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IN BRIEF

MICROBIOME

Microbial mobilomes differ between societies

Brito *et al.* compared the mobile DNA components of human microbiomes from North American and Fijian individuals. The dissemination of mobile genes between geographically separated microbiomes was not strongly restricted by dispersal limitation, as 62% of mobile genes were found in both sets of microbiomes. However, at least some mobile genes seemed to be subject to environmental selection, as the abundances varied between the two cohorts and even between neighbouring Fijian villages, despite similarities in overall microbiome compositions. Consistent with the dietary habits of agrarian societies, mobile genes that encode GH13 glycoside hydrolases, which degrade plant cell wall carbohydrates, were enriched in the Fijian cohort. Differences in commonly used antibiotics were also reflected in the data, with mobile genes that mediate resistance to quinolones enriched in the Fijian cohort and mobile genes that mediate resistance to cephalosporins enriched in the North American cohort.

ORIGINAL ARTICLE Brito, I. L. *et al.* Mobile genes in the human microbiome are structured from global to individual scales. *Nature* http://dx.doi.org/10.1038/nature18927 (2016)

BACTERIAL GENETICS

A new class of Hfq-like sRNA chaperones?

Hfq is the only known chaperone for *trans*-acting small RNAs (sRNAs) in Gram-negative bacteria. However, Attaiech *et al.* show that RocC and RocR are a chaperone and *trans*-acting sRNA, respectively, that together mediate post-transcriptional silencing of competence in the human pathogen *Legionella pneumophila*. Silencing by RocC–RocR seems to occur by a mechanism similar to that commonly mediated by Hfq–sRNA: RocC enables duplex formation between RocR and the 5′ UTR of target mRNAs, thereby masking the ribosome binding site. Interestingly, RocC–RocR provides the first example of post-transcriptional regulation of competence, which is otherwise only known to be regulated by transcriptional activators. Although RocR and RocC specifically silenced genes that are involved in competence, the ProQ/FinO domain, which was responsible for sRNA binding by RocC, is widespread in Proteobacteria and, the authors suggest, might define a class of RNA chaperones that mediate sRNA silencing.

ORIGINAL ARTICLE Attaiech, L. *et al.* Silencing of natural transformation by an RNA chaperone and a multitarget small RNA. *Proc. Natl Acad. Sci. USA* http://dx.doi.org/10.1073/pnas.1601626113 (2016)

BACTERIAL PATHOGENESIS

Gut bugs in the lung link sepsis to ARDS

The gut microbiota has long been known to be fundamental to the aetiology of sepsis and acute respiratory distress syndrome (ARDS); however, the mechanistic role of the gut microbiota in lung pathology has remained unknown. Now, Dickson *et al.* report that the lung microbiota in both sepsis and ARDS is enriched for bacteria that are usually found in the lower gastrointestinal tract. Sequencing 16S rRNA from established mouse models of sepsis and fluid from the lungs of individuals with ARDS enabled the identification of these gut bacteria, which are not detectable by conventional culturing techniques. The authors also observed that the abundance of gut bacteria in the human ARDS samples was correlated with disease severity. These findings indicate that gut–lung bacterial translocation might provide a common mechanism for the development of sepsis and ARDS.

ORIGINAL ARTICLE Dickson, R. P. *et al.* Enrichment of the lung microbiome with gut bacteria in sepsis and the acute respiratory distress syndrome. *Nat. Microbiol.* **1**, 16113 (2016)