IN BRIEF

SYNTHETIC BIOLOGY

Building a designer yeast genome

An international team of researchers has embarked on the creation of a synthetic eukaryotic genome and now report the synthesis of a redesigned *Saccharomyces cerevisiae* chromosome. Boeke and colleagues built a fully functional chromosome III (which they term synIII) that contained hundreds of alterations, including the removal of introns, transposons and tRNA genes to increase the stability of the re-engineered chromosome. In addition, 98 *loxP* sites were inserted to enable genetic reshuffling of the chromosome as desired. Replacement of chromosome III with synIII generated a viable yeast strain that had negligible fitness costs and a highly similar transcriptome compared with the original strain. The synthesis of complete bacterial and viral genomes has already been accomplished, but this is a landmark achievement that paves the way for the construction of entirely synthetic, tailor-made eukaryotic genomes.

ORIGINAL RESEARCH PAPER Annaluru, N. *et al.* Total synthesis of a functional designer eukaryotic chromosome. *Science* http://dx.doi.org/ 10.1126/science.1249252 (2014)

CLINICAL MICROBIOLOGY

Recombination turns one clade into two

Clinical isolates of carbapenem-resistant *Klebsiella pneumoniae* that belong to multilocus sequence type 258 (ST258) have emerged as important nosocomial pathogens, and it has been proposed that all of these isolates are derived from a single genetic clone that has spread globally. However, genome sequencing and phylogenetic analysis of 83 ST258 clinical isolates from a range of geographical locations now reveals that there are two distinct genetic clades, which disproves the single-clone hypothesis. DeLeo *et al.* identified a ~215 kb region that accounts for most of the genetic divergence between the clades, which also seems to be a hot spot for recombination. Thus, the authors suggest that the genetic plasticity associated with this recombination hot spot — which includes the genes involved in the synthesis of the polysaccharide capsule (a major contributor to immune evasion) — might underlie the global success of ST258 isolates as human pathogens.

ORIGINAL RESEARCH PAPER DeLeo, F. R. *et al.* Molecular dissection of the evolution of carbapenem-resistant multilocus sequence type 258 *Klebsiella pneumoniae*. *Proc. Natl Acad. Sci. USA* http://dx.doi.org/10.1073/pnas.1321364111 (2014)

BACTERIAL PATHOGENESIS

sRNA promotes *S. aureus* persistence

Romilly *et al.* report the first example of a conserved, small non-coding RNA (sRNA) that functions as a virulence suppressor in *Staphylococcus aureus*. The authors found that the RsaA sRNA inhibits the expression of MgrA — a master regulator of transcription — primarily via the formation of an imperfect duplex between RsaA and the Shine–Dalgarno sequence of the *mgrA* mRNA, thereby repressing the translation of *mgrA*. This led to increased biofilm formation and decreased capsular polysaccharide synthesis, both of which result in reduced protection against opsonophagocytic killing by neutrophils. Furthermore, deletion of the *rsaA* gene increased *S. aureus* invasion in a mouse sepsis model. Together, these data identify RsaA as a component of a complex regulatory pathway, in which it functions as a virulence suppressor to promote persistence and chronic infection.

ORIGINAL RESEARCH PAPER Romilly, C. *et al.* A non-coding RNA promotes bacterial persistence and decreases virulence by regulating a regulator in *Staphylococcus aureus*. *PLoS Pathog.* **10**, e1003979 (2014)