An RNA Binding Protein from Plasmodium vivax apicoplast.

P07-04

S.M. García-Mauriño[I], **M. Hernández-Vellisca**[I], F. Rivero-Rodriguez[I], A. Díaz-Quintana[I], I. Díaz-Moreno[I]

[I]Instituto de Investigaciones Químicas (IIQ) – Centro de Investigaciones Científicas Isla de la Cartuja (cicCartuja), Universidad de Sevilla – Consejo Superior de Investigaciones Científicas (CSIC), Sevilla, Spain

Malaria parasites harbor an essential vestigial plastid-like organelle, the apicoplast. This organelle contains a ~35 kb circular genome; however, the mechanisms by which transcription and RNA translation are regulated remain poorly understood. The annotation of the *Plasmodium vivax* genome reveals a putative nuclear encoded RNA Binding Protein (RBP), namely apiRBP, that was predicted to be trafficked into the apicoplast. Although the 3D-structural model of apiRBP corresponds to a canonical RNA Recognition Motif fold, protein production trials were nevertheless unsuccessful due to protein aggregation. Theoretical solvation analysis of an apiRBP model supported these findings, highlighting an exposed hydrophobic region close to the C-terminus. Hence, in this work, we use a C-term-GFP-fused chimera to stabilize the highly insoluble apiRBP and determined its ability to bind 10-mer and 25-mer U-rich RNA stretches. The affinity (K_D in the μM range) of apiRBP towards such RNAs is highly dependent on ionic strength, suggesting that the apiRBP-RNA complex is driven by electrostatic interactions rather than π-stacking. Altogether, apiRBP represents a very attractive tool for apicoplast transcriptional studies and anti-malarial drug design.