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Söderlund-Venermo, Maria

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World Society for Virology First International Conference: Tackling Global Virus Epidemics

Maria Söderlund-Venermo^{1*}, Anupam Varma², Deyin Guo³, Douglas P. Gladue⁴, Emma Poole⁵, Flor H. Pujol⁶, Hanu Pappu⁷, Jesús L Romalde⁸, Laura Kramer⁹, Mariana Baz¹⁰, Marietjie Venter¹¹, Matthew D. Moore¹², Michael M Nevels¹³, Sayeh Ezzikouri¹⁴, Vikram N. Vakharia¹⁵, William C. Wilson¹⁶, Yashpal Malik¹⁷, Zhengli Shi¹⁸, Ahmed S. Abdel-Moneim^{19*}

1. Department of Virology, University of Helsinki, Helsinki, Finland
2. Advanced Centre for Plant Virology Indian Agricultural Research Institute, New Delhi, India
3. Center for Infection and Immunity Study, School of Medicine, Sun Yat-sen University, Guangzhou, China
4. Plum Island Animal Disease Center, ARS, USDA, Greenport, USA
5. Department of Medicine, University of Cambridge, Addenbrooke's Hospital, Hills Road, Cambridge, UK
6. Laboratorio de Virología Molecular, Centro de Microbiología y Biología Celular Instituto Venezolano de Investigaciones Científicas, Caracas, Venezuela
7. Department of Plant Pathology, Washington State University, Pullman, WA, USA
8. Department of Microbiology and Parasitology, CRETUS & CIBUS-Faculty of Biology, Universidad de Santiago de Compostela, Santiago de Compostela, Spain
9. Arbovirus Laboratory, Wadsworth Center, New York State Department of Health, Albany, New York, USA
10. WHO Collaborating Centre for Reference and Research on Influenza, Peter Doherty Institute, Melbourne, Victoria, Australia and Research Center in Infectious Diseases of the CHU of Québec and Université Laval, Québec City, Quebec, Canada
11. Zoonotic Arbo- and Respiratory Virus Research Program, Centre for Viral Zoonosis, Department of Medical Virology, University of Pretoria, Pretoria, South Africa
12. Department of Food Science, University of Massachusetts, Amherst, MA, USA
13. Biomedical Sciences Research Complex, University of St Andrews, St Andrews, UK
14. Virology Unit, Viral Hepatitis Laboratory, Institut Pasteur du Maroc, Casablanca, Morocco.
15. Institute of Marine & Environmental Technology, University of Maryland, Baltimore County, Baltimore, MD 21202, USA.
16. Arthropod Borne Animal Diseases Research Unit, Agricultural Research Service, United States Department of Agriculture, Manhattan, KS, USA
17. Indian Veterinary Research Institute (IVRI), Izatnagar, 243 122, Bareilly, Uttar Pradesh, India.
18. CAS Key Laboratory of Special Pathogens and Biosafety, Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, Hubei, China
19. Microbiology Department, Virology Division, College of Medicine, Taif University, Al-Taif, Saudi Arabia, Virology Department, Faculty of Veterinary Medicine, Beni-Suef University, Beni-Suef, Egypt.

*corresponding authors

Authors' names are arranged in alphabetical order, except for the first and last authors.

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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.

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).

General information of 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).

Plenary Keynote Sessions:

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 long-term surveillance for emerging human-needed to prevent emerging infectious diseases caused by this group of viruses.

Marion Koopmans, 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 (Figuerola et al., 2021; Hotez et al., 2021).

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, Montreal 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.

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 meta-transcriptomics 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; Lopez-Labrador et al., 2021; Simmonds et al., 2017).

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.

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.

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).

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 commercialization 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).

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 immunodiagnosics (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, Skolkovo, 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).

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).

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 antitumorogenic 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).

PARALLEL 6 | PHAGE 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).

Mylène 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).

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 ([Supplement 1](#)) and the Abstract booklet of the meeting (WSV2021-Abstracts, 2021).

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.

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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.

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

References

- Abdel-Moneim, A.S., 2021. WSV2021 Welcome talk, Prof. Ahmed S. Abdel-Moneim, Founding President of the World Society for Virology (WSV), in: <https://www.youtube.com/watch?v=L7XaKKaqmQY>.
- Abdel-Moneim, A.S., Moore, M.D., Naguib, M.M., Romalde, J.L., et al., 2020. WSV 2019: the first committee meeting of the World Society for Virology. *Viol. Sin.* 35, 248–252.
- Abdel-Moneim, A.S., Varma, A., Pujol, F.H., Lewis, G.K., et al., 2017. Launching a global network of virologists: the world society for virology (WSV). *Intervirology* 60, 276–277.
- Abergel, C., Claverie, J.M., 2020. Giant viruses. *Curr. Biol.* 30, R1108–r1110.
- Ackerman, C.M., Myhrvold, C., Thakku, S.G., Freije, C.A., et al., 2020. Massively multiplexed nucleic acid detection with Cas13. *Nature* 582, 277–282.
- Angelova, A., Ferreira, T., Bretscher, C., Rommelaere, J., et al., 2021. Parvovirus-based combinatorial immunotherapy: a reinforced therapeutic strategy against poor-prognosis solid cancers. *Cancers* 13.
- Arunachalam, P.S., Scott, M.K.D., Hagan, T., Li, C., et al., 2021. Systems vaccinology of the BNT162b2 mRNA vaccine in humans. *Nature* 596, 410–416.
- Bello, M.B., Mahamud, S.N.A., Yusoff, K., Ideris, A., et al., 2020. Development of an effective and stable genotype-matched live attenuated Newcastle disease virus vaccine based on a novel naturally recombinant Malaysian isolate using reverse genetics. *Vaccines (Basel)* 8.
- Bertram, F.M., Thompson, P.N., Venter, M., 2020. Epidemiology and clinical presentation of west nile virus infection in horses in South Africa, 2016-2017. *Pathogens* 10.

- Bhatia, B., Furuyama, W., Hoenen, T., Feldmann, H., et al., 2021. Ebola virus glycoprotein domains associated with protective efficacy. *Vaccines (Basel)* 9.
- Claverie, J.M., Abergel, C., 2018. Mimiviridae: an expanding family of highly diverse large dsDNA viruses infecting a wide phylogenetic range of aquatic eukaryotes. *Viruses* 10.
- Cobbin, J.C., Charon, J., Harvey, E., Holmes, E.C., et al., 2021. Current challenges to virus discovery by meta-transcriptomics. *Curr. Opin. Virol.* 51, 48–55.
- De, S., Pollari, M., Varjosalo, M., Mäkinen, K., 2020. Association of host protein VARICOSE with HCPro within a multiprotein complex is crucial for RNA silencing suppression, translation, encapsidation and systemic spread of potato virus A infection. *PLoS Pathog.* 16, e1008956.
- de Vries, J.J.C., Brown, J.R., Couto, N., Beer, M., et al., 2021. Recommendations for the introduction of metagenomic next-generation sequencing in clinical virology, part II: bioinformatic analysis and reporting. *J. Clin. Virol.* 138, 104812.
- Dobner, M., Auerbach, M., Mundt, E., Preisinger, R., et al., 2019. Immune responses upon in ovo HVT-IBD vaccination vary between different chicken lines. *Dev. Comp. Immunol.* 100, 103422.
- Figuroa, J.P., Hotez, P.J., Batista, C., Ben Amor, Y., et al., 2021. Achieving global equity for COVID-19 vaccines: stronger international partnerships and greater advocacy and solidarity are needed. *PLoS Med.* 18, e1003772.
- Gallo, R.C., 2020. HIV/AIDS research for the future. *Cell Host Microbe* 27, 499–501.
- Gao, C., Xia, J., Zhou, X., Liang, Y., et al., 2021. Viral characteristics of the warm atlantic and cold arctic water masses in the Nordic seas. *Appl. Environ. Microbiol.* 87, e0116021.
- García-Dorival, I., Cuesta-Geijo, M., Barrado-Gil, L., Galindo, I., et al., 2021. Identification of Niemann-Pick C1 protein as a potential novel SARS-CoV-2 intracellular target. *Antivir. Res.* 194, 105167.
- Grau, K.R., Zhu, S., Peterson, S.T., Helm, E.W., et al., 2020. The intestinal regionalization of acute norovirus infection is regulated by the microbiota via bile acid-mediated priming of type III interferon. *Nat. Microbiol.* 5, 84–92.
- Gustavsen, J.A., Suttle, C.A., 2021. Role of phylogenetic structure in the dynamics of coastal viral assemblages. *Appl. Environ. Microbiol.* 87.
- Hotez, P.J., Batista, C., Amor, Y.B., Ergonul, O., et al., 2021. Global public health security and justice for vaccines and therapeutics in the COVID-19 pandemic. *EClinicalMedicine* 39, 101053.
- Jablonski, M., Poghossian, A., Severins, R., Keusgen, M., et al., 2021. Capacitive field-effect biosensor studying adsorption of tobacco mosaic virus particles. *Micromachines* 12.
- Kenney, S.P., Wang, Q., Vlasova, A., Jung, K., et al., 2021. Naturally occurring animal coronaviruses as models for studying highly pathogenic human coronaviral disease. *Vet. Pathol.* 58, 438–452.

- Konakalla, N.C., Bag, S., Deraniyagala, A.S., Culbreath, A.K., et al., 2021. Induction of plant resistance in tobacco (*Nicotiana tabacum*) against tomato spotted wilt orthotospovirus through foliar application of dsRNA. *Viruses* 13.
- Koopmans, M., Daszak, P., Dedkov, V.G., Dwyer, D.E., et al., 2021. Origins of SARS-CoV-2: window is closing for key scientific studies. *Nature* 596, 482–485.
- Kuhn, R., 2021. WSV2021-Welcome Talk by Prof. Richar Kuhn, President Elect of the World Society for Virology (WSV), in: <https://www.youtube.com/watch?v=bhBx1ChbRoA>
- Labadie, T., Garcia, D., Mutuel, D., Ogliastro, M., et al., 2021. Capsid proteins are necessary for replication of a parvovirus. *J. Virol.* 95, e0052321.
- L'opez-Labrador, F.X., Brown, J.R., Fischer, N., Harvala, H., et al., 2021. Recommendations for the introduction of metagenomic high-throughput sequencing in clinical virology, part I: wet lab procedure. *J. Clin. Virol.* 134, 104691.
- Martinez, M.G., Boyd, A., Combe, E., Testoni, B., et al., 2021. Covalently closed circular DNA: the ultimate therapeutic target for curing HBV infections. *J. Hepatol.* 75, 706–717.
- Mbu'u, C.M., Mbacham, W.F., Gontao, P., Sado Kamdem, S.L., et al., 2019. Henipaviruses at the interface between bats, livestock and human population in Africa Vector. *Borne Zoonotic Dis* 19, 455–465.
- Medina, G.N., Azzinaro, P., Ramirez-Medina, E., Gutkoska, J., et al., 2020. Impairment of the DeISGylation activity of foot-and-mouth disease virus Lpro causes attenuation in vitro and in vivo. *J. Virol.* 94.
- Mishra, S., Mindermann, S., Sharma, M., Whittaker, C., et al., 2021. Changing composition of SARS-CoV-2 lineages and rise of Delta variant in England. *EClinicalMedicine* 39, 101064.
- Monsanto-Hearne, V., Johnson, K.N., 2018. miRNAs in insects infected by animal and plant viruses. *Viruses* 10.
- Mosterd, C., Moineau, S., 2021. Primed CRISPR-Cas adaptation and impaired phage adsorption in *Streptococcus mutans*. *mSphere* 6.
- Mugimba, K.K., Byarugaba, D.K., Mutoloki, S., Evensen, Ø., et al., 2021. Challenges and solutions to viral diseases of finfish in marine aquaculture. *Pathogens* 10.
- Murulitharan, K., Yusoff, K., Omar, A.R., Peeters, B.P.H., et al., 2021. Rapid generation of a recombinant genotype VIII Newcastle disease virus (NDV) using full-length synthetic cDNA. *Curr. Microbiol.* 78, 1458–1465.
- Najmuddin, S.U.F., Amin, Z.M., Tan, S.W., Yeap, S.K., et al., 2020. Oncolytic effects of the recombinant Newcastle disease virus, rAF-IL12, against colon cancer cells in vitro and in tumor-challenged NCr-Foxn1nu nude mice. *PeerJ* 8, e9761.
- Nilon, A., Robinson, K., Pappu, H.R., Mitter, N., 2021. Current status and potential of RNA interference for the management of tomato spotted wilt virus and thrips vectors. *Pathogens* 10.

- Noel, E., Notaro, A., Speciale, I., Duncan, G.A., et al., 2021. Chlorovirus PBCV-1 multidomain protein A111/114R has three glycosyltransferase functions involved in the synthesis of atypical N-glycans. *Viruses* 13.
- O'Donnell, K., Marzi, A., 2020. The Ebola virus glycoprotein and its immune responses across multiple vaccine platforms. *Expert Rev. Vaccines* 19, 267–277.
- Oikarinen, M., Bertolet, L., Toniolo, A., Oikarinen, S., et al., 2020a. Differential detection of encapsidated versus unencapsidated enterovirus RNA in samples containing pancreatic enzymes-relevance for diabetes studies. *Viruses* 12.
- Oikarinen, M., Puustinen, L., Lehtonen, J., Hakola, L., et al., 2020b. Enterovirus infections are associated with the development of celiac disease in a birth cohort study. *Front. Immunol.* 11, 604529.
- Oude Munnink, B.B., Worp, N., Nieuwenhuijse, D.F., Sikkema, R.S., et al., 2021. The next phase of SARS-CoV-2 surveillance: real-time molecular epidemiology. *Nat. Med.* 27, 1518–1524.
- Poghossian, A., Jablonski, M., Molinnus, D., Wege, C., et al., 2020. Field-Effect sensors for virus detection: from Ebola to SARS-CoV-2 and plant viral enhancers. *Front. Plant Sci.* 11, 598103.
- Poirel, L., Nordmann, P., de la Rosa, J.M.O., Kutateladze, M., et al., 2020. A phage-based decolonisation strategy against pan-resistant enterobacterial strains *Lancet. Inf. Disp.* 20, 525–526.
- Roca Suarez, A.A., Testoni, B., Zoulim, F., 2021. HBV 2021: new therapeutic strategies against an old foe. *Liver Int.* 41 (Suppl. 1), 15–23.
- Röltgen, K., Nielsen, S.C.A., Arunachalam, P.S., Yang, F., et al., 2021. mRNA vaccination compared to infection elicits an IgG-predominant response with greater SARS-CoV-2 specificity and similar decrease in variant spike recognition. *medRxiv*. <https://doi.org/10.1101/2021.04.05.21254952>.
- Rosenfeld, A.B., Warren, A.L., Racaniello, V.R., 2019. Neurotropism of enterovirus D68 isolates is independent of sialic acid and is not a recently acquired phenotype. *mBio* 10.
- Rusanen, J., Kareinen, L., Levanov, L., Mero, S., et al., 2021a. A 10-minute "mix and read" antibody assay for SARS-CoV-2. *Viruses* 13.
- Rusanen, J., Kareinen, L., Szirovicza, L., Ugurlu, H., et al., 2021b. A generic, scalable, and rapid time-resolved Förster resonance energy transfer-based assay for antigen detection-SARS-CoV-2 as a proof of concept. *mBio* 12.
- Saif, L.J., Jung, K., 2020. Comparative pathogenesis of bovine and porcine respiratory coronaviruses in the animal host species and SARS-CoV-2 in humans. *J. Clin. Microbiol.* 58.
- Simmonds, P., Adams, M.J., Benk"o, M., Breitbart, M., et al., 2017. Consensus statement: virus taxonomy in the age of metagenomics. *Nat. Rev. Microbiol.* 15, 161–168.

Söderlund-Venermo, M., 2021. WSV2021-Welcome talk by Dr. Maria Söderlund- Venermo. The Head of the Scientific Organizing Committee and Vice President of the World Society for Virology (Europe). https://www.youtube.com/watch?v=riheETul_X8

Speciale, I., Laugieri, M.E., Noel, E., Lin, S., et al., 2020. Chlorovirus PBCV-1 protein A064R has three of the transferase activities necessary to synthesize its capsid protein N-linked glycans. *Proc. Natl. Acad. Sci. U. S. A.* 117, 28735–28742.

Stenseth, N.C., Dharmarajan, G., Li, R., Shi, Z.L., et al., 2021. Lessons learnt from the COVID-19 pandemic. *Front Public Health* 9, 694705.

Steyn, J., Botha, E., Stivaktas, V.I., Buss, P., et al., 2019. West Nile virus in wildlife and nonequine domestic animals, South Africa, 2010-2018. *Emerg. Infect. Dis.* 25, 2290–2294.

Subbarao, K., 2019. The critical interspecies transmission barrier at the animal-human interface. *Trav. Med. Infect. Dis.* 4.

Tremblay, K., Rousseau, S., Zawati, M.H., Auld, D., et al., 2021. The Biobanque qu'eb'ecoise de la COVID-19 (BQC19)-A cohort to prospectively study the clinical and biological determinants of COVID-19 clinical trajectories. *PLoS One* 16, e0245031.

van der Vaart, J., Lamers, M.M., Haagmans, B.L., Clevers, H., 2021. Advancing lung organoids for COVID-19 research. *Dis. Model Mech.* 14.

Varma, A., 2021a. WSV2021-Welcome Talk by Prof. Anupam Varma, WSV-President in: <https://www.youtube.com/watch?v=aKCMJC6k-w>

Varma, A., 2021b. Closing Speech by WSV President: The first WSV conference (WSV2021), in: <https://www.youtube.com/watch?v=uLjBe0U-t20&t=12s> (Ed.).

Visser, L.J., Aloise, C., Swatek, K.N., Medina, G.N., et al., 2020. Dissecting distinct proteolytic activities of FMDV L_{pro} implicates cleavage and degradation of RLR signaling proteins, not its deISGylase/DUB activity, in type I interferon suppression. *PLoS Pathog.* 16, e1008702.

Volz, E., Mishra, S., Chand, M., Barrett, J.C., et al., 2021. Assessing transmissibility of SARS-CoV-2 lineage B.1.1.7 in England. *Nature* 593, 266–269.

Walker, F.C., Hassan, E., Peterson, S.T., Rodgers, R., et al., 2021. Norovirus evolution in immunodeficient mice reveals potentiated pathogenicity via a single nucleotide change in the viral capsid. *PLoS Pathog.* 17, e1009402.

Wong, L.R., Li, K., Sun, J., Zhuang, Z., et al., 2020. Sensitization of non-permissive laboratory mice to SARS-CoV-2 with a replication-deficient adenovirus expressing human ACE2 STAR. *Protoc* 1, 100169.

Worrall, E.A., Bravo-Cazar, A., Nilon, A.T., Fletcher, S.J., et al., 2019. Exogenous application of RNAi-inducing double-stranded RNA inhibits aphid-mediated transmission of a plant virus. *Front. Plant Sci.* 10, 265.

WSV2021, Abstracts. <https://www.ws-virology.org/wp-content/uploads/2021/06/Abstract-Booklet-WSV.pdf>, First Meeting of the World Society for Virology: Tackling Global Viral Epidemics. World Society for Virology, (Online event).

Zakharova, N., Kozyr, A., Ryabokon, A.M., Indeykina, M., et al., 2021. Mass spectrometry based proteome profiling of the exhaled breath condensate for lung cancer biomarkers search. *Expert Rev. Proteomics* 18, 637–642.

Zhang, Y.Z., Chen, Y.M., Wang, W., Qin, X.C., et al., 2019. Expanding the RNA virosphere by unbiased metagenomics. *Annu Rev. Virol* 6, 119–139.

Zheng, J., Wong, L.R., Li, K., Verma, A.K., et al., 2021. COVID-19 treatments and pathogenesis including anosmia in K18-hACE2 mice. *Nature* 589, 603–607.

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
<ol style="list-style-type: none"> 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. 	<ol style="list-style-type: none"> 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
<ol style="list-style-type: none"> 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. 	<ol style="list-style-type: none"> 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
<ol style="list-style-type: none"> 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. 	<ol style="list-style-type: none"> 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
<ol style="list-style-type: none"> 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. 	<ol style="list-style-type: none"> 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
<ol style="list-style-type: none"> 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. 	<ol style="list-style-type: none"> 1. Karyn Johnson: Antiviral defences in insects: The impact of miRNA. 2. Myléne Ogliaastro: 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.

Supplement

Submitted talks:

SARS-CoV-2 & COVID-19

This section was subdivided into 5 sessions: *Disease and pathogenesis*, *Immunity*, *Diagnosis & intervention*, *Molecular virology*, and *Transmission & epidemiology*.

A total of 9 submitted talks were provided in the first session about ***Disease and pathogenesis***. These talks reported the effects of SARS-CoV-2 infection on disease outcomes; analysis of the effects of infection on the psychological health and performance of medical students by Nada Eidhah Algethami, effects of disease on cerebral activity by Raphael Gaudin, gastrointestinal symptom predictors of disease outcome by Ghoshal Ujjala, and COVID-19 in the Makkah and high altitude regions of Saudi Arabia, by Fathiah Zakham and RMM Althaqafi, respectively. There were also studies on the effects of inflammatory cytokines as mediators of disease severity by Tracey L. Freeman, comparative analysis of cytokine storms in hospitalized versus non-hospitalized patients by Zaiga Nora-Krukke, detection of virus in various clinical samples by Liba Sokolovska, and analysis of persistent/ chronic infections by Anda Vilmane.

The **session on *SARS-CoV-2 immunity*** comprised 7 talks on the serological cross-neutralization of SARS-CoV-2 spike and NP proteins by Huttunen Moona, neutralization of SARS-CoV-2 variants with BNT162b2 mRNA COVID-19 vaccine by Pinja Jalkanen, pediatric 82% seroprevalence and disease burden of seasonal human coronaviruses by Pekka Kolehmainen, similar immune responses to SARS-CoV-2 or vaccines in HIV-positive versus -negative patients by Jumari Snyman, development of pseudovirion-based immunosensors for SARS-CoV-2 by Maria-Cristina Navas, identification of novel epitopes in SARS-CoV-2, targeted for vaccine development by Shailendra Saxena, and characterization of SARS-CoV-2 antibodies in COVID-19 patients in Latvia by Samanta Strojėva.

The ***Diagnosis & intervention*** session had 8 talks describing the development of a sensitive and specific automated antigen test for SARS-CoV-2 (mariPOC[®]) by Janne O. Koskinen, a SolaVAX whole-virion SARS-CoV-2 vaccine by Izabela Ragan, an intranasal vaccine with ChAd-SARS-CoV2-S by Ahmed Hassan, compounds that block the binding of SARS-CoV-2 with ACE2 by Benjamin Bailly, fusion inhibitory peptides for SARS-CoV-2 infection by Said Mougari, an engineered water nanostructure-based surface disinfection technique against coronaviruses by Anand Soorneedi, and inhibition of SARS-CoV-2 by bismuth drugs by Tao Xuan, and by the ATPase blocker diphyllylin by Štefánik Michal.

Five talks were delivered in the ***Molecular virology*** session. The research presented included analysis of cellular factors required for virus replication, by Aleksandra Synowiec, ARF6-dependent endocytosis into HUH-7 hepatoma cells of SARS-CoV-2, by Carmen Mirabelli, the inhibition of replication using PAMPS-PAaU, by Botwina Pawel, syncytia formation by SARS-CoV-2 variants, by Maaran Rajah, as well as molecular barriers to SARS-CoV-2 in bat cells, by Sophie-Marie Aicher.

Lastly, the session on ***Transmission & epidemiology*** included 5 talks on SARS-CoV-2 concentration for wastewater-based epidemiology by David Goad, wastewater processing for SARS-CoV-2 detection by John Dennehy, viable SARS-CoV-2 particle detection in aerosols, by Fabrizio Spagnolo, and in bivalve mollusks and marine sediments by Jesús Romalde. Finally, William Wilson described the potential role of insect vectors on SARS-CoV-2 transmission.

Human Virology

This theme comprised 3 sessions: *Clinical virology*, *HIV & hepatitis*, and *Molecular virology*. The ***Clinical virology*** track comprised 15 talks on persistence of parvovirus B19 in blood vessels and lymphoid follicles of the intestinal mucosa by Man Xu, on high prevalence of viral DNAs in the human body by Lari Pyöriä, on rotavirus genotyping in children from severe diarrhea in Nigeria by Babalola Oluyemi, on the modular norovirus-like particle vaccine platform by Vili Lampinen, and on polynuclear platinum complexes (PPCs) as antiviral agents on viruses by shielding cells from virus entry, by Benjamin Bailly. The short talks included the use of a nanopore-based sensing technology for real-time detection of noroviruses by Minji Kim, epidemiology of group A rotaviruses in children under 5 in India by Yengkhom Devi, a multiplexed high-throughput serological assay for human enteroviruses by Niila Saarinen, re-infection or re-activation of human bocavirus 1 resulting in neurological deficits and deaths of two young adults by Rajita Rayamajhi Thapa, how viruses may affect cardiac inflammation and myocarditis by Ashwin Badrinath, a positive correlation between EBV and dengue 2 virus infection and in human specimens by Xiao-Mei Deng, an *in-silico* approach to designing subunit-based Zika-virus vaccines by Ezzeman Wahiba, an *in-silico* alternate mechanism for development of anti-influenza virus molecules by Priyanka Saha, inactivation of foodborne viruses with cinnamaldehyde nanoemulsions by Pragathi Kamarasu, and hospital experiences with parvovirus B19 infections and how this could lead to better diagnosis and management by Nema Shashwati.

The ***HIV & hepatitis*** session comprised 7 talks, on HIV-exposed seronegative women expressing high levels of regulatory T cells and low immune activation in the cervical mucosa, by Kristina Broliden, cytotoxic T cell-epitopes of HIV polymerase during early and chronic infection, by Paballo Nkone, diarrheal HIV patients that have frequent co-infection of cosavirus of the *Picornaviridae*, by Esmeralda Vizzi, inflammatory biomarkers and the impact of antiviral therapy in Moroccan HIV patients, by Haddaji Asmaa, the genotypes and drug resistance mutations of hepatitis C virus in Colombia, by Maria Lopez-Osorio, co-infection of hepatitis B and delta viruses as a public-health issue in Colombian indigenous communities, by Melissa Montoya, and the association between TLR4/TLR9 polymorphisms and the risk of hepatocellular carcinoma in Morocco by Zerrad Chaimaa.

A total of 14 submitted talks were provided in the ***Molecular Virology*** track on virus-host interactions involving miRNA profiling of rotavirus-infected cells by Irene Hoxie, in-situ imaging of cutavirus in cutaneous T-cell lymphoma lesions by Ushanandini Mohanraj, characterization of adenoviruses in South Africa by Michaela M. Davids, use of magnetic ionic liquids to concentrate nonenveloped viruses by Sloane Stoufer, the use of oncolytic MVM parvoviruses for anticancer applications, by T. Calvo-López and Carlos Gallego-García, characterization of enterovirus D68 structural protein by Jacqueline S. Anderson and enterovirus D94 entry by Jianing Fu, virus-host interactions of herpes simplex 1 by Jingjing Li and Xueying Liang, the role of host factors in pathogenesis of hepatitis viruses by Tanouti Ikram-Allah and Abounouh Karima, the role of HIV infection on modification of host mRNAs by Masyelly Rojas, and the role of host factors in development of AIDS by Meryem Bouqdayr.

Zoonotic Virology

The abstracts on zoonotic viruses were divided into 2 sessions: *Clinical and Molecular virology*.

The ***Clinical virology*** session included 10 submitted talks, covering the zoonotic impact, epidemiology, and control of camel pox by Ahmed Elhag, small molecule-based inhibitors of emerging RNA viruses by Ludec Eyer, knowledge of Chikungunya virus in medical students in the Caribbean's, by HP Nepal, the WNV circulation in Lebanon by Nabil Haddad, new surveillance approaches for tick borne encephalitis virus by Arnoldas Pautienius, the cache valley virus and Jamestown Canyon virus mosquito vectors across North America by C Dieme, effects of Zika virus infection on RNA editing, inflammatory and antiviral responses in *Aedes albopictus* by Maria Onyango, the incidence of Sindbis virus in hospitalized patients with acute neurological signs in South Africa by Kgothatso Meno, quantification of the transcriptional response of human macrophage cells infected with CHIKV by Madison Gray, and first detection of lymphocytic choriomeningitis virus in neurological cases in Iraq by Hussein Alburkat.

The ***Molecular virology*** session included 11 talks on filovirus VP24 proteins regulating Rig-I and MDA5-dependent IFN- λ 1 promoter activation by Ilkka Julkunen, the structural landscape of dengue- and Zika-virus antibody repertoire by Madhumati Sevvana, mutations within the prM and E protein transmembrane helices disrupting infectious flavivirus particle formation by Conrad Nicholls, AaFurin1 that may have a role in proteolytic cleavage of arboviruses in mosquitoes affecting their infectivity by Carlos Brito-Sierra, new insights into flavivirus biology through high-resolution EM structures of Usutu virus by Baldeep Khare, and the molecular mechanisms of inhibition of tick-borne encephalitis virus by monoclonal antibodies by Daniel Ruzek. Brief reports were also included in this session, on the genetic and in vitro biological characterization of tick-borne Tribec orbivirus, by Tomáš Csank, the role of filovirus VP24 proteins on interferon-induced innate-immunity pathways by Hira Khan, the genomic and structural characterization of Dobrava-Belgrade orthohantavirus in Turkey by Mert Erdin, the anti-chikungunya potency of thymoquinone, a natural drug compound targeting the capsid by Ravi Kumar, and chikungunya antiviral therapy targeting the stress response pathway, by Supreeti Mahajan.

Animal Viruses/Veterinary Virology

This section was subdivided into four sessions: *Molecular virology*, *Veterinary virology*, *Epidemiology*, and *Novel or endogenous viruses*.

Five talks were submitted to the ***Molecular virology*** session covering the characterization of the capsid structure of a novel insect parvovirus by Judith Penzes, the effect of a key signaling protein (protein kinase B) during infection of murine noroviruses by Irene Owusu, the molecular characterization of the bovine Lumpy skin disease, by Shashi Sudhakar, the expression profiles of toll-like receptors of Koala retroviruses by Mohammad Kayesh, and the functions associated with canine parvovirus NS2 in the modification and egress of mRNA, by Salla Mattola.

Three talks of the ***Veterinary virology*** session were about vaccines; the development of an inactivated pentavalent Indian vaccine against Bluetongue virus by Minakshi Prasad, the development of an effective cell culture-adapted attenuated vaccine for African swine fever virus by Manuel Borca, and vaccine cross-protection against circulating canine parvoviruses by Karmar Kour. The three other talks presented the virulence of different viral haemorrhagic septicaemia viruses affecting over 32 fish species, and host responses by Bartolomeo Gorgoglione, the emergence of Tilapia tilapine- and parvoviruses responsible of economic

losses by Win Surachetpong, and the expression of glycoprotein in diagnostic tests for the porcine reproductive and respiratory syndrome virus by Fatema Akter.

The **Epidemiology** session comprised 8 talks, presenting surveys of Bluetongue virus in ruminants of Morocco and camels in Sudan by Soukaina Daif and Shamsaldeen Saeed, respectively, a survey of neurological Middelburg and Sindbis alphavirus in equine and wildlife species in South Africa by Elise Bonnet, a study on the prevalence and evolution of low-pathogenic avian influenza H9N2, affecting poultry in Morocco by Fatima-Zohra Sikht, the first detection and whole-genome analysis of three low-pathogenicity avian influenza viruses in Peru by Gina Castro-Sanguinetti, a surveillance study of West Nile virus in animals displaying neurological disease in South Africa by Caitlin MacIntyre, the epidemiological and molecular characterization of canine bufal- and cachaviruses in grey wolves from Canada by Kelsi Fry, and molecular characterization of canine parvovirus-2, causing hemorrhagic gastroenteritis in domestic dogs in Caribbean island of Nevis by Kerry Gainor.

The session on **Novel and endogenous viruses** included 8 talks about metatranscriptomics from 711 arthropod species, uncovering over 1300 novel RNA viruses by Tianyi Chang, the discovery of a novel fox protoparvovirus, prevalent in Canada by Marta Canuti, the transmission mode and pathogenesis of Koala retroviruses in joeys from Japan, by Abul Hash, the seroprevalence and sequence of atypical porcine pestivirus circulating in Swedish wild boars by Hedvig Stenberg, the phylogenetic characterization of a Bagaza virus from the Himalayan monal pheasant with neurological signs in South Africa by Adriano Mendes, the identification of a novel iridovirus in deep-sea cladorhizid sponges by Gabrielle Large, the development of a rhabdovirus nested RT-qPCR identifying a novel vesiculovirus from bats in the Mediterranean region by Dongsheng Luo, and the non-primate hepacivirus spillover in horses and dogs in Morocco, by Islam Abbadi.

Plant Virology

Interesting studies were also presented by 12 speakers on *Novel plant viruses* and *Molecular plant virology*.

The first session on **Molecular virology** contained 7 talks, which included major developments related to determination of virus-triggered metabolic adjustments to infection by Richard Manasseh, interplay between the host proteins and viruses like potato virus Y by Gnanasekaran Prabu, silencing suppressor and virulence functions of begomovirus-coded proteins by Zhai Ying, demonstration of a novel pro-viral role of host ARGONAUTE1 by Pollari Maija, that virus-coded RNase III (CSR3) suppresses antiviral RNA silencing defense of plants by Linping Wang, the use of RNA interference (RNAi) to manage diverse viruses by Basavaprabhu Patil, and transcriptomic Response to Begomovirus infection in vector *Bemisia tabaci* by Aarthi Nekkanti.

The **Novel virus** session comprised 5 talks about robust diagnostic systems by Susheel Kumar Sharma, RNA datasets having helped in the identification of known and novel and putative novel viruses infecting important crops like spices by Ishwara Bhat, common bean by Aflaq Hamid, and endangered plant species by Kavi Sidharthan; and detection of infectious plant viruses and monitoring of SARS-CoV-2 in wastewater by Ravnika Maja.