

## IN BRIEF

**➤ VIRAL EVOLUTION****Closely monitoring influenza virus**

Human infections with highly pathogenic avian influenza (HPAI) H7N9 viruses have been detected in China, which raises concerns of a future pandemic, particularly if these viruses acquire efficient human-to-human transmissibility. However, the replication capacity, pathogenicity and transmissibility of human HPAI H7N9 isolates in mammals were unknown. Kawaoka and colleagues characterized a human HPAI H7N9 isolate and its recombinant derivatives that represent neuraminidase inhibitor-sensitive and -resistant subpopulations *in vitro* and *in vivo*. HPAI H7N9 viruses replicated efficiently in mice, ferrets and nonhuman primates and were more pathogenic than low-pathogenic H7N9 viruses in mammals. Moreover, HPAI H7N9 viruses transmit via respiratory droplets among ferrets and exhibit low sensitivity to neuraminidase inhibitors in mice. The findings suggest that the highly pathogenic H7N9 virus has pandemic potential and should be closely monitored.

**ORIGINAL ARTICLE** Imai, M., Watanabe, T., Kiso, M., Nakajima, N., Yamayoshi, S., Iwatsuki-Horimoto, K., Hatta M. *et al.* A highly pathogenic avian H7N9 influenza virus isolated from a human is lethal in some ferrets infected via respiratory droplets. *Cell Host Microbe* <http://dx.doi.org/10.1016/j.chom.2017.09.008> (2017)

**➤ MARINE MICROBIOLOGY****Synchronized rhythms in the ocean**

Viruses are key components of marine ecosystems; however, the temporal dynamics, diversity and variability of viruses in these ecosystems are not well understood. The authors surveyed the diversity and temporal dynamics of viral assemblages over daily and seasonal timescales in waters of the North Pacific Subtropical Gyre. Using metagenomics and quantitative transcriptomics, they monitored the temporal abundance and transcriptional activities of the most abundant double-stranded DNA viruses in the euphotic zone of the ocean and report synchronized diel coupling of viral and cellular replication cycles in both photoautotrophic and heterotrophic bacterial hosts. Moreover, dominant viruses persisted for extended time periods, which suggests that both core viral genomes and viral community structure are conserved over interannual periods. Thus, viruses are intrinsically synchronized with the daily and seasonal rhythms of marine microbial community processes.

**ORIGINAL ARTICLE** Aylward, F. O. *et al.* Diel cycling and long-term persistence of viruses in the ocean's euphotic zone. *Proc. Natl Acad Sci. USA* <http://dx.doi.org/10.1073/pnas.1714821114> (2017)

**➤ TECHNIQUES & APPLICATIONS****Expanding the genetic toolbox for fungi**

*Candida albicans* is a common fungal pathogen of humans, but genetic interaction analysis has been limited in this diploid organism. To overcome the technical restrictions, Shapiro, Chavez *et al.* developed a CRISPR–Cas9-based gene drive array (GDA) platform that can efficiently generate homozygous double-gene deletion mutants, and they present the first large-scale genetic epistasis analysis in this fungal pathogen. The authors generated double-gene deletion libraries, targeting antifungal efflux pumps and biofilm adhesion factors to determine how drug pumps and cellular adhesins interact to govern tolerance to xenobiotics and biofilm formation, respectively, in *C. albicans*. The authors anticipate that the GDA platform can be adapted to study other clinically relevant fungal pathogens.

**ORIGINAL ARTICLE** Shapiro, R. S., Chavez, A. *et al.* A CRISPR–Cas9-based gene drive platform for genetic interaction analysis in *Candida albicans*. *Nat. Microbiol.* <http://dx.doi.org/10.1038/s41564-017-0043-0> (2017)