Virology 566 (2022) 114–121

Contents lists available at ScienceDirect

Virology

journal homepage: www.elsevier.com/locate/virology

World Society for Virology first international conference: Tackling global virus epidemics

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ARTICLE INFO

Keywords:
Conference report
Meeting report
Tackling global viral epidemics
WSV
World Society for Virology

ABSTRACT

This communication summarizes the presentations given at the 1st international conference of the World Society for Virology (WSV) held virtually during 16–18 June 2021, under the theme of tackling global viral epidemics. The purpose of this biennial meeting is to foster international collaborations and address important viral epidemics in different hosts. The first day included two sessions exclusively on SARS-CoV-2 and COVID-19. The other two days included one plenary and three parallel sessions each. Last not least, 16 sessions covered 140 on-demand submitted talks. In total, 270 scientists from 49 countries attended the meeting, including 40 invited keynote speakers.

Abbreviations: WSV, World Society for Virology.

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https://doi.org/10.1016/j.virol.2021.11.009
Received 24 September 2021; Received in revised form 18 November 2021; Accepted 26 November 2021
Available online 6 December 2021
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1. World Society for Virology

The World Society for Virology (WSV) is a non-profit organization established in 2017 to connect virologists around the world without restrictions, boundaries, or membership fees to build a network of experts across low-, middle- and high-income countries (Abdel-Moneim et al., 2017). By fostering cross-sectional collaboration between experts who study viruses of humans, animals, plants and other organisms as well as leaders in the public health and private sectors, the WSV strongly supports the One Health initiative. The WSV is a steadily growing society with a current membership of more than 1500 from 86 countries across all continents. Members include virologists at all career stages including leaders in their field as well as early career researchers and postgraduate students interested in virology. The WSV has established partnerships with The International Vaccine Institute, the Elsevier journal Virology (the official journal of the WSV) and an increasing number of other scientific organizations including national virology societies in China, Colombia, Finland, India, Mexico, Morocco and Sweden (Abdel-Moneim et al., 2017, 2020).

2. General information about the conference

The first global conference of WSV: *Tackling Global Viral Epidemics* was organized in virtual mode on June 16–18. 2021, due to COVID-19 travel restrictions. The meeting was introduced with talks by Maria Söderlund-Venermo, WSV-Vice President and Head of the Scientific Organizing Committee from University of Helsinki, Finland (Söderlund-Venermo, 2021), Ahmed S. Abdel-Moneim, WSV founding President, Taif University, Al-Taif, Saudi Arabia and Beni-Suef University, Beni-Suef, Egypt (Abdel-Moneim, 2021), Richard Kuhn, WSV-President Elect, Purdue University, West Lafayette, Indiana, USA (Kuhn, 2021), and Anupam Varma, WSV-President, the Advanced Centre for Plant Virology at the Indian Agricultural Research Institute, New Delhi, India (Varma, 2021a). The cost of participation was kept comparatively low so scientists from low-income countries could participate. The fact that we had to take into account a global audience and speakers from around the world was challenging due to the dramatically different time zones.

We were proud and happy that altogether 40 distinguished Keynote speakers, who are all top experts in their fields, covered areas of global interest to virology (Table 1). We were further pleased to receive over 140 exciting abstract submissions, which were divided into 16 sessions of 1–2 h, under 5 themes: SARS-CoV-2, Human, Zoonotic, Animal and Plant viruses. Unfortunately, these submitted talks were too many to fit into the live 4-h window, so they were kept as pre-recorded on-demand talks. However, questions for authors could be submitted through our platform Q&A panel. Because of the multitude of talks in only three days of conference, we decided to record all sessions to allow viewing for one month. An Abstract book is available online (WSV2021-Abstracts, 2021).

3. Plenary keynote sessions

3.1. Plenary I | SARS-CoV-2: evolution and control

The first plenary keynote session, chaired by Zhengli Shi, Wuhan University, Wuhan, China, and Deyin Guo, Sun Yat-sen University, Guangzhou, China, comprised lectures on the evolution, epidemiology, vaccine development, and challenges for the effective management of the COVID-19 pandemic:

Zhengli Shi, Wuhan University, China, presented the wide diversity of coronaviruses (CoV), and that both SARS-CoV and SARS-CoV-2 originated from bat coronaviruses and use the same receptor, angiotensin converting enzyme (ACE2), for cell entry. Some SARS-related-CoVs (SARSr-CoVs) in wildlife have acquired the capability to deploy the human ACE2 with different efficiency necessitating the need for

Table 1
Titles of keynote talks in different plenary and parallel sessions.

Plenary session 1: SARS-CoV-2: evolution and control	Plenary session 2: COVID-19: pathogenesis and immune responses
1. Zhengli Shi: From SARS-CoV to SARS-CoV-2, understanding of interspecies infection of bat coronaviruses. 2. Marion Koopmans: Searching for the origins of SARS-CoV-2. 3. Neil M Ferguson: How vaccines and variants are shaping epidemiology and policy in the COVID-19 pandemic. 4. Jerome Kim: COVID-19 vaccines: Taking a shot beyond efficacy.	1. Stanley Perlman: Animal models of COVID-19 and immune responses 2. Bart Haagmans: Pathogenesis of SARS-CoV-2. 3. Kari Nadeau: Reactive immune responses to COVID and its vaccines. 4. Emilia Liana Falcone: The post-COVID-19 condition: from clinical evaluation to pathophysiology through the researcher's lens.
Plenary session 3: From small to giant through the ages	**Plenary session 4: One Health, One World**
1. Vincent Racaniello: Enteroviruses and childhood. 2. Chantal Abergel: The concept of virus in the giant virus era. 3. Edward Holmes: The RNA virosphere: From ecosystems to emergence. 4. Murilo Zerbini: Contagium vivum fluidum: Virus taxonomy from the origins of virology until the 21st century.	1. Curtis Suttle: Unveiling the virosphere. 2. Andrea Marzi: Fighting the beast – a vaccine against Ebola virus. 3. Linda Saif: COVID-19 and global emerging coronaviruses of humans and animals. 4. Robert Gallo: HIV: Yesterday, Today and Tomorrow.
Parallel sessions	
Avian and aquatic viruses	**Animal viruses**
1. Kanta Subbarao: Interspecies transmission of avian influenza viruses. 2. Khatijah Yusoff: Repurposing engineered Newcastle disease virus in modern vaccinology. 3. Egbert Mundt: Infectious Bursal Disease Virus: Deep understanding of viral molecular biology supports controlling the disease. 4. Øystein Evensen: Fish viral vaccines for global aquaculture.	1. Anne Balkema-Buschmann: Bats as reservoirs for henipaviruses. 2. Marietjie Venter: One Health investigations of West Nile virus lineage 2 in South Africa. 3. Teresa de los Santos: FMDV modulation of the host immune response. 4. Covadonga Alonso: Insights in viral uncoating and fusion.
Plant viruses	**Clinical virology**
1. Neena Mitter: RNAi in a drum: Can it work for viruses? 2. Kristiina Mäkinen: A viral ribonucleoprotein complex guards potato virus A RNA genome all the way from replication to stable particle formation. 3. Hanu Pappu: Continued threat of tospoviruses: New insights into virus-host interactions and RNAi strategies. 4. James Van Etten: Chloroviruses have a sweet tooth.	1. Heikki Hyöty: Enteroviruses and diabetes. 2. Fabien Zoulim: The path towards a cure of chronic HBV infection. 3. Jean Rommelaere: Tumor suppression by oncolytic parvoviruses: from bench to bedside and back. 4. Stephanie Karst: Host and microbial regulation of norovirus pathogenesis.
New winds in virus diagnostics	**Phage and insect viruses**
1. Klaus Hedman: FRET-POC – a revolutionary immunodiagnostic concept. 2. Evgeny Nikolaev: Identification of the SARS-CoV-2 virus by mass spectrometry. 3. Christina Wege: Plant virus-based nanotools: Novel functionality and shapes for biosensing. 4. Cameron Myhrvold: Massively multiplexed CRISPR-based viral diagnostics.	1. Karyn Johnson: Antiviral defences in insects: The impact of miRNA. 2. Myléne Ogliastro: Densoviruses for insect biocontrol: something old, something new. 3. Sylvain Moineau:The ongoing battle between phages and CRISPR-Cas systems. 4. Mzia Kutateladze: Phage Therapy: Experience and Perspectives.

long-term surveillance for emerging human-infecting CoVs with risk of potential interspecies transmission. Long-term surveillance is needed to prevent emerging infectious diseases caused by this group of viruses (Stenseth et al., 2021).

Marion Koopmans, Erasmus Medical Centre, The Netherlands, presented interesting data about the first phase of the pandemic in Wuhan. Bat-human or bat-pangolin-human transmissions are the most likely scenarios of virus spillover to humans. From May 2017 to Nov 2019, prior to the discovery of SARS-CoV-2, 38 wild animal species (pangolin not included) were found in Wuhan live markets. Later on, these animals were found to pose potential risk of susceptibility to infection with SARS-CoV-2. Large-scale serological survey of virus circulation in China, Italy, and Spain, as well as in fur animal farms in Asia and bats in the neighboring countries of China are required (Koopmans et al., 2021; Oude Munnink et al., 2021).

Neil M Ferguson, Imperial College London, UK, highlighted the influence of vaccines and variants on epidemics and policies. The Alpha variant (B.1.1.7) accounted for 2/3 of COVID deaths in UK with 40–80% increase of transmissibility from the wild type. The Delta variant (B.1.617.2) was 40–80% more transmissible than the Alpha variant. The COVID-19 vaccination program of the UK has been highly successful but not perfect. The vaccine efficacy was 50.2% and 33.2% following the first vaccine dose but increased following the second dose to 88.4% and 80.8% against Alpha and Delta, respectively (Mishra et al., 2021; Volz et al., 2021).

Jerome Kim, International Vaccine Institute, Seoul, South Korea, presented a critical overview on vaccines and the significance of their efficacy. There is a challenge between the proof of efficacy and impact as well as the successful mitigation of the burden of COVID-19 disease globally. To achieve 70% global coverage, the world needs 10–14 billion doses of COVID-19 vaccines. Accordingly, logistics and human capacity to ship, store, and administer COVID-19 vaccines need to be strengthened globally. A multivalent variant vaccine with optimized dose/schedule that correlates with protection and effectiveness is the current global challenge.

The message from these presentations is that we must go beyond the immediate health crisis of COVID-19 management and aim for sustainable long-term solutions (Figueroa et al., 2021; Hotez et al., 2021).

3.2. Plenary II | COVID-19: pathogenesis and immune responses

The second plenary session, chaired by Ziad Memish, College of Medicine, Alfaisal University, Saudi Arabia, and Ilkka Julkunen, Institute of Biomedicine, University of Turku, Finland, concentrated on the development of laboratory animal models, molecular pathogenesis and the immune response to SARS-CoV-2, as well as clinical evaluation and management of "long-COVID".

Stanley Perlman, University of Iowa, Iowa, USA, presented the development of mouse models for studying COVID-19 pathogenesis. Mice are modified to express hACE2 by Ad5-hACE2 transduction, hACE2-Tg mice, hACE2-knock-in mice or modify the virus so that it can bind to mACE2. Both approaches require 1–2 amino acid changes in mACE2 or SARS-CoV-2 to change virus/receptor-binding affinity. Mice infected with this virus are not only useful for studying the pathogenesis of COVID-19 in the lungs, but also for other manifestations, including anosmia and ageusia (Wong et al., 2020; Zheng et al., 2021).

Bart Haagmans, Erasmus Medical Centre, The Netherlands, discussed molecular mechanisms in the pathogenesis of SARS-CoV-2, and identification of biomarkers that could block virus replication by modulating the host response involved in the pathogenesis of this virus. The use of alveolar and airway organoids to obtain data on the molecular mechanisms of the pathogenesis of SARS-CoV-2 was highlighted (van der Vaart et al., 2021).

Kari Nadeau, Stanford University, Palo Alto, CA, USA, compared the immune response to the virus and its vaccines. After one dose of mRNA vaccine, individuals with prior infection showed enhanced T-cell immunity and memory B cell response compared to those without prior infection. However, IgG levels in individuals with prior infection after one dose of mRNA vaccine were similar to those without prior infection after two doses of vaccine, and the levels of the antibody measured before vaccination in individuals with prior infection were similar to those without prior infection after one dose (Arunachalam et al., 2021; Röltgen et al., 2021).

Emilia Liana Falcone, Montréal Clinical Research Institute, Canada, brought to light the multidisciplinary clinical evaluation and management of the "post-COVID" syndrome. It was demonstrated that at least 10% of all COVID-19 survivors (17 million worldwide) develop long-term COVID, including both adults and children, regardless if they had had mild or severe acute COVID. Post-COVID involves several organs, including the brain, lungs, heart or skin. However, the underlying mechanisms of long-COVID are still unknown and require a multidisciplinary approach combining the clinic and laboratory to improve our understanding and treatment of this disease (Tremblay et al., 2021).

The main outcomes of the session highlight the benefit of using modified lab animals in studying virus pathogenesis and the identification of biomarkers that could block virus replication. Understanding the immune responsiveness to SARS-CoV-2 and its vaccines is also of utmost importance to reach the best way for developing successful vaccines.

3.3. Plenary III | from small to giant through the ages

The third plenary session, chaired by Maria Del Angel, Centre for Research and Advanced Studies (CINVESTAV-IPN), Mexico, and Eric Delwart, University of California, San Francisco, USA, gave valuable information on other important and interesting viruses from small pathogenic enteroviruses of humans to giant viruses of amoebas, and their evolution, phylogeny, taxonomy, and nomenclature through time.

Vincent Racaniello, Columbia University, New York, USA, discussed the role of enteroviruses in childhood paralysis. He started from the first sequencing of a whole poliovirus genome, transfection experiments and vaccine developments, then moved to the emergence in the last years of Enterovirus D68 as an agent of respiratory-induced acute flaccid myelitis. Its neurotropic character and the possible role of host genes on the development of the disease were discussed, as well as some useful approaches to deeper understanding the CNS invasion by EV-D68 (Rosenfeld et al., 2019).

Chantal Abergel, CNRS, Marseille, France, gave a fascinating presentation on the saga of 'giant viruses'. The characterization of the recently discovered mimivirus, pandoravirus and pithovirus, has dramatically changed the classical features of virus description. The viral factory, a virion-based gene dissemination strategy, and the existence of virophages, were presented. Also, the unique ability of Marseillevirus, encoding a full transcription machinery but recruiting the host nuclear proteins, represents a link between exclusively cytoplasmic and nucleic infection cycles. These observations may lead to the abolition of the discontinuity between the viral and cellular worlds (Abergel and Claverie, 2020; Claverie and Abergel, 2018).

Edward Holmes, University of Sydney, Australia, displayed the enormity of the RNA virosphere and the challenges of emerging viruses from fish, birds and insects. He pointed out the need to understand viruses at an ecosystem scale, and to eliminate the bias of viewing viruses only as human pathogens. Evidence was presented on the utility of metatranscriptomics to study different environments, demonstrating a huge phylogenetic diversity of viruses, and the identification of sediments and animal feces as rich sources of viruses. The importance of the study of ancient virus history was also stated, to get clues on the co-divergence and cross-species transmission (Cobbin et al., 2021; Zhang et al., 2019).

Murilo Zerbini, Federal University of Vicosa, Brazil (chair of the ICTV), made a fascinating presentation on virus taxonomy. He discussed the classification of viruses from metagenomic studies, the mega-taxonomy ranks, and the challenges of renaming all the known virus

species following a Linnéan binomial nomenclature. Metagenomic analysis now allow the discovery of an incredible number of novel viruses that, although being not real isolates, will be essential for better understanding of viral ecology and to fill many phylogenetic gaps.

The main outcomes of the session were related to the utility of new research approaches to advance the knowledge of the vast diversity of viruses, their relationships and co-evolution with their hosts, and the role of viruses in the evolution and their place in the tree of life. These fascinating areas of research will be even more relevant in the years to come (de Vries et al., 2021; López-Labrador et al., 2021; Simmonds et al., 2017).

3.4. Plenary IV | one health, one world

The fourth Plenary Session was chaired by Laura Kramer, Wadsworth Centre, USA, and Marietjie Venter, University of Pretoria, South Africa. It comprised four talks that illustrated how viruses impact not only our health but also that of the world. Viruses encompass much of the genetic diversity on Earth, and we coexist with them, leading to interactions on a regular basis. The talks brought out how viruses can be serious human disease agents, such as Ebola, HIV, and SARS-CoV-2, while other viruses serve beneficial roles, acting as major drivers of global biogeochemical cycles, as evidenced by the important role viruses have in the ocean environment.

Curtis Suttle, University of British Columbia, Canada, observed that viruses are the most abundant lifeforms on Earth and have been shaping life on earth for 3 billion years. He emphasized that while we live with viruses continually, only a very small fraction actually do us harm. Globally 91.4% of all sequences from ocean microbes are unidentifiable organisms, thus our knowledge is miniscule. Viruses are key players in oceans – they catalyze the cycling of nutrients, and are critical to global biogeochemical cycles (Gao et al., 2021; Gustavsen and Suttle, 2021).

Andrea Marzi, NIAID Laboratory of Virology, Hamilton MT, USA, presented the pathway to success of the first Ebola vaccine, VSV-EBOV (Ervebo), which is a targeted attenuated single-dose vaccine. Vaccine development which began after the 1976 Yambuko, Zaire [DRC] outbreak and flourished with an influx of bioterrorism funding in 2001, led to the first published study on protection in nonhuman primates in 2005, its use in the West African outbreak 2013-16, and ring vaccination in Guinea. Currently there are at least 4 Ebola vaccines (2 FDA approved) and approximately 350,000 people worldwide that have been vaccinated (Bhatia et al., 2021; O'Donnell and Marzi, 2020).

Linda Saif, Ohio State University, Wooster OH, USA, discussed the continual evolution and global emergence of coronaviruses, and highlighted the concern for reverse zoonoses of SARS-CoV-2 and establishment in animal reservoirs. Domestic cats and dogs also can become infected but there is no transmission back to humans as was observed with farmed mink. She discussed the ecology and chronology of coronavirus emergence, with spillover from bats to humans. Bats are the likely ancestral host reservoir of SARS-CoV-2, with pangolins as possible intermediate hosts. The coronaviruses are genetically diverse with frequent mutations and recombination, giving them great plasticity (Kenney et al., 2021; Saif and Jung, 2020).

Robert Gallo, University of Maryland, USA, discussed the advances made in control of HIV/AIDS since the pandemic in the eighties and the need to build scientific leadership through Global Virus Network. A major advance came with the ability to maintain virus in continuous cell line culture in 1983. This led to a blood test that could be used to verify etiology, a key advance in prevention of new infections. Big advances were made in 1984–1988, including a therapy specific to the viral reverse transcriptase, leading the way for development of non-toxic long-acting therapeutics (Gallo, 2020).

The talks provided background on the pursuit by scientists to understand, prevent, and treat, harmful viruses and their spread; as well as also gain knowledge of viruses beneficial for the wellbeing of our planet.

4. Parallel keynote sessions

In addition to the plenary talks discussed above, a number of parallel sessions were presented on a diverse set of topics from basic to applied aspects of viruses affecting humans, other animals, plants, and microbes, as well as numerous tools and treatments for these viruses.

4.1. Parallel 1 | avian and aquatic viruses

In this session, chaired by Mariana Baz, WHO Collaborating Centre for Reference and Research on Influenza, Peter Doherty Institute, Melbourne, Australia, and Vikram Vakharia, Institute of Marine & Environmental Technology, University of Maryland, USA, viruses affecting poultry and aquaculture industries were reviewed, such as avian influenza virus which can be transmitted to humans; engineered avian Newcastle disease virus which can be used as a vectored vaccine and for oncolytic therapy; new approaches to treat immunosuppression caused by bursal disease virus in chickens, and applied research on the development of fish viral vaccines for global aquaculture.

Kanta Subbarao, WHO Collaborating Centre for Reference and Research on Influenza and University of Melbourne at the Peter Doherty Institute, Australia, provided a summary of the risk that avian influenza A viruses (IAVs) pose to humans. Although some avian IAVs have not yet caused a pandemic, these viruses have crossed the species barrier to infect mammals including pigs and humans. She discussed viral and host factors that are key determinants of the ability of avian IAVs to infect and spread in humans, including receptor specificity, tropism, infectivity, virulence and polymerase complex (Subbarao, 2019).

Khatijah Yusoff, Universiti Putra, Malaysia, discussed Newcastle disease virus (NDV), which causes one of the most important avian respiratory diseases affecting poultry production worldwide. She described the generation and in vitro and in vivo characterization of the first genotype VII NDV reverse-genetics system to be used as a vectored vaccine platform. She also presented her recent studies using the oncolytic property of NDVs and their potential to be used for therapy against human cancer (Bello et al., 2020; Murulitharan et al., 2021; Najmuddin et al., 2020).

Egbert Mundt, Boehringer Ingelheim Veterinary Research Centre, Hannover, Germany, developed and utilized reverse genetics to decipher the molecular determinants of virulence in infectious bursal disease virus (IBDV), using genotype-specific neutralizing antibodies. Based on this information, a new generation of cell-culture adapted, scalable and effective IBDV vaccines were designed to control the disease in the field (Dobner et al., 2019).

Øystein Evensen, Norwegian University of Life Sciences, Oslo, Norway, discussed the presence of different viral diseases in a variety of fish species for which the vaccines (mainly inactivated) are currently available, but not for all; focusing on important viruses affecting salmon, groupers, tilapia, carp and trout; methods for delivery of vaccines and use of oil-adjuvants; development of DNA vaccines; and correlates of immune response in fish (Mugimba et al., 2021).

4.2. Parallel 2 | plant viruses

In this session, chaired by Anupam Varma, Advanced Centre for Plant Virology Indian Agricultural Research Institute, New Delhi, India, and Hanu Pappu, Washington State University, Pullman, WA, USA. Detailed discussions were held on the threat of emerging viruses, latest developments in the use of RNAi for managing viral infections in plants, the role of ribonucleoprotein complexes in modulating viral infections, and the complexities of unique chloroviruses.

Neena Mitter, University of Queensland, Brisbane, Australia, showed the unique approach for topical application of dsRNA for triggering RNAi-based resistance to plant viruses. Spraying degradable layered double hydroxide clay particles as carriers of dsRNA provided protection against virus infection for up to 20 days. For effective commercialisation

of the technology, resolution of factors such as cost-effective production of dsRNA, stability, risk mitigation strategies, regulatory landscape and community acceptance were discussed (Nilon et al., 2021; Worrall et al., 2019).

Kristiina Mäkinen, Helsinki University, Helsinki, Finland, presented research on potato virus A-host interactions, specifically by providing structural and functional elucidation of interactions related to potato virus A RNA stability as well as viral protein manipulation to neutralize host antiviral proteins. These interactions are crucial for the accumulation of stable virus particles required for systemic infection of host by potato virus A (De et al., 2020).

Hanu Pappu, Washington State University, Pullman WA, USA, showed Tomato spotted wilt virus-host interactions at the transcriptome level in tomato genotypes – with or without the resistance gene, Sw5. The viral genome was differentially targeted in these genotypes, and distinct differences were found in the small RNA profiles of the viral genome in resistant versus susceptible genotypes. Success in RNAi-based management of the destructive tospoviruses was also reported (Konakalla et al., 2021; Nilon et al., 2021).

James Van Etten, University of Nebraska, USA, showed that chloroviruses are unique viruses to encode enzymes that synthesize extracellular polysaccharides and presented information on glycosylation of the major capsid protein (MCP), and characterization of the chlorovirus-encoded glycosyltransferases (GTases) and methyltransferases (MTases) involved in glycosylation. Genetic, structural, and hydrolytic analyses indicate that protein A111/114R, which is conserved in all chloroviruses, is a GTase with three domains: galactosyltransferase, xylosyltransferase, and fucosyltransferase (Noel et al., 2021; Speciale et al., 2020).

4.3. Parallel 3 | new winds in virus diagnostics

In this session, chaired by Matthew D. Moore, University of Massachusetts, Amherst, MA, USA, and Maria Söderlund-Venermo, University of Helsinki, Helsinki, Finland, four interesting new technologies were reviewed that can be used in diagnosing virus infections; a rapid and wash-free immunodiagnostic concept, mass-spectrometry for viral and host proteins, versatile viral nanotools, and multiplexed CRISPR-Cas13, along with discussion of the future of the fast-evolving diagnostic field.

Klaus Hedman, University of Helsinki, Helsinki, Finland, presented several different detection approaches based on Time-Resolved Förster Resonance Energy Transfer (TR-FRET) technology, for homogenous, wash-free, rapid, and highly specific and sensitive immunodiagnostics (IgM, IgG and/or antigen detection), in both serum and urine. So far, the technique has been used for the serology of Puumala, B19V, Zika and SARS-CoV-2 virus infections and coeliac disease (IgA) (Rusanen et al., 2021a, 2021b).

Evgeny Nikolaev, Skolkovo Institute of Science and Technology, Skolkova, Moscow, Russia, reported on a mass-spectrometry (MS)-based fast and sensitive method for detection of the N protein of SARS-CoV-2 in patient samples utilizing a simple preparation procedure, including tryptic digestion of the eluate sediment from swab samples. Interestingly, MS approaches can be created for detection of both viral and human proteins in various physiological fluids to also study the human response to viral infections, such as in the case of prolonged "long-COVID" patients (Zakharova et al., 2021).

Christina Wege, University of Stuttgart, Stuttgart, Germany, talked about plant viral nanoparticles with multivalent protein shells, which can serve as advantageous carrier scaffolds – straight, branched or star-shaped TMV nanotubes – for displaying biomolecules for various purposes, including diagnostics. These versatile opportunities provided by TMV-based hybrid structures point at many potential uses, due to the easy handling and high availability of the natural plant-made building blocks (Jablonski et al., 2021; Poghossian et al., 2020).

Cameron Myhrvold, Princeton University, Princeton, New Jersey, USA, introduced an exciting "Combinatorial Arrayed Reactions for Multiplexed Evaluation of Nucleic acids" (CARMEN) technology that enables parallelized CRISPR-Cas13 detection with up to 5000 crRNA-target pairs tested in a single assay. CARMEN increases multiplexing and throughput while simultaneously decreasing the reagent cost per test by >300-fold. Using CARMEN-Cas13, they designed and extensively tested a 169-plex assay and found it to simultaneously differentiate nearly all human-associated viruses for which sequences are available (Ackerman et al., 2020).

4.4. Parallel 4 | animal viruses

This session, chaired by William C. Wilson, Agricultural Research Service, United States Department of Agriculture, Manhattan, KS, USA, and Michael M. Nevels, University of St Andrews, St Andrews, UK, covered important pathogens belonging to the *Asfarviridae, Flaviviridae, Paramyxoviridae* and *Picornaviridae*.

Anne Balkema-Buschmann, Friedrich-Loeffler-Institute, Greifswald-Insel Riems, Germany, presented recent work on paramyxoviruses of the *Henipavirus* genus, which includes the zoonotic and highly pathogenic Hendra and Nipah viruses. Various species of fruit bats (flying foxes) serve as their natural hosts. Two breeding colonies of African fruit bats have facilitated studies on the tissue distribution, pathogenesis and shedding, and have enabled serology and challenge studies. The findings are relevant to assessing the risk of transmission of highly pathogenic henipaviruses to livestock or humans in Africa (Mbu'u et al., 2019).

Marietjie Venter, University of Pretoria, Pretoria, South Africa, talked about the West Nile Virus (WNV), a flavivirus causing mosquito-borne disease. A One Health surveillance program detected a large WNV outbreak among animals in South Africa in 2017. Her team investigated the epidemiology and phylogenetic relationship of WNV in humans, animals and vectors across several provinces. They conclude that WNV, especially lineage 2, contributed to severe neurological and febrile disease in humans and animals between 2017 and 2020, with *Culex* species being the likely vectors. Their findings highlight that WNV disease in South Africa remains underreported (Bertram et al., 2020; Steyn et al., 2019).

Teresa de los Santos, Plum Island Animal Disease Centre, Greenport NY, USA, summarized a body of work on the picornavirus foot-and-mouth disease virus (FMDV), a dreaded pathogen in cloven-hoofed animals. The FMDV leader proteinase (Lpro) affects the innate immune response including the expression of interferon-stimulated genes (ISGs). In addition to its conventional protease activity, Lpro acts as a deubiquitinase and deISGylase. Mutations in Lpro result in increased levels of the ubiquitin-like protein ISG15, which limit viral replication. This study highlights the potential use of Lpro mutants as live attenuated vaccine candidates and of ISG15 as an antiviral agent (Medina et al., 2020; Visser et al., 2020).

Covadonga Alonso, National Institute for Agricultural and Food Research and Technology, Madrid, Spain, presented insights into the infectious cycle of African swine fever virus (ASFV), an asfarvirus causing hemorrhagic fever in domestic pigs. ASFV enters the host cell via endocytosis, but how the virus exits the endosome has remained unclear. The cholesterol transporter proteins Niemann-Pick C type 1 (NPC1) and 2 (NPC2), were identified as critical components in membrane fusion and virus uncoating, revealing new targets for antiviral intervention (García-Dorival et al., 2021).

4.5. Parallel 5 | clinical virology

In this session, chaired by Flor Pujol, Centro de Microbiología y Biología Celular Instituto Venezolano de Investigaciones Científicas, Caracas, Venezuela, and Kristina Broliden, Karolinska Institutet, Stockholm, Sweden, recent advances in the pathogenesis of some important viruses and their role in the development of chronic diseases like diabetes and hepatitis were reviewed. The role of environmental factors regulating infection, as well as of the development of oncolytic

virotherapy and immune interventions were discussed.

Heikki Hyöty, Tampere University, Tampere, Finland, nicely reviewed and highlighted the strong link between the group B coxsackieviruses and type 1 diabetes, based on both epidemiological data and that they, in *in vitro* and *in vivo* studies, infect pancreatic beta-cells. The first trials of antiviral drugs among diabetic patients and of a vaccine against the group B coxsackieviruses are in progress and are foreseen to be promising strategies to prevent type 1 diabetes (Oikarinen et al., 2020a, 2020b).

Fabien Zoulim, Lyon University, Lyon, France, described that, despite the availability of a highly efficient vaccine against hepatitis B, this disease is still an unsolved problem. In the path toward a cure of chronic HBV infection (CHB) he stressed the importance of addressing the persistence of episomal covalently-closed circular DNA form (cccDNA) as a major challenge, although new antiviral drug combinations with immune interventions to reinvigorate the exhausted immune response could help to achieve the functional cure of CHB (Martinez et al., 2021; Roca Suarez et al., 2021).

Jean Rommelaere, German Cancer Research Centre (DKFZ), Heidelberg, Germany, presented the tumor-suppressive properties of rodent protoparvoviruses, in particular the rat H-1 parvovirus (H–1PV), and the development of promising oncolytic virotherapy. In addition to inducing selective cancer cell death, these viruses are also able to exert immunostimulatory effects, prompting establishment of an antitumorigenic proinflammatory tumor microenvironment. Therefore, further clinical development of H–1PV as a partner drug combined immunotherapy against cancer is of great importance (Angelova et al., 2021).

Stephanie Karst, University of Florida, Gainesville, FL, USA, described the suitability of murine norovirus as a model to study human norovirus pathogenesis, with special emphasis on the crosslink between host and environmental factors that regulate norovirus infection. Interestingly, she discussed the consequences of norovirus infection of host immune cells, as well as the role host bile acid has in promoting and influencing norovirus pathogenesis [(Grau et al., 2020; Walker et al., 2021).

4.6. Parallel 6 | phages and insect viruses

In this session, chaired by Yigang Tong, College of Life Science and Technology, Beijing University of Chemical Technology, Beijing China, and Myléne Ogliastro, University of Montpellier, France, the proviral and antiviral impact of miRNA in insects, parvoviruses used for insect biocontrol, the ongoing battle between phages and their bacterial host, and the history and new developments in phage therapy were reviewed.

Karyn Johnson, University of Queensland, Brisbane, Australia, reviewed functions of widespread miRNAs regulating gene expression across many biological functions including antiviral defense in insects. Using the *Drosophila* model, it was demonstrated that miRNAs can have a considerable proviral or antiviral impact on virus infection (Monsanto-Hearne and Johnson, 2018).

Myléne Ogliastro, University of Montpellier, France, talked about the intriguing densoviruses, parvoviruses of insects, which are used as tools for biocontrol. She described the interesting research done on densovirus pathogenesis, virus-host interactions, metagenomics, and their diversity in the ecosystem, highlighting their use in biocontrol in the agroecosystem of today (Labadie et al., 2021).

Sylvain Moineau, Université Laval, Quebec, Canada, talked about the ongoing battle between phages and CRISPR-Cas systems. Interestingly, phages can bypass CRISPR immunity through point mutation or deletion of the CRISPR target or PAM in their genome as well as by the production of anti-CRISPR proteins (ACRs). He told about the roles played by virulent phages in the understanding of CRISPR-Cas systems and the development of industrially relevant phage-resistant bacteria (Mosterd and Moineau, 2021).

Mzia Kutateladze, Eliava Institute, Tbilisi, Georgia, talked about phage therapy, which was aimed to become a standard part of the healthcare systems in Eastern Europe and the USSR during the late 20th century. Phages are widely and successfully used to treat acute and chronic infections caused by antibiotic-resistant bacteria (Poirel et al., 2020).

5. Submitted talks

In addition to the Keynote talks reviewed above, a total of 140 abstracts were also submitted to this conference, which were divided into 16 descriptive 1–2 h sessions according to the topics of the talks, belonging under 5 themes: SARS-CoV-2 & COVID-19, Human-, Zoonotic-, Animal/Veterinary-, and Plant Virology. Due to space constraints, further details are not presented here but can be found in (Supp1.) and the Abstract booklet of the meeting (WSV2021-Abstracts, 2021).

6. Closing remarks and welcome to WSV2023

WSV 2021 came to a close with summary remarks by the WSV-President with thanks to all speakers, attendees, and sponsors (Varma, 2021b). The WSV2021 conference clearly demonstrated the enormity of challenges in managing emerging and re-emerging viruses and the need for concerted efforts by all the virologists of the world to work for minimizing the global risk of emergence of new pathogenic human, animal or plant virus infections. A strong network of the academic societies is essential to engage with policy makers for greater and continued investment in virology research for the benefit of humanity and global health. WSV can play a key role in this effort along with additional national virology societies. The 2nd WSV conference, WSV2023, is planned to be held in the city of Riga, Latvia, during 15–17 June 2023.

CRediT authorship contribution statement

Maria Söderlund-Venermo: Conceptualization, Writing – original draft, Writing – review & editing. **Anupam Varma:** Writing – review & editing. **Deyin Guo:** Writing – review & editing. **Douglas P. Gladue:** Writing – review & editing. **Emma Poole:** Writing – review & editing. **Flor H. Pujol:** Writing – review & editing. **Hanu Pappu:** Writing – review & editing. **Jesús L. Romalde:** Writing – review & editing. **Laura Kramer:** Writing – review & editing. **Mariana Baz:** Writing – review & editing. **Marietjie Venter:** Writing – review & editing. **Matthew D. Moore:** Writing – review & editing. **Michael M. Nevels:** Writing – review & editing. **Sayeh Ezzikouri:** Writing – review & editing. **Vikram N. Vakharia:** Writing – review & editing. **William C. Wilson:** Writing – review & editing. **Yashpal S. Malik:** Writing – review & editing. **Zhengli Shi:** Writing – review & editing. **Ahmed S. Abdel-Moneim:** Conceptualization, Writing – original draft, Writing – review & editing.

Declaration of competing interest

☒ The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgements and funding

We are extremely grateful for the help of our event organizers, Vetlink Conferences from South Africa; they were very flexible for our needs and requests. We would further like to thank our sponsors, who made this conference possible: Boehringer Ingelheim (Platinum Level Sponsor), NanoString Technologies Inc. (Gold), Optolane Technologies Inc (Gold), and Inqaba biotec (Silver), as well as Prof. Janusz T. Paweska, the Centre for Emerging and Zoonotic Diseases, National Institute of Communicable Diseases, South Africa, for his kind donation directed to sponsorship of scientists from developing countries.

The Melbourne WHO Collaborating Centre for Reference and Research on Influenza is supported by the Australian Government Department of Health. The conclusions in this report are those of the authors and do not necessarily represent the views of the USDA.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.virol.2021.11.009.

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