In the news

CANDIDA AURIS' POTENTIAL LINK TO CLIMATE CHANGE

Since its first identification in an ear canal swab from a Japanese hospital patient in 2009, several different lineages of the pathogenic fungus *Candida auris* have emerged independently. *C. auris* is difficult to diagnose and treat, often exhibiting multidrug resistance and causing outbreaks in healthcare settings that are associated with high mortality rates. Its emergence has puzzled the scientific community so far (STAT, 23 July 2019), as outbreaks in Asia, Africa and South America emerged at the same time but were caused by three distinct clades. Now, Casadevall et al. propose that global warming might be linked to the concurrent emergence of different *C. auris* clades.

Casadevall says that the simultaneous emergence of three genetically distinct clades on three continents is "mystifying" and adds that "this implies some common trigger in geographically distant sites and given that climate change is occurring globally we decided to focus on that variable" (Newsweek, 23 July 2019). The vast majority of fungi are adapted to environmental temperatures and thus do not grow well at the relatively high temperatures found in humans, which is one reason why only few fungal species are human pathogens. It was already noted in the first description of C. auris in 2009 that the fungus grew well at 40°C. Casadevall et al. compared the temperature tolerance of C. auris with its close relatives, revealing that C. auris can grow at higher temperatures than most of the examined species. This comparison led Casadevall to say "that as the climate has gotten warmer, some of these organisms, including Candida auris, have adapted to the higher temperature, and as they adapt, they break through humans' protective temperatures" (CNN, 23 July 2019). The authors propose a scenario in which global warming has led to the evolution of greater thermal tolerance of C. auris in the environment, potentially in wetlands, which has enabled it to spread to birds and subsequently to humans.

Without the isolation and detailed characterization of more strains, including from the environment, such a scenario remains speculative. Tom Chiller from the CDC and co-authors concluded in an earlier study that "rising temperatures might have played a role in its emergence, but given an absence of knowledge about its natural habitat, it is impossible at this time to determine whether climatic changes played a role in its recent emergence as a human pathogen". They also note that C. auris is not the only fungal pathogen that emerged globally in recent years, mentioning chytridiomycosis in amphibians and white-nose syndrome in bats. The spread of both of these wildlife fungal diseases is complex and multifactorial but temperature, precipitation and extreme weather events might have a role. For chytridiomycosis, a link to climate change has been proposed (BBC News, 12 August 2012).

Although much about the links between climate change and the emergence of infectious diseases remains to be determined, Casadevall et al. call for greater vigilance and continuous monitoring for emerging fungi.

Ursula Hofer

■ VIRAL INFECTION

Spindle-shaped predators

Ammonia-oxidizing archaea (AOA), which are members of the phylum Thaumarchaeota, mediate ammonia oxidation and have key roles in nitrogen cycling in marine ecosystems. Given this crucial role, changes in the abundance, distribution and composition of these thaumarchaeal communities will affect the biogeochemical processes involved in nitrogen cycling in the oceans. One factor that can influence microbial activity and community structure is viral predation. However, so far the impact of viral infection on AOA abundance and metabolism remained unexplored, and a virus that can infect thaumarchaea had not been isolated.

In this study, Rhee and colleagues report the identification and characterization of spindle-shaped viruses that infect a marine ammoniaoxidizing thaumarchaeon and that are distinct from other known marine viruses.

The authors isolated AOA-infecting *Nitrosopumilus* spindle-shaped viruses (NSV1, NSV2 and NSV3) from seawater and showed that the viruses are similar in size, have a short tail at one pole and are well-adapted to environmental fluctuations such as varying pH, salinity and temperature. Moreover, NSVs have a narrow host range and they interact with the archaeal cell surface, with a large fraction of the virions remaining attached to their host.

Further analysis revealed that NSVs have linear double-stranded genomes and that although they are closely related to each other, they do not display sequence similarity to other known archaeal or bacterial viruses. Thus, the authors speculate that NSVs belong to a new archaeal virus family, which they term 'Thaspiviridae'.

SYNTHETIC BIOLOGY

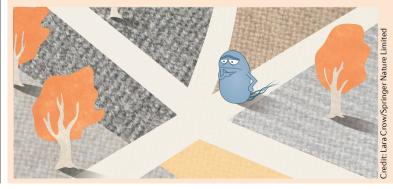
Differentiating bacteria

Synthetic microorganisms hold great promise for a range of applications, from producing biofuels and drugs to detoxifying contaminants in the environment; however, synthetic microorganisms are relatively simple compared with multicellular organisms, limiting their potential in applications that require complex behaviours such as the compartmentalization of functions and spatiotemporal control.

Multicellular organisms achieve

their complexity through asymmetric cellular divisions and cellular differentiation. Now, two studies report synthetic genetic circuits for inducible asymmetric cell division that give rise to cellular differentiation in Escherichia coli.

In the first study, Molinari et al. engineered an asymmetric plasmid partitioning (APP) system that controls partitioning by sequestering plasmids in a single position within the cell. During division, plasmids are retained



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