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SPOTLIGHT

Articles of Significant Interest Selected from This Issue by the Editors

Seeing Is Believing: Intravital Imaging of *Candida*-Phagocyte Warfare

Candida albicans is a potentially lethal human fungal pathogen normally kept in check by the immune system. To dissect the mechanisms of *Candida*-innate immune system interaction, Brothers et al. (p. 932–944) developed a model of disseminated candidiasis in transparent zebrafish larvae. This model shares important traits with mammalian candidemia—virulence-associated fungal dimorphism and dependence on the phagocyte oxidase for immunity—yet *in vivo* imaging revealed a phagocyte-pathogen impasse not previously described *in vitro*. The authors also found an unappreciated role of the phagocyte oxidase activity in limiting filamentous growth. This new model will enable dissection of the *C. albicans*-host interaction *in vivo* and promises to allow chemical and genetic screening in a vertebrate host.

Targeting the Hexosamine Pathway in African Trypanosomes

The African trypanosomes are highly dependent on their glycoproteins, not least the variant surface glycoprotein coat. Both the N-glycosylation and glycosylphosphatidylinositol anchor pathways require UDP-GlcNAc to power their GlcNAc-transferases. Mariño et al. (p. 985–997) further dissect the hexosamine pathway of *Trypanosoma brucei* that leads to UDP-GlcNAc by characterizing the enzyme glucosamine 6-phosphate *N*-acetyltransferase. They show that it is located in the glycosome—adding to the evidence that all of sugar nucleotide biosynthesis may occur in this organelle—and demonstrate that it is essential. They further provide a high-resolution crystal structure that suggests this essential enzyme may be selectively druggable over the human counterpart.

Role of the TbISWI Chromatin Remodeler in an Organism with Little Transcriptional Control

The African trypanosome *Trypanosoma brucei* shows little regulation of transcription and constitutively transcribes most of its genome as polycistronic arrays. Exceptions include the mono-allelically expressed *VSG* expression sites, which are transcribed by RNA polymerase I (Pol I). Stanne et al. (p. 964–976) show that the chromatin remodeler TbISWI regulates various Pol I-transcribed loci. Additionally, TbISWI is particularly abundant at the strand switch regions between Pol II transcription units, which are enriched in modified histones and histone variants. TbISWI therefore appears to be a multifunctional chromatin remodeler involved in the regulation of both Pol I and Pol II transcription in *T. brucei*.