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IN BRIEF

MICROBIOME

Salmonella breathe out Clostridia

The microbial community in the mammalian intestine confers protection from the expansion of pathogenic bacteria. However, the disruption of microbial community composition has been linked to the emergence of infections, and treatment with antibiotics promotes the relapse of gastroenteritis caused by *Salmonella enterica* subsp. *enterica* serovar Typhimurium (*S.* Typhimurium). Now, Rivera-Chávez *et al.* show that treatment with streptomycin reduces the abundance of butyrate-producing Clostridia in the mouse intestinal lumen; the resulting decrease in butyrate availability increases the oxygenation of epithelial cells and promotes the aerobic expansion of *S.* Typhimurium. Lumenal expansion was shown to be driven by the bacterial cytochrome *bd*-II oxidase, and could be diminished by increasing the abundance of Clostridia and by restoring hypoxia. Finally, infection with *S.* Typhimurium in mice that are genetically resistant to *S.* Typhimurium depleted Clostridia in the absence of antibiotic treatment through virulence factor-induced intestinal inflammation, thus enabling the aerobic growth of the pathogen.

ORIGINAL ARTICLE Rivera-Chávez, F. *et al.* Depletion of butyrate-producing Clostridia from the gut microbiota drives an aerobic luminal expansion of *Salmonella*. *Cell Host Microbe* http://dx.doi.org/10.1016/j.chom.2016.03.004 (2016)

STRUCTURAL BIOLOGY

Expanding the pilus family

Pili are multimeric structures comprising linked pilin subunits that protrude from the bacterial surface and have varied roles in pathogenicity. Now, Xu *et al.* determine and analyse the crystal structures of FimA-like pilins from Bacteroidia in the human gut microbiome and identify a possible new pilin superfamily (type V). The structures revealed that the amino-terminal and larger carboxy-terminal domains have a transthyretin-like fold that contains seven core β-strands. Furthermore, the authors propose a proteinase-mediated donor-strand exchange mechanism for the assembly of type V pili that is distinct from that of other known pili. Furthermore, the structural and biochemical findings from this study suggest that members of this superfamily may have a role in both symbiotic relationships and pathogenesis in the human microbiome.

ORIGINAL ARTICLE Xu, Q. *et al.* A distinct type of pilus from the human microbiome. *Cell* http://dx.doi.org/10.1016/j.cell.2016.03.016 (2016)

SYSTEMS BIOLOGY

'Cache-ing' in on PAS domains

PER–ARNT–SIM (PAS) domains are found in many bacterial proteins and were originally described as intracellular sensor modules. Subsequently, several structural studies reported PAS-like domains in extracellular regions of transmembrane receptors; however, sequence-derived PAS domain models did not confirm the structure-based classification. Other reports suggested that these extracellular modules are related to the Cache sensory domain superfamily. Indeed, Upadhyay *et al.* now show that so-called PAS-like domains belong to the Cache superfamily, which is homologous to, but distinct from, PAS domains. Using 3D structures of bacterial cell surface receptors, the authors constructed computational models to identify new proteins that contain Cache domains. Furthermore, their data suggest that this domain is the most common extracellular sensor module in many organisms, including important pathogens.

ORIGINAL ARTICLE Upadhyay, A. A. *et al.* Cache domains that are homologous to, but different from PAS domains comprise the largest superfamily of extracellular sensors in prokaryotes. *PLoS Comput. Biol.* **12**, e1004862 (2016)