao Wu, Virol Mycol 2017, 6:1(Suppl)
http://dx.doi.org/10.4172/2161-0517.C1.017

Cofilin is a clinical marker of HIV-mediated CD4 T cell dysfunction

Yuntao Wu
George Mason University, USA

HIV infection leads to the gradual depletion of blood CD4 T cells. It has long been recognized that the residual peripheral blood CD4 T cells in HIV-infected patients have numerous functional abnormalities such as loss of T helper function, T cell anergy, abnormal T cell homing and migration. Given the low number of infected T cells found in the peripheral blood, these T cell defects largely result from a bystander effect. It is possible that chronic immune activation, persistent exposure to viral proteins, or abortive infections may trigger persistent signals in CD4 T cells, pushing them towards dysfunctioning. Nevertheless, a molecular marker clinically representing HIV-mediated T cell dysfunction is lacking. Cofilin is an actin-depolymerizing factor that regulating actin dynamics for T cell migration and activation. Previously, we demonstrated that during HIV-1 infection of blood resting CD4 T cells, the viral envelope protein triggers CXCR4 signaling to activate cofilin to overcome the static cortical actin restriction in resting CD4 T cells. We have also speculated that in HIV-infected patients, cofilin activity could be abnormally altered by gp120-CXCR4/CCR5 signaling. To test this hypothesis, we conducted a clinical trial to example the cofilin status in blood resting CD4 T cells of HIV-infected MSM cohort in the AIDS Clinical Center of China Medical University. Cell lysates from un-stimulated blood resting CD4 T cells were prepared and analyzed by a reverse phase phospho-cofilin microarray (performed by Theranostics Health Inc. Rockville, MD). We found that there is a significant difference in cofilin phosphorylation between infected and healthy controls. HIV-infected patients carry significantly higher levels of active cofilin (dephosphorylated). Surprisingly, ART treatment did not restore cofilin phosphorylation to the healthy control level. These results demonstrate that cofilin could serve as a new clinical marker to quantify HIV-mediated T cell dysfunction; complementary therapies additional to ART may also be required to restore cofilin phosphorylation to a healthy level.

Biography

Yuntao Wu has completed his PhD from Queen's University at Kingston, Ontario, Canada, and Post-doctoral studies from the National Institute of Health, Bethesda, Maryland, USA. He is a Professor at the National Center for Biodefense and Infectious Diseases, George Mason University, Virginia, USA. He has published more than 50 papers in reputed journals (*Cell, Science, PLos Patho, J. Virol, Virology, J. Bio. Chem*), and has been serving as an Editorial Board Member of a number of virology journals.

ywu8@gmu.edu

Notes:

Anil Kumar, Virol Mycol 2017, 6:1(Suppl)
http://dx.doi.org/10.4172/2161-0517.C1.017

HIV-1 gp120 and Methamphetamine-Mediated toxicity in the brain

Anil Kumar
University of Missouri, USA

HIV associated neurocognitive disorder (HAND) remains a major concern for patients infected with HIV. The viral envelope protein, gp120 has been extensively studied and some of its neurotoxic effects are due to the increased expression of various proinflammatory cytokines. Additionally, it has been well documented that various drugs of abuse can exacerbate HAND, but the mechanism by which this occurs is still poorly understood. The present study was based on the central hypothesis that HIV-1 gp120 and methamphetamine (MA) interact with each other to increase the cytotoxicity in the astrocytes, which is mediated via induction of various pro-inflammatory cytokines/chemokines and oxidative stress. In order to test these hypothesis four different studies were designed. We also investigated the mechanism(s) and pathways involved in the functional interaction between gp120 and MA. Furthermore, in order to understand the functional implications of the interaction between MA and gp120, we examined the combined effect of MA and gp120 to produce oxidative stress and apoptotic cell death. We also studies the involvement of ER stress in the HIV-1 gp120-mediated cell death in the astrocytes. We investigated the role of gp120 in the cytokine production in astrocytes. SVGA astrocytes and human fetal astrocytes were either transfected with a plasmid coding gp120 or treated with recombinant gp120 protein and the expression levels of various cytokines at RNA and protein levels were measured. In order to better explain the role of gp120 in the induction of proinflammatory cytokines/chemokines, 3 major and highly induced cytokines/chemokines were screened and further mechanistic studies were aimed with these 3 cytokines/chemokines. We investigated the role of NF- κB pathway in the transcriptional regulation followed by studies to identify molecular mechanisms.

In conclusion, we have shown that both MA and gp120 independently and in combination increased the production of pro-inflammatory cytokine/chemokines via different pathways. The functional consequences for the interaction between gp120 and MA led to oxidative stress and ER stress, which resulted in apoptotic cell death in astrocytes. Thus, our current studies provide the evidence and underlying mechanisms for the neurotoxic potential of HIV protein, gp120 and substance of abuse, methamphetamine.

Biography

Anil Kumar completed his education in Kanpur University, Kanpur, India, 1987. He is currently working as an Chair and Professor, University of Missouri-Kansas City School of Pharmacy Division of Pharmacology. He is current Research Interests on Effect of drug and alcohol abuse on pathogenesis of AIDS, Identification of target of immune responses in HIV-1 during natural infection, Compartmentalization of HIV during natural infection, Vaccine approaches in monkey model of AIDS.

kumaran@umkc.edu

Notes:

Catherine H Schein, Virol Mycol 2017, 6:1(Suppl)
http://dx.doi.org/10.4172/2161-0517.C1.017

The opposing faces of interferon

Catherine H Schein
University of Texas, USA

Interferon (IFN) were among the first cytokines to be produced recombinant, and the first antiviral proteins to be marketed. Since initial cloning in the late 1970ies, many types of IFNs and a host of cellular proteins induced by IFNs have been identified that are important in attacking viruses directly (e.g., through nuclease induction) or indirectly, through affecting cellular proteins that are required for their replication. The most pathogenic viruses (for example, Ebola) have developed mechanisms to directly interfere with these pathways, which limits the use of IFN as a direct treatment. However, mediators capable of upregulating later steps in IFN-controlled pathways may provide novel therapies to evade these pathogen induced, intracellular blockades.

The antiviral activity of IFN is "hit and run" in nature. Typically, IFN concentrations rise rapidly in the first days after infection, and then drop to undetectable levels as antibody-based responses deal with circulating virus. There is mounting evidence that this decrease in IFN levels is essential. Chronically high levels of IFN, used in treating Hepatitis C infection or diseases without clear viral etiology, such as multiple sclerosis can cause side effects. High circulating concentrations of IFN and IFN-induced proteins are found in diseases characterized by systemic inflammation, including lupus erythematosus and rheumatoid arthritis. Thus a new group of anti-IFN therapeutics is now in testing, to control immune responses to these important biological response factors.

Biography

Catherine H Schein developed the first industrial scale methods for producing recombinant interferons and related cytokines at Biogen SA. After transitioning to academia, her research group explored the differences in control of nuclease function mediated by type 1 and 2 IFNs and how this related to their different structures. Her current research at FfAME, an institute that specializes in polymerase design, novel nucleotides and viral diagnostics, uses viral sequence data to define pathogenic signatures that direct host and organ targeting, physicochemical property consensus sequences for multivalent vaccine design and identifying inhibitors of enterovirus replication.

chschein@ffame.org

Notes:

Ausama A Yousif, Virol Mycol 2017, 6:1(Suppl)
http://dx.doi.org/10.4172/2161-0517.C1.017

LSDV100 and LSDV101 lumpy skin disease virus-specific PCR and real-time PCR for rapid diagnosis and vaccine quality control

Ausama A Yousif
Cairo University, Egypt

Capripoxviruses are genetically and antigenically similar. Sheeppox virus (SPPV) and goatpox virus (GPV) cause diseases in ovines and caprines, respectively. Lumpy skin disease virus (LSDV) causes lumpy skin disease (LSD) in cattle. LSD is endemic in Africa and the Middle East, and was recentrly introduced into Europe and Russia . Live attenuated SPPV is used as a vaccine in endemic areas. Cattle vaccinated using SPPV can develop LSD due to induction of partial protection, or as a result of vaccine seed contamination with non-highly-attenuated LSDV. LSD control and vaccine production can be enhanced by differentiation between LSDV and SPPV using a highly specific, simple, rapid, and inexpensive PCR assay. In this study, primers were designed to specifically amplify conserved LSDV sequences spanning parts of LSDV100, and LSDV101 genes. The design allowed the amplification of a 503 bp PCR product that was used for diagnosis. An alternative reverse primer allowed the amplification of a LSDV-specific 1583 bp PCR product for sequencing. The diagnostic assay detection limit was 585 genome-copy-equivalents of LSDV/5 ul of extract. A real-time assay was 10 times more sensitive. LSDV DNA was detected in skin samples collected from 1988 to 2015. Amplification of LSDV sequences was not affected by lesion size and distribution (localized or generalized) on infected animals. Application of the developed assay for the quality control of local LSD vaccines resulted in the detection of LSDV contamination of a local SPPV vaccine. The incorporation of the developed assay in LSD control programs was recommended.

Biography

Ausama A Yousif graduated at the Faculty of Veterinary Medicine, Cairo University. He was awarded his PhD in 2002 at South Dakota State University. He published several papers on developing diagnostic reagents and vaccines for the control of emerging transboundary pathogens like lumpy skin disease virus. He was first to isolate a pestivirus from camels. Professor Yousif also worked with the industry on several aspects of the production and quality control of several vaccines, including Rift Valley fever virus, foot and mouth disease virus, and camelpox virus vaccines. His current research focus is on improving vaccines and vaccine-based control programs.

ausama_yousif@cu.edu.eg

Notes:

Amal Souiri, Virol Mycol 2017, 6:1(Suppl)
http://dx.doi.org/10.4172/2161-0517.C1.017

Serological detection and genetic characterization of *Pepino mosaic virus* in Moroccan tomatoes

Amal Souiri
University of Hassan II Casablanca, Morocco

Pepino mosaic virus (PepMV) has become an emerging pathogen that causes significant losses in tomato crops worldwide. Several interception reports of PepMV on Moroccan tomato fruit have been stated, but the current situation of the disease is unlikely and the molecular characterization of PepMV population in Morocco has not been determined yet. A primary aim of this work was to develop a monoclonal antibody-based double antibody sandwich ELISA (DAS-ELISA) with sufficient sensitivity and specificity to detect PepMV in tomato. Another aim was to determine the genetic composition of Moroccon PepMV population. For this purpose, first we generated hybridoma cell lines secreting PepMV-specific Mab. Besides, the genomic nucleotide sequences of a part of RNA-dependent RNA polymerase (RdRp), triple gene block (TGB) and coat protein (CP) were determined. As results, the developed DAS-ELISA test was able to detect PepMV with a suitable sensitivity. Furthermore, the phylogenic relationship among isolates and the known genotypes showed that the Moroccan population shares a very high sequence identity with CH2 strains. As well, Moroccan isolates reveal some specific single nucleotide polymorphisms that lead to distinct variants. Thus, this study will contribute to a timely and rapid detection of PepMV and the genotype determination would be a prerequisite for prevention and deploying effective strategies in disease management.

Biography

Amal Souiri is a PhD student from the Faculty of Science, University Mohammed V, Rabat, Morocco. She's a young researcher on virology, molecular biology and cell culture. She has contributed in the development of monoclonal antibodies against *Pepino mosaic virus* infecting tomato crops in Morocco and the genetic characterization of Moroccan PepMV strains. She published several papers in reputed journals and communicated its studies in many international congresses. Also, she participated in the previous edition of Eurovirology organized by OMICS international.

amal.souiri@hotmail.com

Notes:

Ulrich Desselberger, Virol Mycol 2017, 6:1(Suppl)
http://dx.doi.org/10.4172/2161-0517.C1.017

The role of cellular lipid droplets in rotavirus replication: Compounds disturbing lipid droplet homeostasis decrease rotavirus replication

Ulrich Desselberger
University of Cambridge, UK

Rotaviruses (RVs) are a major cause of severe gastroenteritis in infants and young children worldwide. Rotavirus-associated disease is associated with a mortality of >200,000 children/annum. Rotavirus vaccines licensed since 2006 have significantly decreased RV-associated disease and mortality, however with variable efficacy. The molecular biology of RV replication is well studied. Recently, the interaction of viroplasms (cytoplasmic inclusion bodies in which RV RNA replication and early morphogenesis take place) with the cellular organelles lipid droplets (LDs) has been discovered. Viroplasms recruit LDs early during viral replication. Compounds disturbing LD homeostasis (in non-toxic concentrations), such as inhibitors of fatty acid biosynthesis (TOFA, C75 and Triacsin C) or compounds eliciting lipolysis (isoproterenol+IBMX), inhibit RV replication by 4-6-fold (viral RNA replication) and 20-50-fold (infectivity of viral progeny). Compounds disturbing LD homeostasis may have the potential to become antivirals.

Biography

Ulrich Desselberger is the Professor in the Department of Medicine, University of Cambridge, UK. He is having above 100 publications in peer review journals.

ud207@medschl.cam.ac.uk

Notes:

Oksana F Blotska, Virol Mycol 2017, 6:1(Suppl)
http://dx.doi.org/10.4172/2161-0517.C1.017

Emerging and re-emerging diseases: African swine fever in Ukraine

Oksana F Blotska
University of Ukraine, Ukraine

In accordance with OIE classification, African swine fever (ASF) is attributed to especially dangerous diseases. ASF is caused by highly pathogenic DNA virus, which provokes severe economic losses and expansion threats. No specific protection or vaccine against ASF is available. Currently, 22 genotypes of African swine fever virus (ASFV) were registered. The first case of ASF in Ukraine was registered in 1977 year in Odeska region, where all pig population was destroyed not only in the outbreak of the disease, but also in the 30-kilometer zone. Later in 2012, it was next case in domestic swine in the Zaporozhye region. Ukraine reacted in time to detect the disease, and the virus did not spread. But unfortunately in 2014 year 16 cases of ASF: 12 incidents in wild boars and 4 cases in domestic pigs were fixed. Since the beginning of 2015 in Ukraine, detected 39 points disadvantaged in relation to ASF: 5 incidents in wild boars and 34 cases in domestic pigs. In 2016, 5 cases of ASF: 2 incidents in wild boars and 3 cases in domestic pigs was revealed. The situation with regard to wild and domestic pigs changed in 2015-2016. Sequencing of three independent areas of the genome of ASFV, that were discovered in Ukraine showed, that the isolates was 100% homologous with isolates that caused the outbreaks in Eastern Europe, starting with the entry of the virus in Georgia in 2007. That made it possible to include the virus strain that caused the disease of ASF in Ukraine to genotype II. Course of the disease of ASF at pigs in Ukraine is the incubation period duration of 2-6 days. For II genotype of ASF as a rule only acute form for 3-7 days. Scientists of our institute developed, tested and registered, in the established order, the test kit for the diagnosis of ASF for molecular genetic techniques. However, ASF problem is that it's not just a question of the security of Ukraine, but also the European Union as a whole. These things should be done in our opinion on the national and international level in order to control the situation regarding to ASF: Acquire the most new knowledge by monitoring the spread of the ASF in the world; carry out risk analysis; expand bank of diagnostic material; and control the number of wild boars per 1 sq.km.

Biography

Oksana F Blotska, DVM has completed her PhD at the age of 34 years from Institute of Veterinary Medicine, Kyiv, Ukraine. She is Head of the Division of Check and Industrial Virus Strains Support of the Department of Biotechnology and Control of Quality of Viral Preparations of The State Science-Control Institute of Biotechnology and Strains of Microorganisms. She has published more than 30 papers in reputed journals.

blotskaya@ua.fm

Notes:

Weifeng Liang, Virol Mycol 2017, 6:1(Suppl)
http://dx.doi.org/10.4172/2161-0517.C1.017

Study on the noninvasive markers of liver fibrosis and inflammation in chronic hepatitis B patients

Weifeng Liang
Zhejiang University, China

Liver biopsy is the gold standard in assessing histological abnormalities of the liver. The widely accepted indicator for antiviral therapy for chronic hepatitis B (CHB) in China is that the serum alanine aminotransferase (ALT) is more than two times the upper limit of normal (ULN). Although the role of ALT as an effective predictor of liver inflammation has been not definitively proven. It needs more effective non-invasive markers for assessing liver inflammation and fibrosis. We retrospectively evaluated non-invasive markers of treatment-naïve CHB patients who had done liver biopsy from October 2010 to October 2015. And our aim is to investigate the characteristics of histological abnormalities and find effective indicators to assess liver inflammation and fibrosis. Significant liver abnormality was defined as necroinflammation grade ≥A2 and/or fibrosis stage≥F2. A total of 522 CHB patients were recruited, 268 had normal ALT, 164 had 1-2×ULN ALT and 90 had ALT more than 2×ULN. Serious inflammation and fibrosis could be found in the patients with ALT that less than twice ULN. There are significant differences in age, platelet count (PLT), ALT, aspirate aminotransferase (AST), aspartate aminotransferase and alanine aminotransferase ratio (AAR), aspartate aminotransferase to platelet ratio index (APRI), and fibrosis index based on the 4 factor (FIB-4) between patients with mild and serious necroinflammation , and AST was the independent risk factor in predicting serious necroinflammation. The cut-off value of serious necroinflammation for AST was 29.5 U/L. The differences of age, older than 40 or not, PLT, ALT, AST, APRI, FIB-4 and HBV-DNA were statistically significant, and PLT was an independent factor in assessing the fibrosis stage.A high proportion of CHB patients with normal and 1-2×ULN ALT have serious liver histological abnormalities. AST could be an effective non-invasive marker for liver inflammation for treatment-naïve CHB patients and there is serious liver inflammation in CHB patients with AST more than 29.5U/L.

Biography

Weifeng Liang has completed his PhD in 1997 from Zhejiang University, China. He is the doctoral tutor, professor of Zhejiang University. He is the deputy director of both State Key Laboratory for Diagnosis and Treatment of Infectious Diseases and Collaborative Innovation Center for Diagnosis and Treatment of Infectious Diseases of China. He is the director of Shengzhou Branch of The First Affiliated Hospital of Zhejiang University as well. He has published more than 70 papers in reputed journals and has been serving as an editorial board member of repute. He made outstanding contributions to the prevention and treatment of infectious diseases, especially viral hepatitis and AIDS.

wibahiba@live.fr

Notes: