

## Editorial: An expanded view of viruses

Viruses are ubiquitous, and are important in medicine, biology, biotechnology and ecology. All kinds of cells can be infected with viruses, and sometimes, a particular cell is infected with different viruses at the same time. The virus particle, ‘virion’, is composed of the viral coat proteins sheltering the viral genome, and is often surrounded by a lipid ‘envelope’. A virion is small compared to cells, and when it enters cells gives rise to infection distinct from an intracellular bacterial pathogen (Lwoff 1957). A virus-infected cell has a profoundly altered homeostasis due to numerous interactions between cellular and viral components. This leads to evolutionary pressure on both virus and host, and argues that viruses belong to the tree of life (Ludmir and Enquist 2009).

Our cells can be infected by viruses causing acute disease, such as respiratory disease by influenza virus or rhinoviruses, or chronic disease, such as hepatitis or immune deficiency. However, most viral attacks on cells are fended off, or the spread of viruses in an infected organism is restricted, and infection abrogated. By virtue of triggering host defense, viruses have been major drivers of host evolution, and contributed an estimated 30% of the adaptive changes in the human proteome (Enard *et al.* 2016). This is much more than the well-investigated innate immunity factors, such as interferon or interferon-stimulated genes arguing for the existence of a network of proteins that protects cells from viral attack. Other antiviral networks are based on DNA and RNA immunity mechanisms, and may complement the protein network (Forsdyke, Madill and Smith 2002; Guo and Steitz 2014; Lander 2016). When viruses such as filoviruses or avian influenza change their hosts, they hit networks not adapted to these pathogens and cause extensive human disease. Thus, a key challenge is to understand the nature of the protective networks, and sort out their strengths, weaknesses and adaptability.

In this series of *FEMS Microbiology Reviews*, a set of nine articles provides insights into the wealth and diversity of virus research (for a schematic overview, see Fig. 1). The articles cover filamentous bacteriophages attacking biofilms (Mai-Prochnow *et al.* 2015), and phage–bacteria coevolution (Koskella and Brockhurst 2014). The articles bring together results from computational and wet lab studies of bacteriophage–host interactions (Edwards *et al.* 2016), and provide insights into comparative Ebola virus genomics (Jun *et al.* 2015). The issue also features an impressive layout of the currently understudied and potentially high-risk filoviruses (Burk *et al.* 2016). Other articles discuss zoonotic viruses and their potential pandemic threats (Van Breedam *et al.* 2014; Cruz-Oliveira *et al.* 2015; Richard and Foucher 2016). The issue concludes with a discussion of the recently

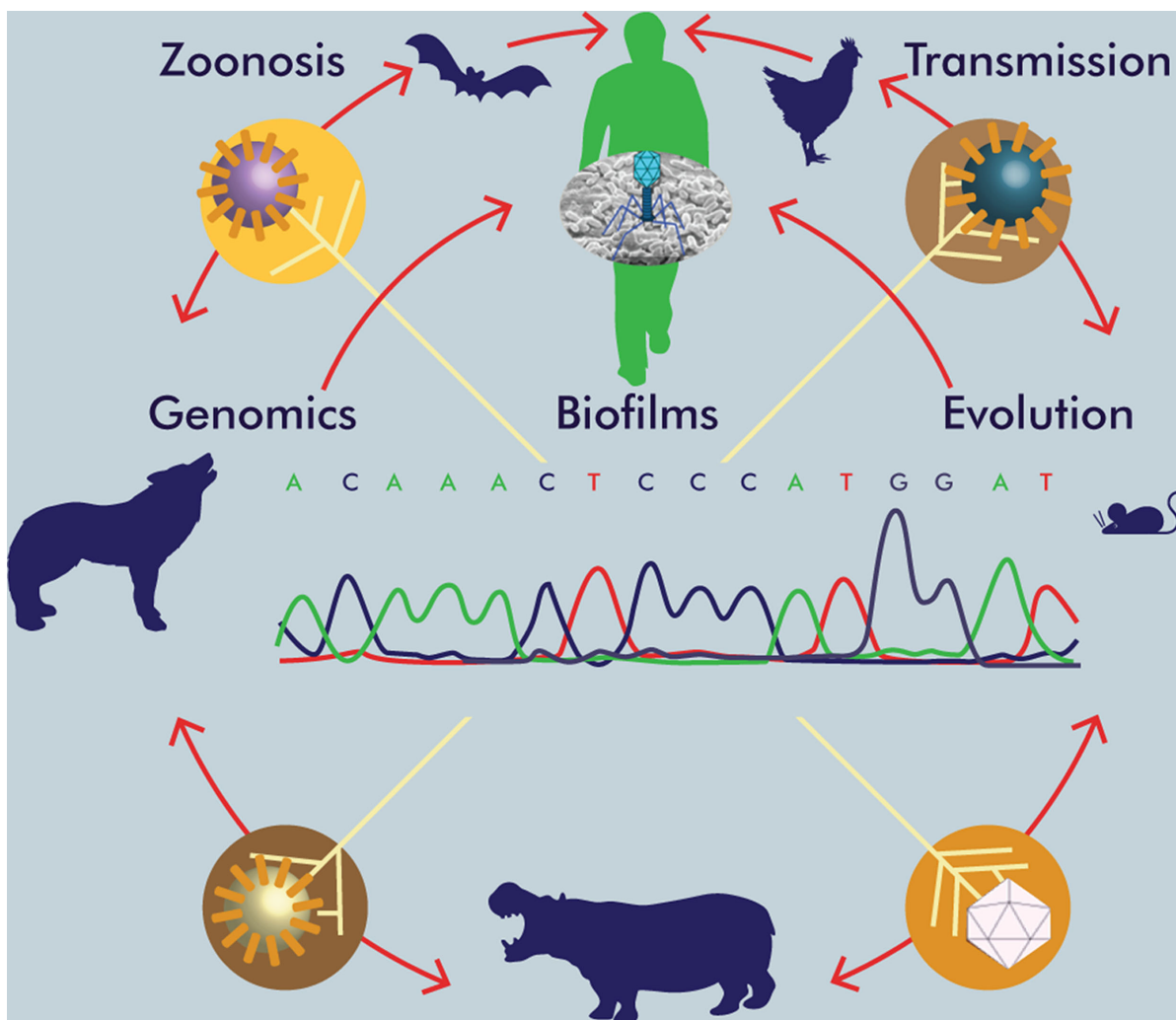
discovered giant viruses, which started to blur the boundaries between viruses and cells (Abergel, Legendre and Claverie 2015).

Virions have many different shapes—spherical, icosahedral, helical, bullet shaped or pleomorphic. Single-stranded DNA or RNA viruses and phages can be as small as a ribosome of about 25 nm, and giant viruses as big as a bacterium of several micrometers. Among the simplest viruses are bacteriophages, arguably the most abundant and diverse biologicals on Earth. Bacteria–phage relationships have far-reaching consequences, which include massive effects on the carbon cycle in the deep sea by turning over bacterial biomass (Danovaro *et al.* 2008). They also include bacterial virulence in eukaryotic hosts. Mai-Prochnow *et al.* (2015) describe how filamentous phages contribute to disease phenotypes caused by bacterial hosts. These phages infect Gram-negative bacteria, and can integrate into the host genome as prophages. For example, the CTXphi phage of *Vibrio cholerae* encodes, and horizontally transfers genes that are genetically modulated in the host. In this way, new variants of cholera toxin genes are created causing epidemic cholera disease. Despite their relatively small genomes, these phages exert significant influence on their hosts. They enhance biofilm development, cell motility or fitness to metal resistance, and contribute to the emergence of new pathogenic bacterial strains.

While phages modulate features of their hosts, bacterium–phage coevolution is an important driver of ecological and evolutionary processes in microbial communities with impact on particular bacterial traits. Koskella and Brockhurst (2014) discuss the dynamics of gene networks of coevolving bacteria and phages, and the impact on host communities and environments. This relatively new field offers unique opportunities for studying in real-time coevolutionary processes in both host and parasite under laboratory and natural conditions, and provides glimpses into the impact of environmental factors on coevolution.

Metagenomics is the analyses of viral genetic material isolated directly from the environment. Although it identifies viral genomes in ecosystems, the nature of the hosts remains unknown in many cases. Edwards *et al.* (2016) describe how the use of sequence homology approaches aids in identifying known phage–host pairs. Together with compositional and abundance-based methods, they argue that this is a powerful approach to identify the unknown sequences in viral metagenomes, and aids in illuminating interactions between phages and their hosts. The hope is to use this and similar approaches to predict unknown phage–host interactions with relevance for medical and biotechnological applications.

An increasingly important impact on human health comes from zoonotic viral transmissions which lead to the infection of



**Figure 1.** Virus–host interaction dynamics. A series of nine articles in this issue of *FEMS Microbiology Reviews* sheds light onto selected features of virus–host interaction dynamics. It describes viral zoonosis, transmission, entry, evolution and the potential of viruses to cause pandemic disease, based on genomics in ecosystems, and novel bioinformatics approaches. Other articles discuss the impact of bacteriophages on human disease caused by bacterial, hemorrhagic fever causing filoviruses or the complexity and evolutionary trajectories of giant viruses. This series illustrates the enormous diversity of viruses and their dynamics. Artwork by Valerie Geiger and Urs Greber.

humans with animal viruses, such as Ebola or influenza virus infections. Zoonotic infections are dangerous, as they break through the protective host networks in unprecedented ways, and have the potential for worldwide pandemic virus spreading. A most recent demonstration of this threat is the outbreak of Ebolavirus having caused an estimated 29 000 infections with ~11 300 deaths. Ebolavirus belongs to the family *Filoviridae*, negative-strand RNA viruses, which cause hemorrhagic fever in humans and primates. Typical for RNA viruses, Ebolavirus is not a single strain, but rather a huge number of variants differing substantially at the nucleotide and amino acid sequence levels. Thus, identifying conserved targets for antiviral drugs and highly conserved epitopes informing vaccine development is a major challenge. However, with the advent of novel sequencing methods and bioinformatics approaches, this challenge can now be met. Jun *et al.* (2015) apply bioinformatics tools and reveal considerable sequence diversity between filoviruses that fall into three distinct genera forming this virus family. Of note, sequence variation is scattered throughout the genome unevenly, allowing the prediction of regions that might correspond to rel-

evant B- and T-cell epitopes as well as possible determinants of virulence. This analysis also underscores that the 2014 West African Ebolavirus strain is clearly different from those having caused earlier outbreaks.

The best-studied filoviruses are Ebola and Marburg virus, but a review by Robin Burk and coworkers competently summarizes that there is much more. In fact, there is a substantial number of filoviruses falling into three genera and a total of eight species (Burk *et al.* 2016). These viruses share an overall comparable genome organization and presumably replication strategy. However, owing to high press coverage and the fact that outbreaks have predominantly been caused by Ebolavirus (and to lesser extent by Sudan and Marburg virus), other filoviruses are largely neglected. This emphasis is short-sighted, because it remains unknown where and how filoviruses occur in nature and how they cause zoonotic outbreaks. It is possible that future outbreaks might be caused by these neglected filoviruses, but our knowledge about their biological properties is poor. Part of the reasons is the lack of adequate tools, but also the current focus on Ebolavirus. Thus, as discussed by Burk and colleagues, more

investment is required to decipher the possible zoonotic potential of neglected filoviruses.

The potential for zoonotic transmission and subsequent spread is also a major concern with influenza viruses as witnessed by several pandemics, the last one in 2009. The hallmark of influenza virus is the segmented genome allowing high genetic plasticity by the exchange of segments in cells coinfecting with two different influenza virus strains. One of the genome segments encodes the envelope glycoprotein HA (hemagglutinin) responsible for binding to and entry into host cells. The specificity of HA to attach to distinct receptors on the surface of human cells or cells of reservoir animal species such as pigs or various birds is a major determinant for efficient virus spread (Richard and Fouchier 2016). However, airborne transmission, critically determining pandemic spread, requires additional features such as HA stability and mutations in the genes for viral polymerase activity. Moreover, the driving forces leading to adaptation of influenza virus to novel hosts have to take into account host and environmental factors. In this way, and by including analogies to other airborne respiratory viruses, such as MERS coronavirus or parainfluenza virus, we might be able to better predict key determinants for airborne transmission within newly emerging pathogenic respiratory viruses.

An important prerequisite for zoonotic transmissions of viruses is that the virion enters both animal donor and human acceptor cells. The article by Van Breedam et al. (2014) discusses how mosquito-borne virions, such as Dengue virus, use polysaccharides on glycoproteins and glycolipids of insect vectors and mammalian cells to modulate host interactions. These so-called glycans can serve as receptors for viral lectins, that is, proteins that bind to carbohydrates, or viruses use glycans to bind to host lectins. Glycan-lectin interactions can directly affect virus entry and endocytic uptake, if receptor pairs are involved, or glycans and lectins alone can indirectly act as facilitators of entry (Mercer and Greber 2013; Boulant, Stanifer and Lozach 2015; Yamauchi and Greber 2016). The review by Van Breedam et al. provides numerous examples for glycan-lectin interactions in the context of viral infection and antiviral immunity, and discusses consequences of their variability.

Along similar lines, Cruz-Oliveira et al. (2015) competently summarize our current knowledge how the most frequent arbovirus, Dengue virus, enters host cells. Several candidate entry molecules have been reported mediating viral entry into mammalian and insect host cells, including glycosaminoglycans, the mannose receptor of macrophages, the adhesion molecule of dendritic cells, the lipopolysaccharide receptor CD14 or heat-shock proteins. Equally promiscuous is the entry route used by Dengue virus that appears to depend on the particular cell system applied to study this process, and that might include a direct entry of the viral RNA genome by capsid protein-mediated RNA translocation at the plasma membrane and the endosome. This breadth of entry factors and pathways is likely a reflection of the broad host range and tropism of this virus replicating in various species and tissues. A speciality of Dengue virus is the requirement for proteolytic cleavage of the envelope 'cofactor' prM. Proteolytic cleavage is mediated by the host cell enzyme furin, and can occur both during exit in the Golgi compartment and during entry in the early endosome, thus increasing infectivity of immature (non-infectious) Dengue virus particles. The latter process appears to be of high importance for the entry of virion-antibody complexes that are taken up into immune cells via the Fc $\gamma$  receptor potentially triggering a cytokine storm, which is the hallmark of fulminant Dengue virus disease.

The compilation ends up with an update on the so-called giant viruses, which are much larger and more complex than common viruses and bacteriophages. Abergel, Legendre and Claverie (2015) describe the history, biogenesis and genetic make-up of four new families of 'giant viruses', Mimivirus, Mollivirus, Pithovirus and Pandoravirus. These viruses can be 'infected' with smaller viruses, and are thought to contain antiviral and perhaps even antibacterial defense systems. The authors end up by providing ideas for new biology, and speculate about the evolutionary origin of DNA viruses.

In conclusion, collective insights from studies summarized in this issue of *FEMS Microbiology Reviews*, and many other data argue for the fact that viruses are virtually without enemies, and may become extinct only if their hosts die out. We have to accept the notion that viruses are part of a tree of life owing to their ever evolving genetic material, which is capable of self-regulation, adaptation and preservation of viral structure and function. The contributions in this issue of *FEMS Microbiology Reviews* also remind us of the dormant potential of viruses to cause unpredictable infectious disease, as has been amply documented in human history (Lederberg 2000).

**Conflict of interest.** None declared.

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