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IN BRIEF

FUNGAL PATHOGENESIS

Defining the fungal filamentous switch

Virulence of the opportunistic pathogen *Candida albicans* correlates with the transition from a single-cell form to a filamentous form. As some of the pathways regulating this dimorphic switch are conserved in the model organism *Saccharomyces cerevisiae*, the authors of this study introduced genome-wide deletion alleles into a filamentous strain of *S. cerevisiae* to identify the genes controlling this phenotype. They identified a set of core genes, many of which encode proteins that regulate the expression of Flo11, one of the key proteins for filamentous growth. Included in this set was the previously uncharacterized gene *MFG1*, which encodes a protein that was shown to physically interact with two *FLO11* transcriptional regulators, Flo8 and Mss11. Deletion of the *MFG1* orthologue in *C. albicans* inhibited filamentation, biofilm formation and invasive growth, and the mutant was less virulent in an *in vivo* infection model. These data suggest that Mfg1 forms part of the conserved circuitry regulating fungal filamentation and pathogenesis.

ORIGINAL RESEARCH PAPER Ryan, O. *et al.* Global gene deletion analysis exploring yeast filamentous growth. *Science* **337**, 1353–1356 (2012)

PARASITE BIOLOGY

Targeting *Plasmodium* epigenetic regulation

Post-transcriptional modification of *Plasmodium falciparum* histones has an important role in virulence gene regulation. Malmquist *et al.* synthesized a library of inhibitors targeting the parasite histone lysine methyltransferases and assessed the potential of these inhibitors as novel antimalarial agents. The library was based on a known inhibitor (BIX-01294) of a human methyltransferase. This compound and its derivative, TM2-115, arrested parasite growth, including growth of multidrug-resistant strains. Flow cytometry and culture analysis revealed that the two compounds were active against all parasite blood stages and exhibited a rapid killing effect *in vitro*, in addition to reducing parasitaemia in infected mice. Importantly, treatment with either compound substantially reduced histone methylation. These new compounds were also selective for parasites over mammalian cells and so could potentially be used as antimalarials.

ORIGINAL RESEARCH PAPER Malmquist, N. A. *et al.* Small-molecule histone methyltransferase inhibitors display rapid antimalarial activity against all blood stage forms in *Plasmodium falciparum*. *Proc. Natl Acad. Sci. USA* 24 Sep 2012 (doi:10.1073/pnas.1205414109)

MICROBIOME

Gut microbiome as a marker for diabetes

Growing evidence indicates that the composition of the gut microbiome is altered in complex diseases. Qin *et al.* carried out a metagenome-wide association study of the gut microbiome from 345 Chinese individuals with type 2 diabetes (T2D) and identified approximately 60,000 microbial markers for the disease. They also developed a new concept for classifying metagenomic data: the metagenomic linkage group, which provides a species-level description of the data without the need for traditional taxonomy. Data analysis indicated that patients with T2D have only moderate intestinal dysbiosis but that butyrate-producing bacteria (which are potentially beneficial) are less abundant and opportunistic pathogens are more abundant in these individuals than in healthy controls. Although a causal link between the observed microbiome changes and T2D has not been shown, the gut microbiome could be used to monitor the risk of T2D development.

ORIGINAL RESEARCH PAPER Qin, J. *et al.* A metagenome-wide association study of gut microbiota in type 2 diabetes. *Nature* 26 Sep 2012 (doi:10.1038/nature11450)