**O1158 In silico identification of human miRNAs predicted to regulate *Plasmodium falciparum* and *P. vivax* genes**

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**Background:** An increase interest has been focused on the role that non-coding smallRNAs might play in host-parasite interaction for the progression, pathogenesis of, and susceptibility to malaria. However, it is still debated whether human miRNA (hsa-miRNA) interacts with malaria transcripts. In this study, we investigated if hsa-miRNAs target *Plasmodium falciparum* and *Plasmodium vivax* 3'- and 5'-UTR sequences using an *in silico* analysis.

**Materials/methods:** Gene transcripts sequences of *P. falciparum* and *P. Vivax* were studied to identify potential hsa-miRNA target sites in their 3'- and 5'-UTRs. The sequences of 3'- and 5'-UTRs were available in the public database for *P. Vivax* but not for *P. falciparum*. Hence, four *P. falciparum* RNA-seq raw data were downloaded from Sequence Read Archive (SRA) and processed to reconstruct the transcript sequence (including UTRs) of the *P. falciparum* transcriptome. Potential hsa-miRNA target sites in *P. falciparum* and *P. Vivax* transcripts were then searched using the miRanda software tool. Gene Ontology enrichment analysis was conducted on the identified *Plasmodium* transcripts presenting hsa-miRNA target site. Statistical significance threshold was defined as Bonferroni adjusted p-value≤0.05.

**Results:** The analyses recognized several hsa-miRNAs that are likely to target *Plasmodium* transcripts. We identified different transcripts of *P. falciparum* and *P. Vivax* as potential targets for hsa-miRNAs as reported as follows:

- *P. falciparum*: PfEMP1 (targeted by hsa-miRNA, miR-494, miR-18b, and miR-7107), GEF (miR-4698), EBL1 (miR-6854) and Stevor (miR-503);
- *P. vivax*: RAD (miR-4706, miR-5009), Phist (miR-557), Plasmodium Exported Protein (miR-4528), ribosomal protein L7a (miR-6865), PREBP (miR-668), eIF2β (miR-6860), SUMO (miR-574), 50SL33 (miR-4668), Phenylalanine-tRNA ligase (miR-4668), 40S518 (548aa), Lactate/malate dehydrogenase (4640), Prefoldins3 (miR-4644), RAB11b (miR-4769), RNA-binding protein (miR-320a) and DNAJ-like molecular chaperone protein (miR-328).

Gene Ontology enrichment analysis showed that these transcripts are mostly involved in a)malaria pathogenesis, b) parasite survival, transmission, and virulence, c) macromolecule biosynthetic process, and d) DNA replication and ribosomal related proteins.

**Conclusions:** *In silico* analysis shows that some *Plasmodium* transcripts might be a target for hsa-miRNA suggesting a novel important mechanism for regulating *Plasmodium* gene expression. These small molecules may represent novel biomarkers to identify patients with severe malaria disease and address treatment decisions. Further studies will be required to investigate functional role.