



Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Elsevier hereby grants permission to make all its COVID-19-related research that is available on the COVID-19 resource centre - including this research content - immediately available in PubMed Central and other publicly funded repositories, such as the WHO COVID database with rights for unrestricted research re-use and analyses in any form or by any means with acknowledgement of the original source. These permissions are granted for free by Elsevier for as long as the COVID-19 resource centre remains active.

Viral abundance and its public health implications

Editorial overview

Marion Koopmans

Current Opinion in Virology 2013, 3:58–60

For a complete overview see the [Issue](#)

Available online 4th February 2013

1879-6257/\$ – see front matter, © 2013 Elsevier B.V.

All rights reserved.

<http://dx.doi.org/10.1016/j.coviro.2013.01.004>

Marion Koopmans^{1,2}

¹ Laboratory for Infectious Diseases and Screening, Center for Infectious Disease Control, National Institute of Public Health and the Environment, Bilthoven, The Netherlands

² Virology Department, Erasmus Medical Center, Rotterdam, The Netherlands
e-mail: m.koopmans@erasmusmc.nl

Marion Koopmans is professor of public health virology and virologist of the national institute of public health. Her research focuses on food-borne and zoonotic viral diseases, with emphasis on molecular epidemiology and development of methods for and approaches to enhancing early detection of new disease clusters and pandemic preparedness.

The recent innovations in sequencing technology have greatly advanced our knowledge of virus diversity [1,2]. The systematic analysis of samples collected in our environment, including specimens from stool, saliva, respiratory tract, urine, blood and organs of wild animals has led to the realization that we are surrounded by an abundance of viruses. These include human, animal, and plant pathogens, viruses that keep bacterial populations in check, and multiple newly identified viruses for which the role in the ecosystem has yet to be discovered. With this, our notion of the virus world has fundamentally changed, certainly from the anthropomorphic perspective: there are vast numbers of viruses on our planet, and occasionally humans get ill when they are exposed. A huge challenge for the public health perspective is if and how we can predict which are the most serious concerns, and what drives emergence of viruses — that may have cohabited with their animal hosts for centuries — into the human population [2]. There are some examples from 2012 that illustrate this need: an outbreak of hantavirus in Yosemite that resulted in the death of 3 visitors who stayed at a specific area triggered a public health response in the US and in 39 other countries, following notification of all overnight visitors (>200 000) that had stayed in the park during the summer months [3,4]. A total of 10 cases were identified. Similarly, a novel coronavirus causing a severe acute respiratory disease in humans in Saudi Arabia and neighboring countries triggered a full public health response because of the parallels with the emergence of SARS (most probably from bats), and the observation that a broad range of cells could be infected with this virus [5,6]. These examples trigger the questions: what makes them jump species, what can we do to prevent that, and the million dollar question: how can we predict the zoonotic risk? How do we therefore assess the risks of finding viruses in our environment? [2,7].

There may be lessons to learn by reviewing experiences from food and water virologists. This field has dealt with the problems of contamination of food and water as a source of human illness for many years. Most research emphasis here lies on known human pathogens, particularly viruses that are shed in stools and through sewage discharge make it into the environment and back into the food chain. Knowledge of the risk assessment framework that is used to control the safety of our food may help identify research gaps for emerging diseases that potentially could transmit by the same routes. This notion was explored in great detail in a public workshop hosted by the Forum on Microbial Threats of the Institute of Medicine, US in 2011 [8]. This issue of Current Opinion in Virology focuses on a seemingly wide range of topics, all addressing viruses and viral diseases in which environmental transmission is crucial for their epidemiology and impact.

Eva Theres Gensberger and **Tanja Kostić** review advances in virus detection methods from environmental samples, in particular water. This work focuses primarily on detection of viruses that are known to be human pathogens.

While there may be parallels with diagnostic medical or veterinary virology, for instance in terms of choice of primer-sets for PCR-based detection methods for diverse groups of viruses, environmental virology has to overcome significant hurdles. Periodic overflows of sewage treatment plants, a situation that occurs regularly after heavy rain, may lead to contamination of environmental waters harboring shellfish production sites, for instance, but this contamination is not constant, and concentrations may be low. In addition, given the abundance of viruses in our environment, detecting mere presence of a virus or viral RNA or DNA is considered to be insufficient evidence for their potential public health impact, as viral genetic material may persist even when particles are no longer infectious. They describe the challenges (particularly at the level of sample preparation), and some interesting developments aiming at addressing the infectivity question.

Ambroos Stals *et al.* go deeper into the discussion on PCR positivity versus infectivity, now focusing on virus detection in food. Again, this deals with mostly human pathogenic viruses, where the increasing awareness of their potential health risks has led to a push for testing of food items that are most often associated with viral disease outbreaks, such as shellfish, soft fruits, among others. The overwhelming presence of viral RNA in such products (the authors quote recent studies finding up about one-third of soft red fruits PCR positive, and even more of the leafy greens and shellfish samples tested) has triggered studies that try to improve the ability to predict if this presence will lead to human illness.

The review contributed by Alexander Murray moves into animal pathogenic viruses for which environmental transmission is essential, namely viruses affecting aquaculture. This sector is one of the fastest growing food production industries, and a review of emerging infectious disease events has highlighted such changes as important risk factors for disease emergence. This is no different for the aquaculture business, which has been plagued with major disease outbreaks. Alexander Murray discusses the major viral diseases affecting salmon (alphaviruses, birnaviruses, and orthomyxoviruses) and reviews the factors that are known to contribute to viral transmission and spread. He also describes the approaches that have been developed to reduce the risk of disease emergence, and that have had some success in the control of bacterial diseases in the same environment.

So far, there is no evidence of potential zoonotic risk of infections that affect aquaculture. However, the same principles that were discussed by Dr Murray apply for other viruses present in the environment, including viruses from wildlife. This is an area that has received increasing interest with the technological developments, allowing profiling of the presence of viral genomes in

many different types of environments, including stool, throat, blood or tissue samples from animals.

Kris Murray and Peter Daszak discuss how the recent new science is changing the way ecologists view the interaction between wildlife habitats and humans, and present two hypotheses that are currently studied addressing the potential effects of land use change on disease emergence. These hypotheses are not mutually exclusive, and it is conceivable that the evidence for either one may differ for different diseases. The perturbation hypothesis assumes that changes in the environment may disturb an equilibrium that is associated with lower risks of transmission of viruses from wildlife to humans. What exactly that equilibrium is may differ for each ecosystem and its components, including the animals and pathogens in there. The second hypothesis, the pathogen pool hypothesis, assumes that disease emergence related to change of land use is explained by increased exposure of humans (or animals, as intermediate hosts) to a rich pool of pathogens from which they were separated before the change occurred. Understanding the complex processes that drive disease emergence can inform risk-based surveillance strategies and might eventually lead to interventions.

Wild animals may harbor viruses that can transmit to humans, and the wild-life reservoir has been linked to a high proportion of emerging infectious disease events. Bats rank at the top of the list, because the bat virome is highly complex and includes many viruses that are lethal to humans and other mammals. This unique balance of pathogens and hosts, and the specific questions raised on the functioning of the bat immune system are a hot area of research. In their contribution, Ina Smith and Linfa Wang focus on the public health implications of bat derived zoonoses, and review evidence on drivers for disease emergence from recent outbreaks. The example of Nipah virus further illustrates how important it is to understand disease ecology in detail: although originating initially from the same host, drivers for Nipah virus outbreaks in Malaysia differ fundamentally from those in Bangladesh, with respect to the mode of transmission of the virus from bats to humans (with pigs as an intermediate host in the Malaysia situation), and subsequent person to person transmission, observed in Bangladesh only, and linked to specific cultural practices. With that, recommendations for surveillance and control measures differ.

Rodents are another group of animals that host zoonotic viruses, as exemplified by the Yosemite outbreak of hantavirus illness. With the advancing technology, the list of newly recognized hantaviruses has been growing exponentially, as described by Chantal Reusken and Paul Heyman. The recent scientific advances also challenge a dogma in hantavirology, namely that there are unique host-virus combinations. Investigations following the

recent increases in the incidence of hantavirus infections in parts of Europe have given some insights in factors that contribute to emergence, including some that could be used for early warning purposes. However, highly disparate disease incidences in adjacent regions again stress the importance of understanding local ecology.

Conclusions

The exponential increase in sequencing capacity has led to the discovery that viruses are much more abundant than previously thought. This realization requires a fundamental shift in our approach of novel virus discoveries. The contributions in this issue illustrate the challenges of assessing the public health relevance of these findings, which typically requires a risk assessment approach. The authors have listed important data gaps, for which research is needed before we can move from response to outbreaks to prediction and prevention. This will require a systems approach to understand virus ecology and the role of humans as potential targets. Therefore, these new challenges in virology require multidisciplinary research collaborations, in addition to in depth pathogen-specific virological expertise.

References

1. Williamson SJ, Allen LZ, Lorenzi HA, Fadrosch DW, Bami D, Thiagarajan M, McCrow JP, Tovchigrechko A, Yooseph S, Venter JC: **Metagenomic exploration of viruses throughout the Indian Ocean.** *PLoS ONE* 2012, **7**:e42047 <http://dx.doi.org/10.1371/journal.pone.0042047> Epub 2012 October 17.
2. Woolhouse M, Scott F, Hudson Z, Howey R, Chase-Topping M: **Human viruses: discovery and emergence.** *Philos Trans R Soc Lond B Biol Sci* 2012, **367**:2864-2871 <http://dx.doi.org/10.1098/rstb.2011.0354>.
3. Centers for Disease Control and Prevention (CDC): **Notes from the field: hantavirus pulmonary syndrome in visitors to a national park — Yosemite valley, California, 2012.** *MMWR Morb Mortal Wkly Rep* 2012, **61**:952.
4. Roehr B: **US officials warn 39 countries about risk of hantavirus among travellers to Yosemite.** *BMJ* 2012, **345**:e6054 <http://dx.doi.org/10.1136/bmj.e6054>.
5. Zaki AM, van Boheemen S, Bestebroer TM, Osterhaus AD, Fouchier RA: **Isolation of a novel coronavirus from a man with pneumonia in Saudi Arabia.** *N Engl J Med* 2012, **367**:1814-1820 <http://dx.doi.org/10.1056/NEJMoa1211721> Epub 2012 October 17.
6. Müller MA, Raj VS, Muth D, Meyer B, Kallies S, Smits SL, Wolny R, Bestebroer TM, Specht S, Suliman T *et al.*: **Human coronavirus EMC does not require the SARS-coronavirus receptor and maintains broad replicative capability in mammalian cell lines.** *MBio* 2012, **3** <http://dx.doi.org/10.1128/mBio.00515-12> pii: e00515-12.
7. Chan JF, Li KS, To KK, Cheng VC, Chen H, Yuen KY: **Is the discovery of the novel human betacoronavirus 2c EMC/2012 (HCoV-EMC) the beginning of another SARS-like pandemic?** *J Infect* 2012, **65**:477-489 <http://dx.doi.org/10.1016/j.jinf.2012.10.002> Epub 2012 October 13.
8. Institutes of Medicine (IOM): *Improving Food Safety Through a One Health Approach.* Washington, DC: The National Academies Press; 2012.
1. Williamson SJ, Allen LZ, Lorenzi HA, Fadrosch DW, Bami D, Thiagarajan M, McCrow JP, Tovchigrechko A, Yooseph S,