Plasma microRNA and Lipid Profile Dynamics in Patients with Malaria: A Prospective Multicenter Study

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Background: Circulating microRNAs (miRNAs) hold potential as biomarkers for predicting severe outcomes and improving patient management in malaria. Acute malaria is associated with alterations in lipid profiles, attributed to systemic inflammation, but the underlying mechanisms remain unclear. Plasma miRNA expression involved in lipid metabolism may clarify these associations.

Materials and Methods: prospective, observational, multicenter study including malaria cases, November 2024-December 2025. Lipid profiles and miRNA (digital PCR-quantified: miR-27, miR-99a, miR-132, miR-143, miR-145, miR-223, miR-146a, miR-451, and miR-486) were measured at diagnosis and six weeks post-treatment.

Results: Ten cases were analyzed (median age 33.5 years, IQR 28–47; 60% male); all acquired in Sub-Saharan Africa. There were 3 migrants, 5 VFRs (visiting friends and relatives), 2 travellers. Nine cases due to Plasmodium falciparum (including 2 severe infections, 1 submicroscopic infection); one P. ovale. Post-treatment (all P. falciparum cases treated with artemisinin derivatives, with IV artesunate used in severe malaria; P. ovale case treated with chloroquine and primaquine), significant increases were observed in total cholesterol, high-density lipoprotein (HDL), low-density lipoprotein (LDL), Apolipoprotein A1 (ApoA1) and Lipoprotein (a) while significant decreases were observed in triglycerides, miR-451, miR-486, miR132 and miR146a (Table 1). Other miRNAs and Apolipoprotein B (ApoB) showed no significant changes.

Conclusion: Malaria treatment results in a significant reduction of plasma miR-451, miR-486, miR132 and miR146a, possibly reflecting erythrocyte destruction, inflammatory activation, and endothelial responses. These changes paralleled significant normalization of lipid profiles. The role of erythrocyte injury, circulating miRNAs, and lipid metabolism during malaria recovery should be investigated further.