

Prediction of MicroRNA Targets in *Anopheles gambiae*: Towards an Understanding of Parasitic Control by Blood-sucking Mosquito

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Plasmodium, the causative agent of malaria, has a complex life cycle between the mosquito and humans. It encounters several obstacles at each of its developmental stages and spatial transitions inside the mosquito. One of the major barriers is the midgut epithelium cell, within which it is attacked by the mosquito's innate immune system. During this stage, the number of parasites drops drastically reaching a minimum, indicating an existence of mosquito factors that regulate development of the parasite.

MicroRNA (miRNAs) are non-coding RNAs, which regulate gene expression at the level of transcription by base pairing to their messenger RNA targets. Due to this regulatory effect, miRNAs modulate the protein levels involved in numerous biological processes. Currently, over 66 miRNAs have been identified in mosquito genome, but the target genes for majority of these miRNAs have not been identified. Recent studies reported that some miRNAs displayed changes in their expression levels during *Plasmodium* infection providing a functional role for miRNAs in controlling parasite infection in the mosquito midgut. In this investigation, prediction of the miRNA targets in *Anopheles gambiae* were performed with an integrated approach incorporating functional ontologies and biological pathways by various target predication algorithms.