RESEARCH HIGHLIGHTS

IN BRIEF

⮞ EVOLUTION

Co-evolution promotes innovation

The interaction between a viral ligand and its cellular receptor is highly specific and limits host range. A recent paper describes a mutant form of bacteriophage λ that targets an alternative receptor after co-evolution with *Escherichia coli*. When phage cl26 was cultured with *E. coli* in conditions that sustained the phage but suppressed expression of the canonical host receptor, LamB (also known as maltoporin), mutant phage particles shifted their specificity from LamB to a new receptor, OmpF. A combination of four mutations in the phage tail protein J were essential for exclusive targeting of OmpF and were present in multiple lineages, an indicator of strong positive selection. Interestingly, not all lineages evolved the capacity to use OmpF, and the authors found that the evolutionary trajectory demanded a fortuitous sequence of mutational events, not only in the phage but also its host, demonstrating the complexity of interactions in a co-evolving population.

ORIGINAL RESEARCH PAPER Meyer, J. R. *et al.* Repeatability and contingency in the evolution of a key innovation in phage lambda. *Science* **335**, 428–432 (2012)

⮞ BACTERIAL GENOMICS

Universal bacterial barcode

Although analysis of 16S ribosomal RNA has revolutionized the ability to classify bacteria and understand their phylogenetic relationships, it is less useful for classifying related strains of bacteria that share similar or identical 16S rRNA gene sequences but exhibit distinct properties. To address this, Jolley *et al.* have developed a ribosomal multilocus sequence typing (rMLST) approach that relies on variations in the 53 *rps* genes that encode the bacterial ribosomal proteins. These genes are ideal candidates, as most bacteria contain all 53, and they are distributed around the chromosome and are under stabilizing selection. Jolley *et al.* created a database comprising whole genome sequences of 1,900 bacteria that can be used to analyse *rps* sequences to allow rapid classification of an isolate. It may be possible to include *rps* sequences from other domains, providing a truly universal classification system.

ORIGINAL RESEARCH PAPER Jolley, K. A. *et al.* Ribosomal multi-locus sequence typing: universal characterization of bacteria from domain to strain. *Microbiology* 26 Jan 2012 (doi:10.1099/mic.0.055459-0)

⮞ VIRAL INFECTION

Promiscuous packaging

The high error rate of viral polymerases allows viruses to rapidly adapt to a new host, and each replication cycle results in a heterogeneous population of viruses with distinct genetic content. Routh *et al.* used an unbiased next-generation sequencing approach to look at the total RNA content of a purified non-enveloped single-stranded RNA virus, Flock House virus (FHV). They showed that, as well as the FHV genome, FHV virions contain a range of host RNAs that account for 1% of the total packaged nucleic acid and include mRNAs, ribosomal RNAs, non-coding RNAs and transposable elements. Such a high incidence of these host RNAs suggests that viruses such as FHV have an important role in horizontal gene transfer. Moreover, the authors found that host RNAs, including transposable elements, are also regularly packaged in virus-like particles (VLPs), which must be taken into account when considering the potential use of VLPs as vehicles for delivering gene therapy.

ORIGINAL RESEARCH PAPER Routh, A. *et al.* Host RNAs, including transposons, are encapsidated by a eukaryotic single stranded RNA virus. *Proc. Natl Acad. Sci. USA* 24 Jan 2012 (doi: 10.1073/pnas.1116168109)