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IN BRIEF

BACTERIAL GENOMICS

Unexpected introns in the 16S

The universal presence and consistent size of the 16S ribosomal RNA gene have defined it as the hallmark phylogenetic marker for classifying bacteria and archaea. Salman *et al.* now challenge this view by revealing that large sulphur bacteria contain a number of self-splicing introns at specific sites in this gene that can increase its size by up to 3.5 kb. The four introns had low sequence identity, and phylogenetic analysis of the most recurrent intron showed that it was probably transferred both vertically and horizontally within this bacterial family. These introns were capable of self-splicing *in vitro* and were removed from precursor 16S rRNA, indicating that they do not disturb ribosome function. The discovery of introns in the most commonly sequenced gene is a surprise and also questions the reliability of this phylogenetic marker for diversity studies because heterogeneity in the size of the 16S rRNA gene is not taken into consideration by many common detection techniques.

ORIGINAL RESEARCH PAPER Salman, V. *et al.* Multiple self-splicing introns in the 16S rRNA genes of giant sulfur bacteria. *Proc. Natl Acad. Sci. USA* **109**, 4203–4208 (2012)

TECHNIQUES & APPLICATIONS

Mastering staphylococcal transformation

The ability to genetically manipulate bacterial organisms is key to understanding their pathogenicity. However, the medically relevant staphylococci resist transformation with foreign DNA owing to expression of the conserved restriction endonuclease *Sau*USI, which cleaves methylated cytosines. By constructing an *Escherichia coli* strain that is defective in cytosine methylation, Monk *et al.* now show that plasmids isolated from this mutant are efficiently transformed into clinical isolates of *Staphylococcus aureus*. The authors also reveal that *Staphylococcus epidermidis* contains an orthologue of *Sau*USI, McrR, which is also by-passed when DNA lacking methylated cytosines is used. By developing this *E. coli* mutant, as well as a new vector for allelic exchange in staphylococci and an improved transformation protocol, the authors have broken some long-standing boundaries in staphylococcal genetics.

ORIGINAL RESEARCH PAPER Monk, I. R. *et al.* Transforming the untransformable: application of direct transformation to manipulate genetically *Staphylococcus aureus* and *Staphylococcus epidermidis*. *mBio* **3**, e00277-11 (2012)

HOST RESPONSE

Pro-angiogenic bacteria in the gut

The mammalian gut microbiota was previously shown to promote angiogenesis in the small intestine by an unknown mechanism. By comparing germ-free and colonized mice, Reinhardt *et al.* show that intestinal bacteria promote glycosylation of the pro-angiogenic tissue factor (TF), thus targeting this receptor to the enterocyte cell surface. Treatment of colonized mice with a TF-specific antibody, or deletion of the phosphorylatable cytoplasmic domain of TF, reduced intestinal vessel density. The authors also found that germ-free mice had lower expression of the downstream receptor PAR1. Moreover, phosphorylation of TF was impaired and vessel density was reduced accordingly in PAR1-deficient mice. These data provide evidence for a new developmental pathway of bacterium-stimulated vascular remodelling in the gut that could potentially be exploited to improve intestinal homeostasis.

ORIGINAL RESEARCH PAPER Reinhardt, C. *et al.* Tissue factor and PAR1 promote microbiota-induced intestinal vascular remodelling. *Nature* **483**, 627–631 (2012)