

IN BRIEF

BACTERIAL PHYSIOLOGY**How LysM binds to peptidoglycan**

LysM is a highly conserved carbohydrate binding module that is present in proteins from all kingdoms, but how LysM binds its substrates is unknown. Mesnage *et al.* now show how a LysM domain from AtlA, an autolysin from *Enterococcus faecalis*, recognizes peptidoglycan. By constructing protein variants that contained a varying number of LysM modules, the authors showed that each module could bind peptidoglycan independently, and that the binding capacity increased with the number of LysM modules. By varying the composition of peptidoglycan, they demonstrated that LysM recognizes a specific motif that includes N-acetylglucosamine (GlcNAc) repetitions — GlcNAc-X-GlcNAc. Free and bound LysM structures were solved by NMR, which revealed a pocket responsible for binding to one of the GlcNAc N-acetyl groups. Furthermore, the peptidoglycan peptide stems were located in shallow grooves at the surface of LysM, on both sides of the glycan backbone, suggesting that these peptide stems modulate the binding of peptidoglycan to LysM and might allow LysM to discriminate between different binding substrates.

ORIGINAL RESEARCH PAPER Mesnage, S. *et al.* Structural basis for bacterial peptidoglycan recognition by LysM domains. *Nature Commun.* <http://dx.doi.org/10.1038/ncomms5269> (2014)

MICROBIOME**New bacteria associated with diarrhoea**

Diarrhoeal diseases are a major cause of childhood mortality in developing countries, yet in most cases no known pathogens can be identified by conventional diagnostic methods. Pop *et al.* used high throughput 16S rRNA sequencing to compare the faecal microbiota composition in 992 children from Gambia, Mali, Kenya and Bangladesh. This analysis established a strong association between diarrhoea and the presence of different organisms in the microbiota that had been previously associated with the disease, such as members of the *Escherichia/Shigella* genus and *Campylobacter jejuni*, and also revealed new associations, including bacteria from the genus *Streptococcus* and *Granulicatella*. By contrast, the presence of *Prevotella copri* and *Lactobacillus ruminis* correlated with protection from acute diarrhoea. Although person-to-person variability was high, the microbiota from children with diarrhoea was enriched in either facultatively anaerobic or microaerophilic bacteria and several obligate anaerobic bacterial lineages were present in healthy controls.

ORIGINAL RESEARCH PAPER Pop, M. *et al.* Diarrhea in young children from low-income countries leads to large-scale alterations in intestinal microbiota composition. *Genome Biol.* <http://dx.doi.org/10.1186/gb-2014-15-6-r76> (2014)

FUNGAL PATHOGENICITY**Dissecting effector effects**

The genome of the fungal phytopathogen *Ustilago maydis* contains several large gene clusters encoding putative secreted effector proteins. Brefort *et al.* present a functional analysis of the largest cluster, cluster 19A, which encodes 24 effectors. Although the virulence of a *U. maydis* strain in which cluster 19A has been deleted is severely attenuated, it can still complete the biotrophic life cycle. Specific functions for several effectors were identified and although each effector analysed makes a modest contribution to virulence, the analysis indicated that they have distinct plant cell targets.

ORIGINAL RESEARCH PAPER Brefort, T. *et al.* Characterization of the largest effector gene cluster of *Ustilago maydis*. *PLoS Pathogens* <http://dx.doi.org/10.1371/journal.ppat.1003866> (2014)