

IN BRIEF

SYNTHETIC BIOLOGY

De novo designed proteins from a library of artificial sequences function in *Escherichia coli* and enable cell growth

Fisher, M. A. *et al.* *PLoS ONE* **6**, e15364 (2011)

To date, synthetic biology has relied on a cut-and-paste approach, using genes, proteins and regulatory elements derived from naturally occurring sequences. To probe whether novel, 'unevolved' DNA sequences might be able to encode functions that enable cell growth, the authors designed a library of artificial genes encoding $\sim 1.5 \times 10^6$ novel amino acid sequences. This library was transformed into 27 *Escherichia coli* auxotrophic mutants, and the ability to restore bacterial growth on minimal media was assessed. Novel proteins that rescued the growth of four mutant strains ($\Delta serB$, $\Delta gltA$, $\Delta ilvA$ and Δfes) were identified. How these novel proteins are able to rescue these strains remains unclear, but these findings suggest that the synthetic biology tool box can be extended to include proteins not found in nature.

SYMBIOSIS

Aphid genome expression reveals host–symbiont cooperation in the production of amino acids

Hansen, A. K. & Moran, N. A. *Proc. Natl Acad. Sci. USA* 31 Jan 2011 (doi: 10.1073/pnas.1013465108)

Animals are unable to synthesize the ten essential amino acids and must therefore obtain them from their diet. Phloem sap contains particularly low levels of these amino acids, meaning that phloem-feeding insects, such as the pea aphid *Acyrtosiphon pisum*, must rely on microbial symbionts to produce them. The bacterium *Buchnera aphidicola* resides in specialized *A. pisum* cells known as bacteriocytes. Although *B. aphidicola* synthesizes essential amino acids for its host, its genome lacks particular genes that are important for the biosynthesis of five of these amino acids. A transcriptomic analysis revealed 404 *A. pisum* genes that are specifically upregulated in the bacteriocyte, including 26 genes thought to be involved in amino acid biosynthesis. Among this group are seven genes that fill the gaps in the essential amino acid synthesis pathways of *B. aphidicola*. Thus, host gene expression in bacteriocytes is intimately linked to the metabolic capabilities of the endosymbionts that they house.

VIROLOGY

Natural and experimental infection of *Caenorhabditis* nematodes by novel viruses related to nodaviruses

Félix, M. A. *et al.* *PLoS Biol.* **9**, e1000586 (2011)

The nematode worm *Caenorhabditis elegans* has become a useful model system for studying immune responses to infecting bacteria and microsporidia. However, a lack of viruses known to naturally infect *C. elegans* has hampered the study of antiviral innate immunity. Now, wild isolates of *C. elegans* and its close relative *Caenorhabditis briggsae* have been observed to be infected with two novel RNA viruses. Distantly related to nodaviruses, both viruses are transmitted horizontally between worms, although Orsay virus (isolated in Orsay, France) infects only *C. elegans*, whereas Santeuil virus (isolated in Santeuil, France) infects only *C. briggsae*. Both *C. elegans* and *C. briggsae* mount an RNA interference response against the viruses, and disruption of the RNA interference pathway in a laboratory strain of *C. elegans* led to higher levels of Orsay viral RNA and increased symptoms of infection. This study represents the first description of viruses that naturally infect nematodes.