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Transcriptomic, proteomic and metabolomics analysis of sexual stage development in Malaria

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The malaria parasite heavily relies on secretory functions for its pathogenesis. Is the parasite is equipped with machinery to tackle perturbations to its secretory pathway? In this talk the author will describe their study revealing a complete absence of genes involved in the canonical unfolded protein response pathway in *Plasmodium falciparum*. Accordingly, the parasite is unable to up-regulate endoplasmic reticulum (ER) chaperones or ER-associated degradation in response to ER stress. Global profiling of gene expression together with proteomic and metabolomics analysis upon redox stress revealed a network of AP2 transcription factors, their targets and specific metabolites being activated and/or upregulated. The overall outcome was an up-regulation of genes involved in protein export and the sexual stage of the parasite life cycle, culminating in gametocytogenesis. Our results suggest that the malaria parasite uses ER stress as a cue to switch to the transmissible, sexual stage.

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