Comparative heterochromatin profiling reveals conserved and unique epigenome signatures linked to adaptation and development of malaria parasites

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Heterochromatin-dependent gene silencing is central to the adaptation and survival of Plasmodium falciparum malaria parasites, allowing clonally variant gene expression during blood infection in humans. By assessing genome-wide heterochromatin proteină1 (HP1) occupancy, we present a comprehensive analysis of heterochromatin landscapes across different Plasmodium species, strains, and life cycle stages. Common targets of epigenetic silencing include fast-evolving multi-gene families encoding surface antigens and a small set of conserved HP1-associated genes with regulatory potential. Many P. falciparum heterochromatic genes are marked in a strain-specific manner, increasing the parasite's adaptive capacity. Whereas heterochromatin is strictly maintained during mitotic proliferation of asexual blood stage parasites, substantial heterochromatin reorganization occurs in differentiating gametocytes and appears crucial for the activation of key gametocyte-specific genes and adaptation of erythrocyte remodeling machinery. Collectively, these findings provide a catalog of heterochromatic genes and reveal conserved and specialized features of epigenetic control across the genus Plasmodium.
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