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IN BRIEF

MICROBIOME

Diving deeper into the communities

The Human Microbiome Project has improved our understanding of microbial and functional diversity. Lloyd-Price, Mahurkar *et al.* now report an expanded data set from the study, comprising 1,631 new metagenomes (2,355 total) from diverse body sites at multiple time points in 265 individuals. Strain-level metagenomic profiles revealed body site-specific subspecies clades and the authors were able to quantify species with phylogenetic diversity that were under-represented in isolate genomes. Moreover, species-level taxonomic profiling revealed co-occurrence patterns between bacterial species and several archaea, eukaryotes and viruses. Using functional profiling methods, the authors classified metabolic core pathways into universal, microbiome-enriched and body site-enriched; the latter being indicative of functional adaptation by the microbiota to a particular niche. Finally, the authors characterized microbial and functional variation over time at different body sites.

ORIGINAL ARTICLE Lloyd-Price, J., Mahurkar, A. *et al.* Strains, functions and dynamics in the expanded Human Microbiome Project. *Nature* http://dx.doi.org/10.1038/nature23889 (2017)

BACTERIAL PHYSIOLOGY

Making a memory

CRISPR–Cas immune systems integrate short fragments of foreign DNA into CRISPR arrays within the host genome as a record against future encounters. Integration into the CRISPR locus is mediated by the CRISPR integrase, a heterohexameric complex of four Cas1 and two Cas2 proteins, and requires integration host factor (IHF); however, how the integration complex recognizes the CRISPR locus is unknown. In a recent study, Wright, Liu *et al.* reported structures of the full CRISPR locus integration complex. The structures revealed that target DNA deformation is required for access of the active site in the Cas1 integrase to the site of integration. In addition, IHF was found to bend the target DNA to bring an upstream recognition motif into contact with Cas1, thus reducing off-target integration. These structures reveal an unexpected mechanism of integrase targeting that occurs during the early stages of CRISPR–Cas immunity.

ORIGINAL ARTICLE Wright, A. V., Liu, J. -J. *et al.* Structures of the CRISPR genome integration complex. *Science* **357**, 1113–1118 (2017)

FUNGAL PHYSIOLOGY

Two for the price of one

Candida albicans is an opportunistic pathogen that forms part of the commensal microbiota. After initial colonization, *C. albicans* adapts to environmental changes, particularly in response to stresses, such as antifungal treatment. For example, gain-of-function mutations in fungal transcription factors confer new phenotypes and are a common cause of antifungal resistance. In a recent study, Hampe *et al.* found that an acquired mechanism of antifungal resistance also enabled escape of host intrinsic immunity. Histatin 5, an antimicrobial peptide that is secreted in the saliva, has fungicidal activity against *C. albicans*. The authors observed that mutant Mrr1 (a transcription factor that upregulates the multidrug efflux pump *MDR1* gene) strains also caused the overexpression of *FLU1*, a gene that encodes an efflux pump that confers histatin 5 resistance. This study demonstrates that antifungal therapy could promote the evolution of *C. albicans* strains that are resistant to host immune defences.

ORIGINAL ARTICLE Hampe, I. A. I. *et al.* An acquired mechanism of antifungal drug resistance simultaneously enables *Candida albicans* to escape from intrinsic host defenses. *PloS Pathog.* **13**, e1006655 (2017)