IN BRIEF

PARASITE BIOLOGY

Immune evasion through silence

Plasmodium falciparum has 60 *var* genes encoding distinct antigenic forms of the virulence protein PfEMP1 (*P. falciparum* erythrocyte membrane protein 1). The parasite expresses only one *var* gene at any time point during infection to avoid detection by the immune system, but the mechanism controlling the silencing of the other 59 *var* genes was unknown. Now, Jiang *et al.* show that *var* gene silencing is regulated by the histone lysine methyltransferase PfSETvs (previously known as PfSET2). Knockout of *PfSETvs* led to a strong reduction in trimethylation of histone H3 lysine 36 along the entire body of *var* genes and to transcription of almost all *var* gene family members. Notably, confocal microscopy showed that knockout of *PfSETvs* resulted in the expression of multiple PfEMP1 variants at the surface of infected red blood cells.

ORIGINAL RESEARCH PAPER Jiang, L. *et al.* PfSETvs methylation of histone H3K36 represses virulence genes in *Plasmodium falciparum*. *Nature* http://dx.doi.org/10.1038/nature12361 (2013)

FUNGAL PATHOGENESIS

Two routes to invasion

Fungal pathogens such as *Magnaporthe oryzae* have numerous effector proteins (involved in, for example, modulating immunity) that are delivered to the host cell and host–pathogen interface during infection. Here, the authors show that *M. oryzae* has two distinct secretion systems to ensure the transport of its effectors and to promote tissue invasion. Effectors that accumulate in the apoplast (the space between plant cells) are secreted through the previously described ER–Golgi secretory pathway. By contrast, cytoplasmic effectors (those that enter the host cell during invasion) preferentially accumulate at the biotrophic interfacial complex, a plant-derived structure that is rich in secretory complexes and is associated with invasive fungal hyphae. The secretion of these effectors depends on a novel pathway involving the exocyst components Exo70 and Sec5, as well as the exocytosis protein t-SNARE, which is known to mediate the docking of secretory vesicles to the target membrane.

ORIGINAL RESEARCH PAPER Giraldo, M. C. et al. Two distinct secretion systems facilitate tissue invasion by the rice blast fungus *Magnaporthe oryzae*. *Nature Commun.* http://dx.doi.org/10.1038/ncomms2996 (2013)

MICROBIOME

A bacterial trigger for liver cancer

Obesity has been associated with a perturbed gut microbiota in both humans and mice, and this study shows that such alterations can lead to obesity-related hepatocellular carcinoma. After establishing that antibiotic treatment blocks hepatocellular carcinoma development, the authors observed that the levels of deoxycholic acid (DCA; a gut bacterial metabolite known to promote DNA damage and to be associated with carcinogenesis) increased in mice fed a high-fat diet and decreased following antibiotic treatment. Importantly, reduced DCA levels blocked hepatocellular carcinoma development, and reciprocally, DCA administration to lean mice had the opposite effect. Further analysis revealed that the main bacterial population responsible for the increased DCA production in mice fed a high-fat diet belonged to *Clostridium* cluster XI, operational taxonomic unit (OTU)-1105.

ORIGINAL RESEARCH PAPER Yoshimoto, S. *et al.* Obesity-induced gut microbial metabolite promotes liver cancer through senescence secretome. *Nature* http://dx.doi.org/10.1038/nature12347 (2013)