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DRUG TARGET VALIDATION USING RNA INTERFERENCE APPROACH IN *SCHISTOSOMA MANSONI*

Marina de Moraes Mourão
Fundção Oswaldo Cruz, Brazil

The *Schistosoma mansoni* genome project identified 10,852 protein-coding genes of which almost half are annotated with unknown function. Those genes could be parasite-specific and represent genes whose biological functions are of interest for basic and applied science. Despite of great advances in the genomic field, application of technologies for schistosomiasis control have not kept pace; treatment of this disease still relies on a single drug and no vaccines are yet available. Therefore, extracting meaningful functional information from the accumulated genomic data is critical to discovering new chemotherapeutics and other novel approaches to disrupting development within the snail and human hosts. Currently, RNA interference (RNAi) is the most effective reverse genetic tools for manipulating gene expression and determining gene function in schistosome parasites, both *in vitro* and *in vivo* in the association with their hosts. Our group has dedicated efforts to understand the role of schistosome genes and their encoded protein products in the host-parasite interaction, with the goal of identifying and validating promising druggable targets. This talk aims at presenting our work applying the RNAi approach in the different parasite life cycle stages to assess the function of diverse genes such as kinases and histone modifying enzymes, to rationally identify efficient therapeutic targets for schistosomiasis control, as well as understanding the mechanisms by which *S mansoni* survives within its hosts.