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The ecological virus

Maureen A. O'Malley

CIRID/ALYSAI, University of Bordeaux, France

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ABSTRACT

Ecology is usually described as the study of organisms interacting with one another and their environments. From this view of ecology, viruses – not usually considered to be organisms – would merely be part of the environment. Since the late 1980s, however, a growing stream of micrographic, experimental, molecular, and model-based (theoretical) research has been investigating how and why viruses should be understood as ecological actors of the most important sort. Viruses, especially phage, have been revealed as participants in the planet's most crucial food webs, even though viruses technically consume nothing (they do not metabolize by themselves). Even more impressively, viruses have been identified as regulators of planetary biogeochemistry, in which they control cycles such as carbon, nitrogen and phosphorus – cycles on which all life depends. Although much biogeochemical research black-boxes the entities filling functional roles, it is useful to focus a little more closely to understand how viruses can be held responsible for the global processes of life. This paper will give a brief overview of the history of virus ecology and tease out the implications of large-scale ecological modelling with viruses. This analysis suggests that viruses should be conceptualized as ecological actors that are at least comparable and possibly equal to organismal actors. Ecological agency can therefore be distinguished from standard interpretations of biological agency.

1. Introduction

Viruses might not be considered organisms, but they are established as biologically important actors. All contributors to this special issue would agree with that sentence, no matter how unhappy they are with the existence of the first belief. Reasons for disbelieving the status of viruses as organisms are straightforward. Even though viruses are recognized as evolving entities, they do not metabolize on their own and nor do they have any self-reproducing capacity. However, there are ways in which to understand biological individuals other than as traditionally conceived organisms (Dupré & O'Malley, 2009). One of these is as distributed agents in ecosystems. My aim is to show how viruses as ecological actors bypass debates about whether they can be conceived as organisms, or whether they are alive in the sense single organisms are alive. The discussion that follows will instead draw attention to the importance of the interplay between viruses and microorganisms for an understanding of how biotic and abiotic factors maintain living systems. For philosophers, this sort of interaction is significant because it deflates the importance we traditionally attach to organismality in understanding biological agency. My analysis suggests that a different view of life – one that distinguishes 'life' in general from single living things (Section 8) – may come about via an examination of virus ecology.

I will make this argument first by sketching the development of virus ecology over the last few decades. Much of the traditional biological importance attributed to viruses is because of the medical and agricultural effects of viruses. Since their discovery, viruses have overwhelmingly been studied as disease-causing agents in humans, other animals and plants (Grafe, 1991; Wilkinson, 2001). Even though these host organisms are ecosystems in their own right, and the viruses infecting these hosts are interacting ecologically with them, these macroorganism-based ecosystems are not

E-mail address: maureen.omalley@u-bordeaux.fr.

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my focus. Instead, I will focus mainly on the viruses that depend on bacterial cells,[1] with the aim of developing a wider view of viruses: one that eventually encompasses the planetary biosphere. Doing so allows me to discuss the implications of viruses for marine food webs and broader biogeochemistry, before reflecting on the extended implications of these viral interactions for questions of agency, individuality, and life.

2. The viral transformation of microbial ecology

The consolidation of virus ecology is often identified with formative papers in the late 1980s, in which surprisingly high numbers of viruses were counted in aquatic environments (Bergh, Borsheim, Bratbak, & Heldal, 1989; Proctor, Fuhrman, & Ledbetter, 1988). Broad notions of virus ecology had been around since the 1950s, due to widespread acceptance that viruses circulated in all ecological environments. Much of this earlier literature focused on the isolation and identification of particular aquatic viruses (e.g., Safferman & Morris, 1963; Anderson, Cline, Harris, & Green, 1967), but was hampered by the lack of appropriate methods for precise quantification of viruses and their effects (Moebus, 1987; Torrella & Morita, 1979). If broader ecological implications were discussed, the focus was often on the viruses of microorganisms in sewage or wastewater, and how these entities fared if they found their way to the ocean and other water bodies (e.g., Clarke & Chang, 1959). A consequent line of inquiry investigated the use of viruses to control 'nuisance organisms', such as the cyanobacteria that produced 'algal' growths in waste treatment facilities (Safferman & Morris, 1964, p. 217). As historiographical work on virology notes and early viral ecologists attest, virology and microbiology have been for much of their history dominated by medical and commercial-industrial interests (Cannon, 1987; Grafe, 1991).[2] In many environments not directly related to humans, and especially marine ones, virus numbers were thought to be so low as to be 'ecologically unimportant' (Bergh et al., 1989, p. 467; Greenberg, 1956; Spencer, 1955; Zobell, 1946). Some work did examine virus abundance in relation to microorganismal abundance (e.g., Mitchell & Jannasch, 1969), but made little quantitative headway.

What changed at the end of the 1980s was the quantification of viruses and the degree of agency attributed to them. Direct counting rather than culture-based studies was the methodological change that introduced ecological analysis to the virus world. It had become increasingly clear that large numbers and perhaps the majority of microorganisms could not be cultured in laboratory settings (Staley & Konopka, 1985; Wommack & Colwell, 2000). If the hosts could not be grown, and if the viruses were host-specific, then they could not be grown either. But even though abundance became more calculable with new visualization methods, particle counts on their own were insufficient: what also had to be shown was that viruses caused the lysis or bursting open of cells (Proctor et al., 1988; Suttle, 1994).[3] A variety of micrographic and experimental methods was used to do this, all of them somewhat inaccurate but nevertheless producing useful and sometimes comparable results (Bratbak, Thingstad, & Heldal, 1994; Suttle et al., 1990; Suttle, 1994; Weinbauer, 2004).[4]

Virus numbers were (and continue to be) calculated as an average of 15 viruses for every prokaryote cell, with wide variations in the virus-prokaryote ratio in different environments (Suttle, 2007). The ocean is estimated to contain about 4×10^{30} viruses, making them the most prolific entities in number (but not biomass) in the oceans (Suttle, 2005). They are highly diverse – far more diverse than cellular life (Rohwer & Barott, 2013) – and very little is known even now about the extent of that diversity. Daily virus-induced mortality rates of the entire marine prokaryote community may be as much as 40%, but this depends very much on the growth dynamics of the hosts, plus environmental variables such as temperature and season that can impact viruses directly as well as indirectly via host-cell growth (Suttle, 2007).

The strongest surge of knowledge about viral ecology has occurred via analyses of marine ecosystems,[5] where many environments are oligotrophic (low nutrient). Finding out just how much biological activity is going on even in these ocean 'deserts' required a major rethink of marine ecology and biodiversity at the microscopic and ultimately macroscopic scale. Rather than having inconsequential roles in ecology, viruses were rapidly perceived as active contributors, primarily through their control of prokaryotic microorganisms, which previously were thought to be regulated entirely by predatory protists (protists are eukaryotic microbes). Viruses became increasingly discussed as 'agents of mortality' that are 'major players in the mortality of marine microorganisms' (Suttle, 2007, p. 800). An additional but somewhat lesser ecological role proposed for viruses is as gene-transfer agents between microorganisms (Bergh et al., 1989; Thingstad, Heldal, Bratbak, & Dundas, 1993). Both these activities bestowed the potential to structure not just the size but the constituents of microbial communities (Section 4).

Viruses thus began to fill a theoretical gap in mathematical modelling knowledge about aquatic dynamics and productivity, including carbon production and cycling in particular (Sections 3–5). Large microorganismal predation of smaller photosynthesizing microorganisms was already recognized as insufficient to explain the latter's mortality rates (Fuhrman & McManus, 1984; Servais, Billen, & Rego, 1985; Sherr, Sherr, & Pedrós-Alió, 1989). Even though the protist–prokaryote relationship could be nicely represented as an oscillatory pattern of the sort central to large-organism ecological models (Azam et al., 1983), this predator-prey dynamic only partly captured the fluctuations of microorganismal biomass. Viruses and the dynamics they cause became the ecological explanations of these gaps.

3. The microbial loop and viral shunt

In the oceans, several ecological roles are the focus of efforts to understand nutrient dynamics and biogeochemistry. A key distinction is made between autotrophic and heterotrophic organisms, with the former being primary producers because they fix their own carbon, and the latter being secondary producers because they use organic carbon fixed by other organisms. 'Virioplankton' is the term for aquatic viruses that infect plankton,

[1] The viruses of bacteria (and more rarely, archaea) are usually called bacteriophage or phage. However, I will use 'virus' generically since my discussion ranges across eukaryotic and prokaryotic viruses.

[2] As a referee of my paper helpfully noted, phage have been much more important to basic biology than to medical microbiology. See Summers (1993) for an important step in how this divergence between viral and phage research occurred.

[3] Lytic viruses burst open cells as viral progeny are released. Lysogenic viruses bide their time inside the host genome, and replicate without lysing the host cell. It is the former that are the focus of my discussion and most of the research it reports, simply because lytic viruses are the most studied (Jiang & Paul, 1998).

[4] Molecular methods began to complement high-powered microscopy especially for identification purposes, and models increasingly used to predict the dynamics of different combinations of environment, organisms and viruses (Thingstad & Lignell, 1997).

[5] However, it is widely recognized that viruses play major ecological roles in other environments, such as soil (Williams, Mortimer, & Manchester, 1987), and some of the more general implications of marine virus ecology will apply to these other systems.

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which are free-living aquatic organisms. Plankton themselves can be divided into zooplankton (heterotrophic eukaryotes), phytoplankton (autotrophic prokaryotes and eukaryotes) and bacterioplankton (heterotrophic prokaryotes). Phytoplankton are crucial for understanding the trophic dynamics (who eats whom) of the oceans, and the biogeochemical cycles of the Earth. As oxygen-generating primary producers, phytoplankton form the very basis of life as we know it on the planet (Falkowski, 2012). The numbers, productivity and fates of plankton, especially the smaller plankton, determine carbon, oxygen, nitrogen and other biologically important elemental budgets in the ocean and beyond. The centrality of these primary producers, and the increasing knowledge about interactions between bacterioplankton, phytoplankton and their consumers, meant that new models had to be constructed of ocean food dynamics (Azam et al., 1983; Azam 1998; Fig. 1). These models in turn made findings about the viral control of plankton abundance an empirically and theoretically significant topic.

Viruses infect not only photosynthesizers (autotrophs), but also heterotrophic prokaryotes — organisms that acquire carbon from other organisms rather than fixing it themselves. Studies in the late 1960s and early 70s had indicated very strongly that heterotrophic bacteria are the major consumers in the oceans. They take greater nutritional advantage of the biomass produced by photosynthesizers than do much larger organisms (Azam et al., 1983; Pomeroy, 1974; Williams, 1981). This addition of a 'microbial loop' to the aquatic food chain transformed the existing model of nutrient dynamics in the ocean (Fig. 1). Rather than being a linear chain of nutrients successively supplied to the largest animal predators, the oceanic food web was reconceived as a complex web, with microbes comprising many of the most crucial nodes (Sherr & Sherr, 1991). The addition of viruses a decade and a half later produced another transformation.

Although all elements essential to life are recycled by microorganisms, including nitrogen and phosphorus (which regulate cell abundance because they are essential for cellular growth and reproduction), a common focus of the reconceptualization of marine food webs has been carbon. Dissolved organic matter (DOM) in the ocean is a vast store of organic carbon that is readily assimilated by heterotrophic microorganisms. It is less available to larger consumers simply because of the difficulties and costs for large organisms to take advantage of such diffuse and minute particles. DOM is produced by excretion and cellular breakdown, and consists of nucleic acids, proteins, lipids and carbohydrates. Particulate organic matter (POM) also forms a tremendous carbon resource of material that is larger in size and thus more valuable to larger organisms.[6] Somewhere around 20% of the carbon fixed by photosynthesizing organisms is 'short-circuited' or 'shunted' by viruses into pools of dissolved organic matter as the viruses lyse living cells (Wilhelm & Suttle, 1999; Fuhrman, 1999; Figs. 2 and 3). These pools are then further recycled, primarily by microorganisms, whose vulnerability to viruses ensures the process loops endlessly, albeit with evolutionary buffering as hosts acquire resistance (Lennon & Martiny, 2008).

What the viral shunt model means biologically and ecologically is that carbon is recycled most intensively within the 'semi-closed' microbial loop (Fuhrman, 1999, p. 545). This shunting changes the dynamics of nutrient flow across all marine ecology, right up to the largest animal consumers.

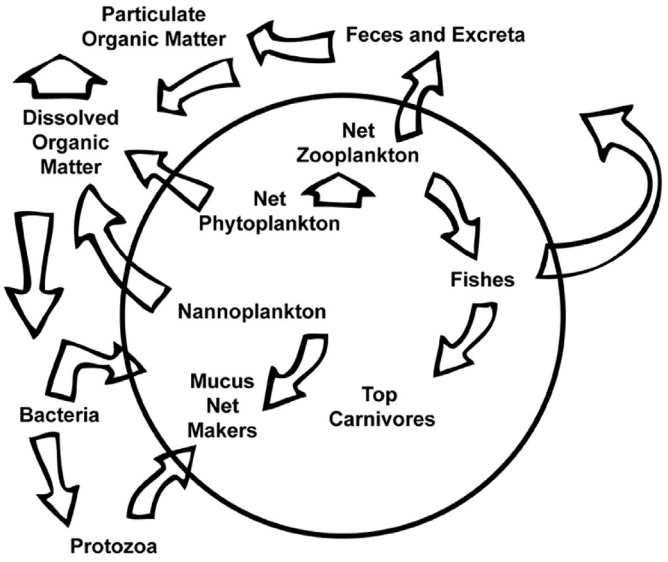

Fig. 1. The microbial loop. Pomeroy (1974) drew the traditional marine food web inside the circle, and the new microbial players and their dynamics as arrows that 'looped' outside it. Azam et al. (1983) coined the term 'microbial loop' and elaborated on its implications. 'Nannoplankton' refers to very small plankton ('nano' is the more conventional spelling), which sometimes include the very smallest 'picoplankton'. Nanoplankton are smaller than 'net' or microplankton. 'Protozoa' are heterotrophic protists, and 'mucus net makers' are suspension feeders that produce extracellular mucous nets to catch and transport food particles (including small organisms). Reproduced with the permission of Oxford University Press (see Pomeroy, 1974).

> 'Ironically, the results of active phage lysis are higher levels of bacterial production and less transfer of organic matter to higher trophic levels' (Wommack & Colwell, 2000, p. 94).

This is 'ironic' because lysis entails the destruction of bacterial cells, and yet that very destruction contributes to the maintenance of the planet as a microbial world. Modelling how this is achieved, both qualitatively and quantitatively, has become a major focus of marine virus ecology.

4. Viral structuring of microbial communities

For microbial populations and communities, viruses can be understood as selective agents. In an important respect, they are agents of negative frequency-dependent selection (Winter, Bouvier, Weinbauer, & Thingstad, 2010). A key model for understanding viral dynamics in microbial communities involves the mechanism of 'killing the winner' (Thingstad & Lignell, 1997, p. 24).[7] Viruses appear to be more likely to infect and lyse fast-growing cells, because this ensures faster viral replication. Any microorganismal population that grows very rapidly will thus be preyed on more heavily by viruses, thereby 'punishing' the 'winners' of interpopulational competition (Thingstad et al., 1993). In other words, the less competitive populations end up surviving and even flourishing — but not too well, or they then become favoured virus targets themselves (Winter, Smit, Herndl, & Weinbauer, 2005). These ongoing oscillations in competitiveness also control virus numbers, which need to be understood better with regard to lysogenic viruses and what switches them to a lytic cycle (Paul, 2008). The

[6] In fact there is a continuum between DOM and POM, which are usually distinguished by the filtration methods (especially filter size) deployed by researchers (Azam & Malfatti, 2007).

[7] Killing the winner is not the only model attempting to represent and explain virus-host dynamics, but it is a major one. For some new but probably non-competing models, see Giovannoni, Temperton, & Zhao (2013).

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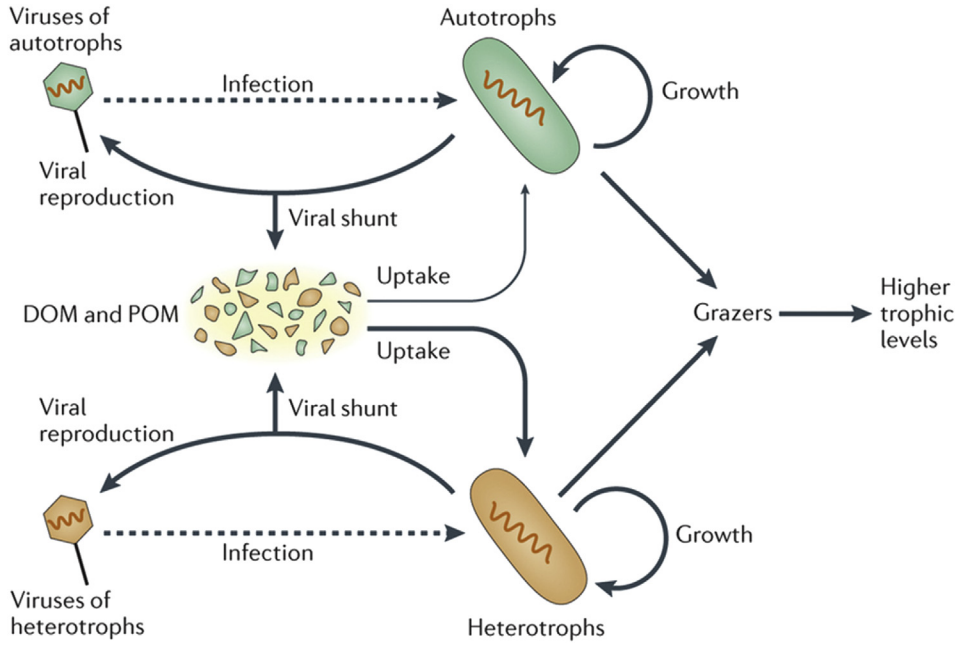

Fig. 2. The viral shunt model, representing trophic roles and carbon-based interactions (Jover, Effler, Buchan, Wilhelm, & Weitz, 2014). DOM = dissolved organic matter; POM = particulate organic matter. Remineralization (converting back to inorganic compounds) of carbon, nitrogen and phosphorus also occurs and is of major biogeochemical importance, but is not represented in the figure. Reprinted by permission from Macmillan Publishers Ltd: Nature Reviews Microbiology (Jover et al.), copyright (2014).

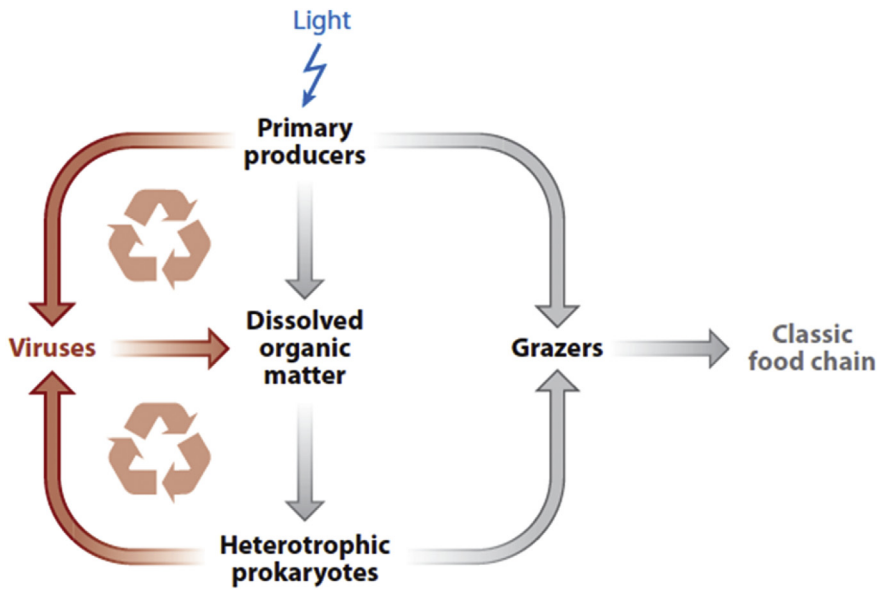

Fig. 3. An even more abstracted version of the viral shunt model (Breitbart, 2012). This visualization represents the key dynamics more schematically than Figure Two, with the viral shunt depicted in red on the left half of the diagram. Reproduced with permission of the Annual Review of Marine Science, Volume 4, 2012. © Annual Reviews.

growth-related culling of populations by viruses produces very different community structures from the 'grazing' of predatory organisms, which would not discriminate their prey in the same way (Fuhrman & Noble, 1995). However, the two processes work together. 'Killing the winner' produces many coexisting species, and these are kept to a size and nutrient-using balance by size-selective predators such as protists (Thingstad, 2000).

What explains this dynamic mechanistically? Resistance and sensitivity are key factors. Resistance to viruses has a cost. Fast-growing microorganisms often jettison resistance and its costs. The most common lineages tend to be, therefore, slow-growing but virus resistant. The other strategy is to grow rapidly but be virus-sensitive and thus prone to 'boom-and-bust' cycles (Jacquet, Miki, Noble, Peduzzi, & Wilhelm, 2010; Suttle, 2007). Population explosions of microorganisms also make it easier for viruses to come into contact with cells and lyse them, and thus contribute to the maintenance of stable host–virus relationships (Brussaard, 2004). In addition, viral lysis may liberate nutrients that then trigger microbial population explosions (Weitz & Wilhelm, 2012). Many limitations of the killing-the-winner model have been recognized (e.g., Hewson & Fuhrman, 2006), but the overall dynamic is detected repeatedly, and simple forms of the model found to be

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highly predictive (Winter et al., 2010). One limitation is that change in nutrients induced by lysis (e.g., more carbon, nitrogen etc) is not part of the model (Winter et al., 2010), and yet one reason for learning about population and community structure is to extrapolate to biogeochemistry (see Section 5).

Another factor that structures microbial populations is the lateral gene transfer (LGT) carried out by viruses (Morgan, this issue; Weinbauer & Rassoulzadegan, 2004). This can occur directly in the form of transduction, which is the process by which viruses transport additional 'foreign' DNA into the host cell and genome. LGT can also happen indirectly in the form of transformation, when environmental DNA from virus-lysed cells and other sources is taken into the cell by 'competent' microorganisms (Fuhrman, 1999; Jacquet et al., 2010). Although many viruses are host-specific, genes are nonetheless known to be available globally through viral action and their global uptake is calculated to be very frequent (Rohwer & Thurber, 2009). The ability of viruses as virions (encapsulated particles) to drift long distances and times between hosts contributes to this distribution and frequency of LGT. Viruses able to target multiple hosts are not uncommon (Hewson & Fuhrman, 2006; Holmfeldt, Middelboe, Nybroe, & Riemann, 2007), even if interkingdom transduction of DNA rarely happens. Much of this virus-transduced DNA may be removed from the host cell's genome, or make no difference over short and long evolutionary periods. Some of it, a tiny minority, may actually benefit the host.

In marine ecology, a famous example of what might initially be understood as beneficial virus genes occurs in cyanophage (viruses of cyanobacteria), which transport photosynthesis genes they cannot use themselves (Mann, Cook, Millard, Bailey, & Clokie, 2003). The proteins synthesized from these genes in the host cell undergo considerable damage from light, and the virus genes may replace broken versions and thus contribute to the robust functionality of photosystems in these hosts (Lindell, Jaffe, Johnson, Church, & Chisholm, 2005; Sharon et al., 2009). Virus genes thereby increase the photosynthesis and carbon fixation rates of the cyanobacteria (Weitz & Wilhelm, 2012), thus adding yet another boost to ongoing geochemical cycling. In an interesting phylogenetic twist to the story, the cyanophage photosynthesis genes are originally cyanobacterial and appear to have been acquired and passed around by viruses (Lindell et al., 2004). In addition, other metabolism genes, particularly those involved in carbon metabolism, have been detected in many marine viruses. Such findings suggest that in many circumstances viruses are 'reprogramming' their hosts metabolically, with accompanying effects on biogeochemical cycles (Hurwitz, Hallam, & Sullivan, 2013; Section 5). These sorts of findings give some empirical heft to the common metaphor of a global gene pool distributed by viruses (e.g., Hendrix, Smith, Burns, & Ford, 1999; Weinbauer & Rassoulzadegan, 2004; Zeidner et al., 2005). It is not just lytic viruses that dip into this 'pool'. Lysogenic viruses in the ocean and elsewhere often carry host fitness-enhancing genes that become integrated in the host genome and expressed (Brüssow, Canchaya, & Hardt, 2004).

But should this 'sharing' be called cooperation? Aren't viruses the ultimate selfish agent (see Pradeu, this issue)? We can think about these questions by going back to the viral photosynthesis genes and their transfer of function to the host. What do such transfers do for the virus? By supplying the relevant photosynthesis genes, which the host normally stops repairing when infected by a virus, cellular metabolism continues and generates more resources for viral replication (Mann, 2005). In other words, the more energy the host produces, the more phage can be reproduced (Lindell et al., 2005). So even though the host can maintain photosynthesis while occupied by a reproducing virus, it gains no advantage itself and probably imperils its neighbouring relatives by increasing virus numbers. The advantages accrue to the virus. However, from a broader ecological point of view things are not so cut and dried. It doesn't actually matter for ecosystems whether the virus behaviour is cooperative or exploitative in a tightly defined evolutionary-theoretic sense. What matters is the ecosystem effect. In other words, 'although viruses can have deleterious effects to the hosts they infect and lyse, they may nonetheless have a stimulatory effect at population and ecosystem scales' (Weitz et al., 2015, p. 1362). We might be tempted to think of this as an ecosystem-scale view of cooperation (or perhaps more neutrally, of collaboration) – a view that will become clearer in Section Eight.

The overall impact of viruses on macrobial communities is largely one of increased resources (e.g., DOM) – including more 'efficient' use of less preferred resources because these are what the less competitive organisms subsist on (Rodriguez-Valera et al., 2009) – and increased diversity due to combinations of gene transfer, arms races, and killing the winner. Viruses can therefore be conceived as driving microbial and other cellular evolution via mechanisms that structure populations ecologically as well as over long-term evolutionary time (Koonin & Wolf, 2012). Ecology, however, focuses on the ecosystem roles of such entities without particularly caring whether they are cellular or non-cellular (see Section 7). And although viruses may have causal impact on the structure of any community, including large-organism communities (Bratbak et al., 1994), it is in the ability of viruses to regulate biogeochemistry that the broadest scope of their activity can be understood.

5. Viruses as biogeochemical agents

Biogeochemical cycles are what make life the way it is on our planet. Every cycle on the Earth, from carbon to oxygen to sulphur, is mediated biologically and often driven by microorganisms (Falkowski, Fenchel, & Delong, 2008). But if the microbial uptake of elements is significantly regulated by viruses, then so are the biogeochemical cycles. Viruses also contain carbon, nitrogen and phosphorus in their virion or particle form (a genome encased in a protein case), and the contribution via these particles can affect the phosphorus and possibly the nitrogen cycle (Bratbak et al., 1994; Jover et al., 2014). But this is a more 'passive' sort of effect, and not what I am interested in. It is virus *activity* that is my focus, and their management of the carbon cycle illustrates very effectively what I mean by this distinction (which is elaborated in Section 7).

The carbon cycle is essentially the conversion of inorganic carbon in the form of carbon dioxide into organic carbon compounds and back again. By removing CO_2 from the ocean, not only do autotrophic microorganisms fix carbon, but they also pump it into the ecosystem for use by heterotrophs. But as side effects, the uptake of CO_2 in the ocean means the waters are less acidic due to the presence of less dissolved inorganic carbon (e.g., carbonic acid), and the atmosphere less of a greenhouse (carbon gases such as CO_2 and methane are often referred to as greenhouse or insulating gases). Plants, also autotrophs, regulate the elemental composition of the atmosphere and carbon availability on land, but despite their far greater size produce only the same amount of organic carbon as phytoplankton (Falkowski, 2012). When viruses are factored into these dynamics as the viral shunt mechanism, they increase primary productivity by making more inorganic nutrients available to the autotrophs, and they boost secondary productivity by increasing the recycling of organic material (Weitz et al., 2015). The implications of such involvement are planet-wide, and encompass climate change.

'Linking viruses to the global climate system may at first seem rather far fetched' (Thingstad et al., 1993, p. 211), but there are

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reasons and models to be less sceptical. Section Three showed how viruses intervene in the biological pump that cycles carbon from the atmosphere through the ocean surface and depths then back again. Phytoplankton, as primary producers, and bacterioplankton as organic carbon consumers and CO_2 releasers, have a global impact on atmospheric CO_2 levels and thus climate (Falkowski, Barber, & Smetacek, 1998). When viruses shuttle carbon from primary to secondary producers, and from secondary producers back into the ocean (including the sequestering of carbon in ocean sediments), they play an important regulatory role that contributes to climate change (Danovaro et al., 2011). The warmer the planet becomes, the stronger this impact is likely to be. Higher temperatures often appear to increase virus activity and numbers, with associated effects on hosts and geochemical cycles. However, predictions about the interactions of viruses, ecosystems, geochemical cycles, and climate change are still vague, because virus interactions and effects are rarely included in climate change models (Danovaro et al., 2011). This is a curious oversight, not just because empirically viruses play major causal roles in processes crucial to climate change, but also because virus activity has tended to be modelled very effectively at other ecosystem scales.

6. Viruses as theoretical agents

So far, I have made a case for viruses as ecological actors mostly on the basis of observations of and interventions in real-world ecologies. An additional and closely connected incentive to understand viruses as ecological actors comes from their role in ecological modelling. Models have made important contributions to virus ecology, right from the early days of micrographic observations. In part this was because data and precise quantification were simply not available. Models had to be used to infer processes from patterns, and allow interpretations of sparse data. Virus–microbe relationships have repeatedly been the focus of models that are mathematical and material (i.e., organismal systems),[8] the latter most notably in chemostats.

Chemostats are input–output devices that support populations and communities of microorganisms and viruses. Resources and population numbers can be tightly regulated and measured repeatedly; they are also captured very effectively by mathematical equations. Early chemostat work elaborated on standard Lotka–Volterra equations describing predator-prey oscillations. Chemostat models can also be used to test the principle of competitive exclusion, which states that different 'species' (often operationalized as genotypes) that are dependent on identical resources cannot coexist (Levin, 1972). An early influential instance of such research used a single limiting resource to grow two bacterial populations that were respectively resistant and sensitive to viruses (Levin, Stewart, & Chao, 1977).[9] By adding the virus as a predator, an amended version of competitive exclusion theory predicts the equilibrium of all the entities concerned (bacteria and viruses). Without the predator, and with two consumers and a limiting resource, one consumer would go extinct (unless mutation and evolutionary divergence, plus niche partitioning in general are factored in). The experimental instantiation of the model in this chemostat research agreed with those theoretical predictions. The material system thus demonstrated important modifications to the basic competitive exclusion model. The addition of a predatory agent (the virus) brought about otherwise unachievable coexistence between the two consumers (Levin et al., 1977).

These results and many subsequent versions of this experimental model system have been carried out materially in chemostats, in which diversity – genetic and environmental – is necessarily underrepresented (Weitz & Wilhelm, 2012). But by drawing parallels to non-specific stable equilibrium models in wider ecology, Levin et al.'s (1977) model demonstrated the value of closer specification of the functional roles of organisms contributing to the equilibrium. Not only do such material implementations become specific and thus biologically realistic enough to be more predictive, but also the theoretical model itself becomes more fine-tuned in the process (Weitz & Dushoff, 2008). Much subsequent modelling work has continued to make mathematical and chemostat models of virus-prokaryote interactions more realistic and precise (e.g., Middelboe, 2000; Bohannan & Lenski, 2000).

A standard concern about material model systems in ecology is that they oversimplify complex relationships (Jessup et al., 2004). Ecological models of virus interactions deal with such concerns by acknowledging the necessary idealization in such models, and by working with the unavoidable tradeoffs between simplicity and complex realisticness (e.g., Thingstad, 1998; Lenski, 1988; Levin et al., 1977). Simplifications are necessary for any modelling process, but models need sufficient biological detail to maximize their explanatory power. Prokaryotic consumers on their own are not sufficient to model marine dynamics, and nor are consumers and their resources. But mathematical and material models that include both of these *plus* viruses are going to capture more effectively the nutrient dynamics that affect the biogeochemical cycles of the earth (Murray & Eldridge, 1994; Thingstad & Lignell, 1997).

7. Viruses as distributed agents

One conclusion that even a brief overview of virus ecology reaches is the importance of viruses as model agents for microbial ecology. At population and community scales, especially but not only in the microbial world, viruses need to be included as ecological actors (or at least their omission justified – see, e.g., Legendre & Rivkin, 2008). And at the scale of nutrient and biogeochemical cycles, major causal forces would be left out if viruses were not part of the modelling (Weitz et al., 2015). Viruses lend themselves so readily to modelling efforts because they are simple structures with specific but strong collective effects. Some viruses are highly tractable in laboratory settings (Lenski, 1988), and can thus be conceived as powerful model 'organisms'. The model-ability of viruses as entities holding roles normally attributed to organisms (i.e., predators) is closely linked to their powers of agency. Put slightly differently, the epistemological value of viruses in models hinges on their biological agency. This suggests that a valuable philosophical lesson from virus ecology is that biological agents of the most active and interactive kinds are not necessarily organismal agents. Although this may be obvious to evolutionary virologists and other biologists, most of whom accept that viruses interact and evolve but are not organisms (e.g., Van Regenmortel, 2010; Moreira & López-García, 2009), it is not always so clear in philosophical discussions of biological agency.

For many philosophers, agents that are not reasoning or feeling are only carrying out 'weak' activities (e.g., Wilson & Shpall, 2012). But weak activity is good enough for this discussion; in fact, we might often want a view of agency or activity that is unencumbered by psychology and cognition. Philosopher Rob Wilson has a helpful ecumenical definition of agents: 'an agent is an individual entity that is a locus of causation or action' (2005, p. 6). All agents are

[8] There is a well-established philosophical tradition of distinguishing mathematical and material models. Both are accepted as genuine models (e.g., Weisberg, 2013).

[9] Levin et al. (1977) initially modelled mathematically and materially the equilibrium achieved between just one consumer (a phage-resistant bacteria) and a phage predator. I discuss only the two-consumer, one-predator models (also mathematical and material).

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causes, but not all causes are agents because they are not necessarily individual entities. As well as organisms, Wilson nominates genes, proteins, biochemical pathways and other entities as agents. But as in many discussions of individualized agents in biology, it is organisms that are paradigmatic mechanistic agents (Wilson, 2005, p. 7). And organisms are 'living agents' (p. 8), which means they have properties additional to biological agents. Is this view of agency what is indicated in the discussion above of viruses as ecological entities?

One thing ecology does in general is diminish the conceptual and epistemic importance of *single* individual organisms. The effects of any single organism are usually insignificant in an ecological framework. Instead, ecology relies on a distributed notion of individual, in which biological coherence and activity are distributed across collections of single organisms and their parts. These distributed agents have causal effects, but that causality is the aggregated activity of a loosely bounded collectivity: the distributed individual. These individuals may be single-species populations, multispecies groups (communities) or functional types (collective ecological actors with specified effects).

Ecology is the study of those populations, communities and ecosystems, all of which are aggregates of single organisms and their parts. Evolutionary biology also studies single-species aggregates of organisms, but very often, evolving populations are being tracked as *outcomes* of cumulative events (i.e., fixation of mutations). In fact, there are arguments against an 'agential' view of evolution, because of problems to do with the notion of purposeful agents (Godfrey-Smith, 2009, p. 10). The main purported difficulty with this sort of agential view is that it offers the wrong epistemic resources to a project that requires less of a 'psychological' narrative and more emphasis on the abstracted modelling necessary to population thinking in evolutionary biology (Godfrey-Smith, 2009). The notion of 'agent' that I am exploring here, however, is a distributed notion of causal individuality, where aggregated individuals have functional effects (e.g., predators, consumers, etc) on different scales of biological organization that range from microorganismal populations to global ecosystems. This notion thus binds together the model-theoretic and empirical senses of agency discussed in the previous sections.

From an ecosystem perspective, causal agents are 'functional types' (Legendre & Rivkin, 2008, p. 290) that carry out particular classes of activity in a designated system, such as viruses do in the ocean. Does this mean ecological agents are not biological agents in a classic organismal sense? Only if that means single organisms must underpin conceptually any account of biological agency. Ecology very clearly offers us an alternative conception: a distributed notion of agency that is central to understanding aggregated and large-scale biological interactions. Biological entities other than viruses also exhibit distributed agency in ecosystems (e.g., particular sorts of microbial metabolizers in biogeochemical cycles), but for many cognitive and epistemic purposes, viruses are an ideal and thought-provoking exemplar of such agency. They are particularly interesting in this regard because of being situated on the cusp of biotic and abiotic material. This means viruses also suggest alternatives to the idea of 'living agents' being biological agents of a privileged sort. Instead, the notion of viruses as distributed agents is conducive to a notion of 'life' as a web of interactions between biological entities.

8. General conclusions about virus ecology

Once viruses are identified as ecological agents, it becomes tempting to reimagine ecology from the viewpoint of viral agency. 'Virocentric ecology' is how some viral ecologists have distinguished the ecological study of viruses from 'our normal anthropocentric' ecology (Hurst & Lindquist, 2000, p. 3). Ecological virocentrism builds on raw empirical facts about viral abundance, ubiquity and genetic diversity. Its proponents argue that sheer numbers combined with extensive causal impact mean that ecology should be understood from a viral perspective (Rohwer & Thurber, 2009). Evolutionary discussions of virocentrism (e.g., Koonin & Dolja, 2013) advocate a view of evolution very compatible with virocentric ecology, in that the former focuses on virus-host coevolution (as would most virus ecologists). However, for ecosystem analysis it is ecological roles that matter (Konopka, Lindemann, & Frederickson, 2015), rather than the phylogenetic lineages emphasized by evolutionary virocentrism. Although some uses of virocentrism might imply that viruses can be seen as little organisms (e.g., Andrewes, 1965), from the distributed agency point of view in ecosystem analysis, organismality doesn't really matter.

Conceiving agents as causal nodes in the function of ecosystems is one reason why biogeochemical ecosystem analysis is (in)famous for its 'blackboxing' of organismal entities as it tracks and models flows of chemistry and energy in the oceans and on the rest of the planet (Odenbaugh, 2006; Rivkin & Legendre, 2002). 'The metaphysics of ecosystem ecology considers organisms indirectly at best in terms of ecological energetics', says philosopher of ecology Jay Odenbaugh (2006, p. 397). Taking this metaphysics a bit further, research in virus ecology shows the necessity of understanding viruses as distributed agents that form various nodes in food chains and biogeochemical cycles. This agency is what explains energetic dynamics and outcomes. The very possibilities of modelling nutrient flows requires conceiving viruses as agents able to bring about and explain multilevel effects on other forms of biological organization, with at least some reasonably predictable outcomes in a network of multiple biological agents (as functional types). This view may extend so far as to explain life and its organization.

In a recent essay, virus ecologists Forest Rohwer and Katie Barott (2013) propose a virus-driven view of life via an ecological-energetic analysis. In their model, the central explanandum is why on Earth there are so very many viruses on the planet. As mentioned in Section Two, there are at least 4×10^{30} viruses in the ocean, and an estimated 1×10^{31} on the whole planet at any given biological moment. This enormous number of viruses replaces itself in entirety every week – a process that involves prodigious amounts of replication and concomitant resource use by the hosts. Rohwer and Barott suggest that by playing such central roles in food webs and biogeochemical cycles, 'Effectively, the viruses are creating conditions to replace themselves' (2013, p. 291). Now this may be an explanatory step too far for some readers, who will hear 'selfish gene' echoes in this claim, but the point of focusing on viruses and asserting virocentrality has the epistemic aim of constructing ecosystem models as if viruses mattered. They matter both for being explained and for explaining ecologies (I have focused on the latter, and Rowher and Barott on the former). Despite being non-organismal, non-metabolic and probably non-cooperative (in a traditional evolutionary-theoretic sense), viruses explain energy flows, community structure, and population dynamics at a microbial scale and beyond. Because the microbial level of analysis goes on to explain much biogeochemistry and ecosystem interaction, then a virocentric perspective becomes a very useful way in which to view the ecological and evolutionary world.

The notion of viruses as ecological agents is not a piece of casual shorthand, which is the agential view Godfrey-Smith (2009) criticizes, when people say things such as 'tubeworms solve their energy problems by acquiring symbionts'. Conceiving and modelling viruses as ecological agents combines a 'bottom-up' (nutrient-driven) approach with a 'top-down' way of modelling ecosystems and biogeochemical cycles (Torsvik, Øvreås, & Thingstad, 2002).

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'Top-down' refers to theorizing nutrient flows and community assemblies as structured by agents, rather than being the inevitable and somewhat passive outcomes of bottom-up nutrient abundances and deficits (Pace & Cole, 1994). These latter causal factors do not have the distributed biological individuality I have suggested that viruses – as a functional type – possess. Viruses are a distributed agent in such frameworks (e.g., Figs. 2 and 3), operating on multiple scales, and their inclusion in ecosystem models has major explanatory benefits. The epistemic virtues of distributed agents are a valuable lesson to learn from viral ecology. And another is that life may best be understood as the combined and often non-linear interactions of biological agents, not all of which are living things. Thinking in this way may help push through problematic issues such as when 'life' began, and where to draw the line between living and non-living. With distributed agents forming networks that count as life, we need not worry for many ecological explanations about thresholds or dividing lines.

The ecological virus thus becomes a philosophically interesting entity that can give insight into the conceptual understanding of agents, activities such as cooperation at the ecosystem scale, and even life itself. Ecological viruses also draw attention to modelling strategies and the comparability of mathematical and material structures for representing and explaining the biological world. Once agents are abstracted from self-contained individuated organisms or other biological entities, they become less concrete and more like mathematical equations in how they explain biological dynamics. All of these virtues are achieved by viewing viruses not as some kind of single individualized agent but as a distributed one with causal effects that occur at different biological scales. For all these reasons, the ecological virus is worth further philosophical consideration.

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References

Anderson, N. G., Cline, G. B., Harris, W. W., & Green, J. G. (1967). Isolation of viral particles from large fluid volumes. In G. Berg (Ed.), *Transmission of viruses by the water route* (pp. 75–88). NY: Interscience.

Andrewes, C. H. (1965). The troubles of a virus: the seventh Marjory Stephenson Memorial Lecture. *Journal of General Microbiology, 40*, 149–156.

Azam, F. (1998). Microbial control of oceanic carbon flux: the plot thickens. *Science, 280*, 694–696.

Azam, F., Fenchel, T., Field, J. G., Gray, J. S., Meyer-Bell, L. A., & Thingstad, F. (1983). The ecological role of water-column microbes in the sea. *Marine Ecology Progress Series, 10*, 257–262.

Azam, F., & Malfatti, F. (2007). Microbial structuring of marine ecosystems. *Nature Reviews Microbiology, 5*, 782–791.

Bergh, O., Borsheim, K. Y., Bratbak, G., & Heldal, M. (1989). High abundance of viruses found in aquatic environments. *Nature, 340*, 467–468.

Bohannan, B. J. M., & Lenski, R. E. (2000). The relative importance of competition and predation varies with productivity in a model community. *American Naturalist, 156*, 329–340.

Bratbak, G., Thingstad, F., & Heldal, M. (1994). Viruses and the microbial loop. *Microbial Ecology, 28*, 209–221.

Breitbart, M. (2012). Marine viruses: truth or dare? *Annual Review of Marine Science, 4*, 425–428.

Brussaard, C. P. D. (2004). Viral control of phytoplankton populations – A review. *Journal of Eukaryotic Microbiology, 51*, 125–138.

Brüssow, H., Canchaya, C., & Hardt, W.-D. (2004). Phages and the evolution of bacterial pathogens: from genomic rearrangements to lysogenic conversion. *Microbiology and Molecular Biology Reviews, 68*, 560–602.

Cannon, R. E. (1987). Cyanophage ecology. In S. M. Goyal, C. P. Gerba, & G. Bitton (Eds.), *Phage ecology* (pp. 245–265). NY: John Wiley.

Clarke, N. A., & Chang, S. L. (1959). Enteric viruses in water. *Journal (American Water Works Association), 51*, 1299–1317.

Danovaro, R., Corinaldesi, C., Dell'Anno, A., Fuhrman, J. A., Middelburg, J. J., Noble, R. T., et al. (2011). Marine viruses and global climate change. *FEMS Microbiology Reviews, 35*, 993–1034.

Dupré, J., & O'Malley, M. A. (2009). Varieties of living things: life at the intersection of lineage and metabolism. *Philosophy and Theory in Biology, 1*(1). http://dx.doi.org/10.3998/ptb.6959004.0001.003.

Falkowski, P. (2012). The power of plankton. *Nature, 483*, S17–S20.

Falkowski, P. G., Barber, R. T., & Smetacek, V. (1998). Biogeochemical controls and feedbacks on ocean primary production. *Science, 281*, 200–206.

Falkowski, P. G., Fenchel, T., & Delong, E. F. (2008). The microbial engines that drive Earth's biogeochemical cycles. *Science, 320*, 1034–1039.

Fuhrman, J. A. (1999). Marine viruses and their biogeochemical and ecological effects. *Nature, 399*, 541–548.

Fuhrman, J. A., & McManus, G. B. (1984). Do bacteria-sized marine eukaryotes consume significant bacterial production? *Science, 224*, 1257–1260.

Fuhrman, J. A., & Noble, R. T. (1995). Viruses and protists cause similar bacterial mortality in coastal seawater. *Limnology and Oceanography, 40*, 1236–1242.

Giovannoni, S., Temperton, B., & Zhao, Y. (2013). Giovannoni et al. reply [to Zhao, et al., 2013]. *Nature, 499*, E4.

Godfrey-Smith, P. (2009). *Darwinian populations and natural selection*. Oxford: Oxford University Press.

Grafe, A. (1991). *A history of experimental virology* (transl. Reckendorf, E.). Berlin: Springer-Verlag

Greenberg, A. E. (1956). Survival of enteric organisms in sea water. *Public Health Reports, 71*, 77–86.

Hendrix, R. W., Smith, M. C. M., Burns, R. N., & Ford, M. E. (1999). Evolutionary relationships among diverse bacteriophages and prophages: all the world's a phage. *Proceedings of the National Academy of Sciences USA, 96*, 2192–2197.

Hewson, I., & Fuhrman, J. A. (2006). Viral impacts on marine bacterioplankton assemblage structure. *Journal of the Marine Biological Association UK, 86*, 577–589.

Holmfeldt, K., Middelboe, M., Nybroe, O., & Riemann, L. (2007). Large variabilities in host strain susceptibility and phage host range govern interactions between lytic marine phages and their *Flavobacterium* hosts. *Applied and Environmental Microbiology, 73*, 6730–6739.

Hurst, C. J., & Lindquist, H. D. A. (2000). Defining the ecology of viruses. In C. J. Hurst (Ed.), *Viral ecology* (pp. 3–40). San Diego: Academic.

Hurwitz, B. L., Hallam, S. J., & Sullivan, M. B. (2013). Metabolic reprogramming by viruses in the sunlit and dark ocean. *Genome Biology, 14*, R123.

Jacquet, S., Miki, T., Noble, R., Peduzzi, P., & Wilhelm, S. (2010). Viruses in aquatic ecosystems: important advancements of the last 20 years and prospects for the future in the field of microbial oceanography and limnology. *Advances in Oceanography and Limnology, 1*, 97–141.

Jessup, C. M., Kassen, R., Forde, S. E., Kerr, B., Buckling, A., Rainey, P. B., et al. (2004). Big questions, small worlds: microbial model systems in ecology. *Trends in Evolution and Ecology, 19*, 189–197.

Jiang, S. C., & Paul, J. H. (1998). Significance of lysogeny in the marine environment: studies with isolates and a model of lysogenic phage production. *Microbial Ecology, 35*, 235–243.

Jover, L. F., Effler, T. C., Buchan, A., Wilhelm, S. W., & Weitz, J. S. (2014). The elemental composition of virus particles: implications for marine biogeochemical cycles. *Nature Reviews Microbiology, 12*, 519–528.

Konopka, A., Lindemann, S., & Frederickson, J. (2015). Dynamics in microbial communities: unraveling mechanisms to identify principles. *ISME Journal, 9*, 1488–1495.

Koonin, E. V., & Dolja, V. V. (2013). A virocentric perspective on the evolution of life. *Current Opinion in Virology, 3*, 546–557.

Koonin, E. V., & Wolf, Y. I. (2012). Evolution of microbes and viruses: a paradigm shift in evolutionary biology? *Frontiers in Cellular and Infection Microbiology, 2*, 119.

Legendre, L., & Rivkin, R. B. (2008). Planktonic food webs: microbial hub approach. *Marine Ecology Progress Series, 365*, 289–309.

Lennon, J. T., & Martiny, J. B. H. (2008). Rapid evolution buffers ecosystem impacts of viruses in a microbial food web. *Ecology Letters, 11*, 1178–1188.

Lenski, R. E. (1988). Dynamics of interaction between bacteria and virulent bacteriophage. In K. C. Marshall (Ed.), *Advances in microbial ecology* (Vol. 10, pp. 1–44). NY: Plenum.

Levin, B. R. (1972). Coexistence of two asexual strains on a single resource. *Science, 175*, 1272–1274.

Levin, B. R., Stewart, F. M., & Chao, L. (1977). Resource-limited growth, competition, and predation: a model and experimental studies with bacteria and bacteriophage. *American Naturalist, 111*, 3–24.

Lindell, D., Jaffe, J. D., Johnson, Z. I., Church, G. M., & Chisholm, S. W. (2005). Photosynthesis genes in marine viruses yield proteins during host infection. *Nature, 438*, 86–89.

Lindell, D., Sullivan, M. B., Johnson, Z. I., Tolonen, A. C., Rohwer, F., & Chisholm, S. W. (2004). Transfer of photosynthesis genes to and from *Prochlorococcus* viruses. *Proceedings of the National Academy of Sciences USA, 101*, 11013–11018.

Mann, N. H. (2005). The third age of phage. *PLOS Biology, 3*(5), e182.

Mann, N. H., Cook, A., Millard, A., Bailey, S., & Clokie, M. (2003). Bacterial photosynthesis genes in a virus. *Nature, 424*, 741.

Middelboe, M. (2000). Bacterial growth rate and marine virus-host dynamics. *Microbial Ecology, 40*, 114–124.

Mitchell, R., & Jannasch, H. W. (1969). Processes controlling virus inactivation in seawater. *Environmental Science and Technology, 3*, 941–943.
Moebus, K.-H. (1987). Ecology of marine bacteriophages. In S. M. Goyal, C. P. Gerba, & G. Bitton (Eds.), *Phage ecology* (pp. 137–156). NY: John Wiley.
Moreira, D., & López-García, P. (2009). Ten reasons to exclude viruses from the tree of life. *Nature Reviews Microbiology, 7*, 306–311.
Morgan, G. J. (2016). What is a virus species? Radical pluralism in viral taxonomy. *Studies in History and Philosophy of Biological and Biomedical Sciences* (in this issue)
Murray, A. G., & Eldridge, P. M. (1994). Marine viral ecology: incorporation of bacteriophage into the microbial planktonic food web paradigm. *Journal of Plankton Research, 16*, 627–641.
Odenbaugh, J. (2006). Struggling with the science of ecology. *Biology and Philosophy, 21*, 395–409.
Pace, M. L., & Cole, J. J. (1994). Comparative and experimental approaches to top-down and bottom-up regulation of bacteria. *Microbial Ecology, 28*, 181–193.
Paul, H. H. (2008). Prophages in marine bacteria: dangerous molecular time bombs or the key to survival in the seas? *ISME Journal, 2*, 579–589.
Pomeroy, L. R. (1974). The ocean's food web, a changing paradigm. *BioScience, 24*, 499–504.
Pradeu, T. (2016). Mutualistic viruses and the heteronomy of life. *Studies in History and Philosophy of Biological and Biomedical Sciences* (in this issue)
Proctor, L. M., Fuhrman, J. A., & Ledbetter, M. C. (1988). Marine bacteriophages and bacterial mortality. *Eos, 69*, 1111–1112.
Rivkin, R. B., & Legendre, L. (2002). Roles of food web and heterotrophic microbial processes in upper ocean biogeochemistry: global patterns and processes. *Ecological Research, 17*, 151–159.
Rodriguez-Valera, F., Martin-Cuadrado, A.-B., Rodriguez-Brito, B., Pašić, L., Thingstad, T. F., Rohwer, F., et al. (2009). Explaining microbial population genomics through phage predation. *Nature Reviews Microbiology, 7*, 828–836.
Rohwer, F., & Barott, K. (2013). Viral information. *Biology and Philosophy, 28*, 283–297.
Rohwer, F., & Thurber, R. V. (2009). Viruses manipulate the marine environment. *Nature, 459*, 207–212.
Safferman, R. S., & Morris, M.-E. (1963). Algal virus: isolation. *Science, 140*, 679–680.
Safferman, R. S., & Morris, M.-E. (1964). Control of algae with viruses. *Journal (American Water Works Association), 56*, 1217–1224.
Servais, P., Billen, G., & Rego, J. V. (1985). Rate of bacterial mortality in aquatic environments. *Applied and Environmental Microbiology, 49*, 1448–1454.
Sharon, I., Alperovitch, A., Rohwer, F., Hanyes, M., Glaser, F., Atamna-Ismaeel, N., et al. (2009). Photosystem 1 gene cassettes are present in marine virus genomes. *Nature, 461*, 258–262.
Sherr, E. B., & Sherr, B. F. (1991). Planktonic microbes: tiny cells at the base of the ocean's food webs. *Trends in Ecology and Evolution, 6*, 50–54.
Sherr, B. F., Sherr, E. B., & Pedrós-Alió, C. (1989). Simultaneous measurement of bacterioplankton production and protozoan bacterivory in estuarine water. *Marine Ecology Progress Series, 54*, 209–219.
Spencer, R. (1955). A marine bacteriophage. *Nature, 175*, 690–691.
Staley, J. T., & Konopka, A. (1985). Measurement of in situ activities of non-photosynthetic microorganisms in aquatic and terrestrial habitats. *Annual Review of Microbiology, 39*, 321–346.
Summers, W. C. (1993). How bacteriophage came to be used by the Phage Group. *Journal of the History of Biology, 26*, 255–267.
Suttle, C. A. (1994). The significance of viruses to mortality in aquatic microbial communities. *Microbial Ecology, 28*, 237–243.
Suttle, C. A. (2005). Viruses in the sea. *Nature, 437*, 356–361.
Suttle, C. A. (2007). Marine viruses – Major players in the global ecosystem. *Nature Reviews Microbiology, 5*, 801–812.
Suttle, C. A., Chan, A. M., & Cottrell, M. T. (1990). Infection of phytoplankton by viruses and reduction of primary productivity. *Nature, 347*, 467–469.
Thingstad, T. F. (1998). A theoretical approach to structuring mechanisms in the pelagic food web. *Hydrobiolgia, 363*, 59–72.
Thingstad, T. F. (2000). Elements of a theory for the mechanisms controlling abundance, diversity, and biogeochemical role of lytic bacterial viruses in aquatic systems. *Limnology and Oceanography, 45*, 1320–1328.
Thingstad, T. F., Heldal, M., Bratbak, G., & Dundas, I. (1993). Are viruses important partners in pelagic food webs? *Trends in Ecology and Evolution, 8*, 209–213.
Thingstad, T. F., & Lignell, R. (1997). Theoretical models for the control of bacterial growth rate, abundance, diversity and carbon demand. *Aquatic Microbial Ecology, 13*, 19–27.
Torrella, F., & Morita, R. Y. (1979). Evidence by electron micrographs for a high incidence of bacteriophage particles in the waters of Yaquina Bay, Oregon: ecological and taxonomical implications. *Applied and Environmental Microbiology, 37*, 774–778.
Torsvik, B., Øvreås, L., & Thingstad, T. F. (2002). Prokaryotic diversity – Magnitude, dynamics, and controlling factors. *Science, 296*, 1064–1066.
Van Regenmortel, M. H. V. (2010). Logical puzzles and scientific controversies: the nature of species, viruses, and living organisms. *Systematic and Applied Microbiology, 33*, 1–6.
Weinbauer, M. G. (2004). Ecology of prokaryotic viruses. *FEMS Microbiology Reviews, 28*, 127–181.
Weinbauer, M. G., & Rassoulzadegan, F. (2004). Are viruses driving microbial diversification and diversity? *Environmental Microbiology, 6*, 1–11.
Weisberg, M. (2013). *Simulation and similarity: Using models to understand the world*. NY: Oxford University Press.
Weitz, J. S., & Dushoff, J. (2008). Alternative stable states in host-phage dynamics. *Theoretical Ecology, 1*, 13–19.
Weitz, J. S., Stock, C. A., Wilhelm, S. W., Bourouiba, L., Coleman, M. L., et al. (2015). A multitrophic model to quantify the effects of marine viruses on microbial food webs and ecosystem processes. *ISME Journal, 9*, 1352–1364.
Weitz, J. S., & Wilhelm, S. W. (2012). Ocean viruses and their effects on microbial communities and biogeochemical cycles. *F1000 Reports Biology, 4*, 17. doi: 103410/B4-17.
Wilhelm, S. W., & Suttle, C. A. (1999). Viruses and nutrient cycles in the sea. *BioScience, 49*, 781–788.
Wilkinson, L. (2001). History of virology. *Encyclopedia of Life Sciences*. http://dx.doi.org/10.1038/npg.els.0003075.
Williams, P. J. leB. (1981). Microbial contribution to overall marine plankton metabolism: direct measurements of respiration. *Oceanologica Acta, 4*, 359–364.
Williams, S. T., Mortimer, A. M., & Manchester, L. (1987). Ecology of soil bacteriophages. In S. M. Goyal, C. P. Gerba, & G. Bitton (Eds.), *Phage ecology* (pp. 157–179). NY: John Wiley.
Wilson, R. A. (2005). *Genes and the agents of life: The individual in the fragile sciences*. Cambridge University Press.
Wilson, G., & Shpall, S. (2012). Action. In E. N. Zalta (Ed.), *Stanford Encyclopedia of Philosophy*. http://plato.stanford.edu/archives/sum2012/entries/action/.
Winter, C., Bouvier, T., Weinbauer, M. G., & Thingstad, T. F. (2010). Trade-offs between competition and defense specialists among unicellular planktonic organisms: the 'killing the winner' hypothesis revisited. *Microbiology and Molecular Biology Reviews, 74*, 42–57.
Winter, C., Smit, A., Herndl, G. J., & Weinbauer, M. G. (2005). Linking bacterial richness with viral abundance and prokaryotic activity. *Limnology and Oceanography, 50*, 968–977.
Wommack, K. E., & Colwell, R. R. (2000). Virioplankton: viruses in aquatic ecosystems. *Microbiology and Molecular Biology Reviews, 64*, 69–114.
Zeidner, G., Bielawski, J. P., Shmoish, M., Scanlan, D. J., Sabehi, G., & Béjà, O. (2005). Potential photosynthesis gene recombination between *Prochlorococcus* and *Synechococcus* via viral intermediates. *Environmental Microbiology, 7*, 1505–1513.
Zobell, C. E. (1946). *Marine microbiology*. Massachusetts: Chronica Botanica.

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