The first draft of the human malaria parasite's genome was released in 2002. Since then, the malaria scientific community has witnessed a steady embrace of new and powerful functional genomic studies. Over the years, these approaches have slowly revolutionized malaria research and enabled the comprehensive, unbiased investigation of various aspects of the parasite's biology. These genome-wide analyses delivered a refined annotation of the parasite's genome, provided a better knowledge of its RNA, proteins, and metabolites, fostered the discovery of new vaccine and drug targets and contributed to the foundation for modern biomedical research.

Despite the positive impacts of these genomic studies, we still have a weak understanding of the molecular mechanisms that regulate parasite virulence. Using recently developed genome-wide approaches; our laboratory is investigating the role of chromatin structure and epigenetics marks in controlling the parasite virulence.

By integrating those newly generated genome-wide data sets, we are starting to unfold the role of chromatin structure in regulating the parasite intensive replication state. All together we showed that the parasite infection is controlled by simple epigenetics characteristics that share common features with undifferentiated plant and mammalian cells. Given the major differences observed in parasite epigenetic features compared to all other eukaryotic organisms, antimalarial strategies developed against Plasmodium-specific epigenetic enzymes have a strong potential against malaria.
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