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Exosomal miR-451a and let-7i-5p Levels Correlate with Sickle Cell Haemoglobin Genotypes and Influence Malaria Parasite Growth

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Introduction

A sizable fraction of the world's population is afflicted by malaria, which will impact 247 million people worldwide in 2021, mostly in Africa. However, some hemoglobinopathies, such as Sickle Cell Trait (SCT), have been associated with a reduction in malaria patients' fatality rates. When both alleles of a haemoglobin mutation including inherited, sickle cell disease (SCD) can result. One allele (HbAS, HbAC) is inherited together with a normal allele in SCT. These genes' ability to protect against malaria may explain why they are so prevalent in Africa. For the diagnosis and prognosis of SCD and malaria, biomarkers are essential. According to studies, there is a difference in the expression of miRNAs in HbSS and HbAS compared to controls, particularly miR-451a and let-7i-5p. Exosomal miR-451a and let-7i-5p levels in Red Blood Cells (RBCs) and infected Red Blood Cells (iRBCs) from various sickle Hb genotypes were studied in our study, as well as their effects on parasite proliferation. We measured the levels of exosomal miR-451a and let-7i-5p in RBC and iRBC supernatants in vitro. In iRBCs from people with various sickle Hb genotypes, exosomal miRNAs had distinctive expression patterns [1].

Description

microRNAs (miRNAs) are short, non-coding RNAs that post-transcriptionally up- or down-regulate the expression of specific genes in the body. Numerous cells create miRNAs and a single miRNA may have several targets. MiRNA profiles vary between healthy and diseased states, making them potential indicators for both diagnosis and prognosis. MiRNAs may be employed as biomarkers for many illnesses, such as cancer and infectious disorders, in bodily fluids. Exosomes, which are Microvesicles (MVs) of 30 to 100 nm in size, are what keep miRNAs alive in plasma. Exosomes can be moved between different types of cells. Exosomal miRNAs have been utilised to provide novel therapeutic and diagnostic tools for cancer, chronic illnesses and infectious disorders [2].

Exosomal miRNAs are stable for long-term storage and are readily accessible in plasma and other bodily fluids, making them useful biomarkers. The function of miRNAs in malaria and SCD, however, is not well understood. By biting a human, a female anopheles mosquito transmits the Plasmodium parasite, which then releases sporozoites that move to the liver. Schizonts are created in the liver stage and burst open, releasing merozoites into the bloodstream, which results in malaria symptoms. Immature trophozoites become mature trophozoites or gametocytes during the blood stage. These gametocytes have five phases and can be passed to the female mosquito after a blood meal [3].

There were four participants per genotype among the 24 participants who were free of *P. falciparum* infection. During the 16-day measurement period, parasites developed in RBCs from persons with various sickle Hb genotypes and shown comparable patterns of overall development. Measurements of the area under the curve (AUC) showed that HbCC had the lowest and HbAA had the highest parasite growth count. Using Turkey's multiple comparison test, we also discovered that there was a significant difference between the two groups' means (p=0.03). To assess group differences while accounting for Type I error inflation, post hoc multiple comparison tests were carried out.

On days 3, 8, 9 and 16, data from daily parasite counts were analysed. The HbAC and HbSC groups had the greatest parasite counts on day three, followed by the HbAS, HbAA, HbCC and HbSS groups. It's interesting to note that on day eight, the parasite levels in HbAA and HbCC were highest. The sickle Hb genotypes did not differ significantly on day eight, despite a pattern that was comparable to day three. It's noteworthy to see that days 3, 8 and 9 had the lowest parasite counts for HbSS. Day 16 saw the lowest parasite count for HbCC, while all the other days saw the lowest parasite count for HbSS [4,5].

Conclusion

We synchronised Pf cultures so that only the ring stage was present at the start of the experiment in order to better understand parasite phase distribution. Illustrates the distribution of various parasite counts in their various morphological stages, such as rings, trophozoites, schizonts and gametocytes. It also demonstrates a modest variation in phase distribution amongst sickle Hb genotypes. Rings were continuously seen throughout the trial, but trophozoites were generally seen in the first eight days and schizonts were mostly seen after day six. AUC analysis was used to calculate the average sum of each parasite phase during the course of the 16-day timeframe. Except for HbCC, which had fewer trophozoites than the other sickle Hb genotypes, we discovered that trophozoite numbers were comparable between all sickle Hb genotypes.

This will have significant implications for the development of theoretical clinical models of mental health disorders, as well as for treatment development. This will have significant implications for the development of theoretical clinical models of mental health disorders, as well as for treatment development. For example, neural regions that exhibit a distinct pattern of decoupling in association with a mental health disorder can be targeted for real-time neural coupling training as a treatment option. Understanding how bATL-fronto-limbic interactions work will thus have important implications for clinical research. Establishing the validity of ATL connectivity as a biomarker of symptoms and treatment efficacy, in particular, should be a major motivator for future research.

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Conflict of Interest

There are no conflicts of interest by author.

References

1. Waller, Karena L., Brian M. Cooke, Ross L. Coppeln and Wataru Nunomura, et al. "Mapping the binding domains involved in the interaction between the *P.falciparum* Knob-Associated Histidine-Rich Protein (KAHRP) and the cytoadherence ligand

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P. falciparum erythrocyte membrane protein 1 (PfEMP1)." *J Biol Chem* 274 (1999): 23808-23813.

2. Ghumra, Ashfaq, Jean-Philippe Semblat, Richard S. McIntosh and Ahmed Raza, et al." Identification of residues in the $C_{\mu}4$ domain of polymeric IgM essential for interaction with *P. falciparum* Erythrocyte Membrane Protein 1 (PfEMP1)." *J Immunol Res* 181 (2008): 1988-2000.

3. Adams, Yvonne, Pongsak Kuhnrae, Matthew K. Higgins and Ashfaq Ghumra, et al. "Rosetting *P. falciparum*-infected erythrocytes bind to human brain microvascular endothelial cells in vitro, demonstrating a dual adhesion phenotype mediated by distinct *P. falciparum* erythrocyte membrane protein 1 domains." *Infect Immun* 82 (2014): 949-959.

4. Deans, Anne-Marie and J. Alexandra Rowe. "*P. falciparum*: Rosettes do not protect merozoites from invasion-inhibitory antibodies." *Exp Parasitol* 112 (2006): 269-273.

5. Wahlgren, M., J. Carlson, R. Udomsangpetch and P. Perlmann. "Why do P.falciparumm -infected erythrocytes form spontaneous erythrocyte rosettes?." *Parasitol Today* 5 (1989): 183-185.

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