Molecular mechanisms underlying cellular aging in controlled human malaria infection (CHMI)

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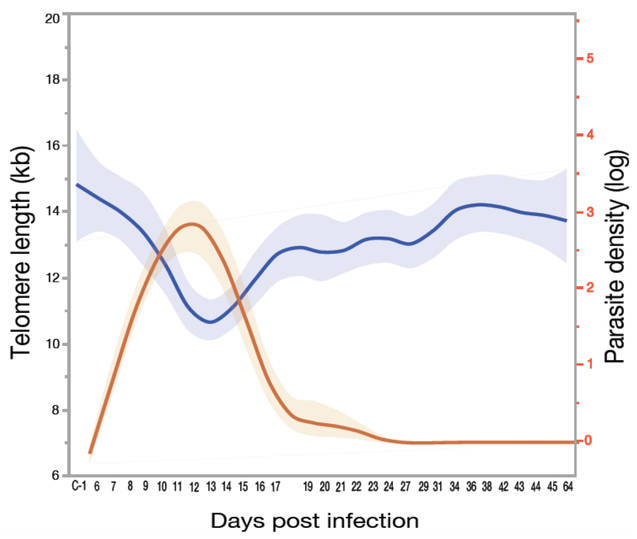
Introduction:

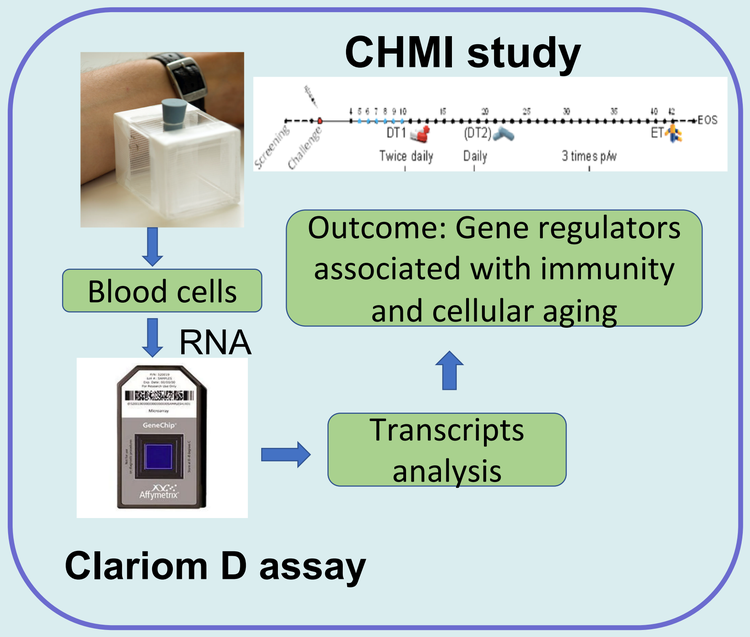
- Acute Malaria infection has a pronounced effect on cellular aging.
- The clinical consequences of acute malaria are well known, but the host could have a hidden long-term cost .
- A previous study showed that malaria infection (CHMI) accelerated telomere shortening (Miglar et al.Sci report 201).



Miglar et al. Scientific Reports 2021.

Aim: To study transcriptional regulation underlying cellular aging in controlled human malaria infection.

Method:



Conclusions: Transcriptome studies in CHMI showed important gene regulators associated with immunity and cellular aging during infection. But, the effect was fully reversed after successful treatment.

Transcriptome analysis showed distinct gene expression during infection in controlled Malaria infection (see: figure 1 A &B).

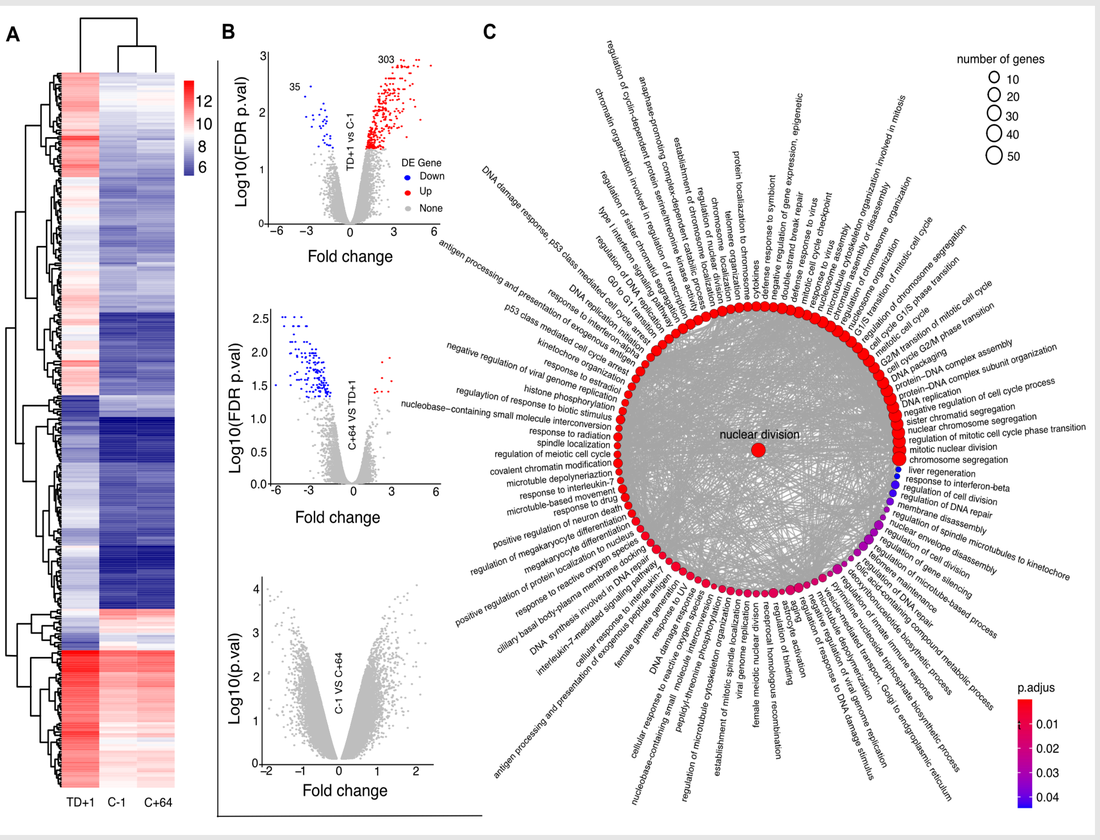


***Figure 1**: A) Heatmap of differentially expressed genes. The column TD+1 represents the infected time point, C-1 represents non-infected control, and C+64 represents the recovery time point. B) Volcano plots of differentially expressed genes in paired comparisons; TD+1 vs C-1 (during infection vs control), C64 vs TD+1 (recovery vs during infection), and C-1 vs C+64 (control vs recovery). C) Gene Ontology enrichment of differentially expressed genes.*

Functionally enriched genes are associated with immunity and different categories hallmarks of aging in controlled malaria infection (see: figure 2 A).

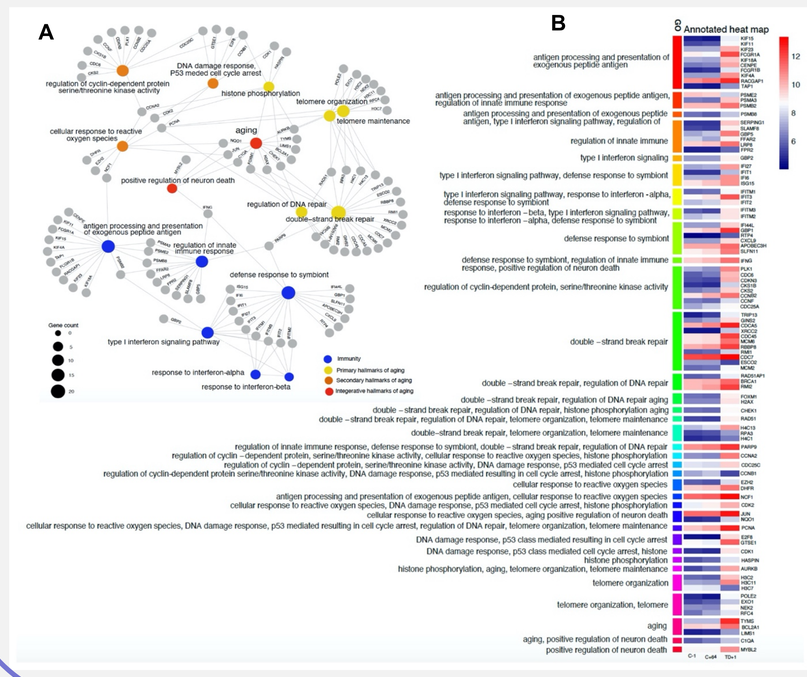


***Figure 2 (left):** A) Network plot representing linkages of important gene regulators and biological pathways; B) Annotated Heatmap representing biological pathways together with gene expressions at C-1 (control), recovery (C+64), and TD+1 (during infection). Annotation at left represents biological pathways, and annotation at right shows gene names.*

Co-expression of microRNA and mRNA showed a possible involvement in cell cycle arrest in controlled malaria infection (see: figure 3 A,B&C).

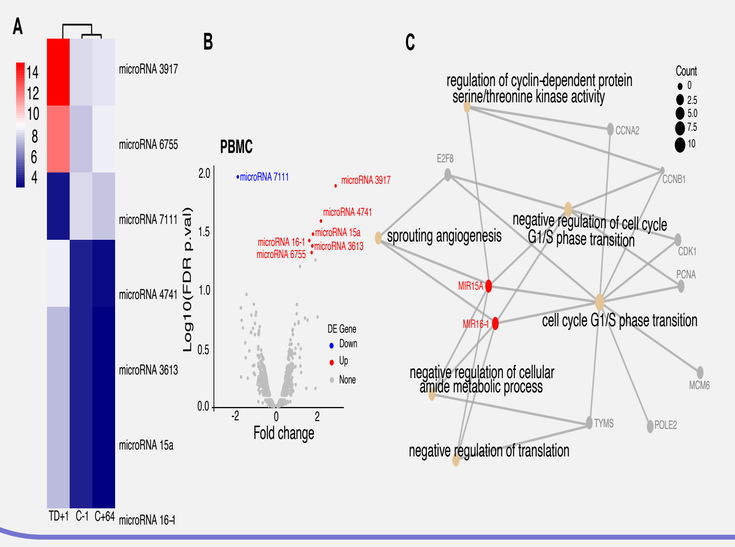


***Figure 3 (right):** A) Heatmap representing microRNA expression, B) volcano plot representing differential microRNA expression and, C) network plot representing the linkages of microRNA-mRNA and biological pathways.*

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