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Abstracts:
Poster Presentations

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Transcriptomic Profiling of *Pseudogymnoascus destructans* Adaptive Responses to Metal Stress.

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The emergence of White-nose syndrome (WNS) by the fungus *Pseudogymnoascus destructans*, presents a grave and imminent threat to diverse bat species inhabiting North America. This fungal disease has led to substantial declines in bat populations, thereby jeopardizing the existence of numerous small cave-dwelling bat communities and casting a shadow of potential extinction. *P. destructans* thrives on hibernating bats, infiltrating their skin and wing tissues, leading to burn-like lesions, and inevitably resulting in death. Understanding how *P. destructans* successfully colonizes its bat host and overcomes its innate immune response will be important to prevent infection. Previous work had suggested from transcriptomic profiling at WNS infection sites that the fungus might be insufficient in vital metal micronutrients. Such a deficiency could potentially expose a vulnerability in the fungus's overall survival strategy. Comparative analysis of transcript levels obtained from WNS infection samples and standard laboratory growth conditions has underscored significant variations in gene expression patterns. Encouraged by these previous studies, we performed a systematic investigation to characterize the *P. destructans* transcriptional response to copper stress. By employing precisely formulated synthetic growth media, we induced conditions of copper restriction by introducing 800 µM BCS, as well as conditions of copper overload by supplementing with 500 µM copper ($CuSO_4$). Leveraging advanced clustering algorithms, the transcriptomic data unearthed substantial shifts in gene expression patterns intricately associated with distinct copper environments. the analysis of differential gene expression shed light on the profound and complex reconfiguration of *P. destructans*' transcriptome when subjected to copper-induced stress. This poster encompasses a comprehensive and in-depth exploration of the extensive analysis conducted on the RNA-seq datasets. the primary focus will center on unraveling the intricacies of the regulated pathways that play a pivotal role in mediating *P. destructans* homeostasis with respect to copper and other essential metal ions.

Protists and Parasites Cell Biology

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Microscopic evidence for malaria infection in viscera tissue of the Medici family .

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The Medici were a powerful family from Florence (Italy) that rose to prominence in the early 15th century. After death, deceased Medici family members were subjected to an embalming process that

included the removal of the viscera which were placed in large terra cotta embalming jars (orci). We subjected viscera tissue from selected orci to microscopic and molecular analyses. During our initial histological analysis, we could identify a possible blood vessel that still contained traces of red blood cells and a potential first indication of a parasite that apparently resided within the red blood cells. Additional experimental approaches indicated the presence of the malaria parasite *Plasmodium falciparum* inside the red blood cells. Our results provide the first potential microscopic evidence for the occurrence of the most fatal form of malaria in the Medici family.

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Proteolytic Processing of Histone Acetyltransferase (PfGCN5) by Cysteine Protease: A unique Phenomenon in *Plasmodium falciparum*.

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Despite over 150 years of studying malaria, the distinct characteristics of the malarial parasite, *Plasmodium*, continue to puzzle us. However, by developing effective elimination methods and gaining a better understanding of the parasite's biology and pathways, we can address this worldwide health issue that impacts approximately 250 million individuals every year. One of the ways, the parasite controls its gene expression is by PfGCN5, an indispensable histone acetyltransferase. the C-terminus region of this 170 kDa chromatin-remodeling enzyme contains the conserved bromodomain (BrD) and acetyltransferase domain (GNAT). In the present study, we report the existence of a novel pathway in nuclear gene regulation of malaria parasites through proteolytic processing of nuclear PfGCN5 by a food vacuolar cysteine protease. For this purpose, we generated endogenous PfGCN5 conditional knockdown parasite line with GFP fusion by 3' replacement. GFP-PfGCN5 protein is constitutively expressed throughout the three intraerythrocytic developmental stages namely, ring, trophozoites, and schizonts in the parasite. PfGCN5 protein is predominantly localized in the nucleus of the parasite as confirmed by immunofluorescence and immunoelectron microscopy. Further, the knockdown of PfGCN5 leads to slower parasite growth which hints towards the essentiality of the protein in the parasite. the full-length protein undergoes unique proteolytic processing mediated by a cysteine protease-like enzyme. This process leads to the formation of multiple protein fragments or mature peptides. This processing is sensitive to well-known cysteine protease inhibitors E64d. the proteolytic cleavage plays a vital role in the in vivo functionality of PfGCN5. Subsequently, interacting partners of PfGCN5 were identified through LC-MS/MS after immunoprecipitation that revealed the presence of Food Vacuolar proteins including Cysteine Proteases Falcipain apart from canonical members of the PfGCN5 complex. Falcipains are known to play a role in various processes such as hemoglobin degradation within the food vacuole, erythrocyte invasion, and rupture. Notably, the cleaving of a nuclear protein PfGCN5 by a food vacuole protease is unique and does not generally occur in eukaryotic organisms. Targeting the proteolytic processing of these proteins and the involved proteases would serve as a new drug development regimen to tackle the emerging resistance in parasites to existing antimalarials.