29th ECCMID Amsterdam, Netherlands 13 – 16 April 2019

The congress of ESCMID

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), 40SS18 (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.