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With a background spanning multiple disciplines, including molecular parasitology, entomology, microbiology, genomics, and bioinformatics, Francis's overarching goal is to comprehend the genetic and epidemiological factors that contribute to persistent malaria transmission despite control strategies. He is interested in understanding how malaria parasites adjust to environmental modifications brought about by different interventions aimed at parasite and vector populations. His focus is on investigating phenotype-genotype surveillance of drug and diagnostic resistance in natural parasite populations to inform local malaria control efforts.

Project

Molecular Epidemiological Surveillance of Plasmodium Falciparum Histidine-Rich Protein-2 Gene Deletion and Impact on Malaria Rapid Diagnostic Test Performance in Chad

Rapid Diagnostic Tests (RDTs) diagnose about 85% of all suspected malaria cases in Chad. The accuracy of the most frequently used *Plasmodium falciparum* histidine-rich protein-2 (*Pfhrp2*) based RDT is currently threatened by deletion in the *Pfhrp2* gene. The criteria of the World Health Organisation (WHO) necessitate accuracy above 95 % as the threshold for selection or withdrawal of RDTs advocating for vigorous *Pfhrp2* gene deletions mapping. The current study seeks to determine the occurrence of *Pfhrp2* gene deletion and assess its influence on RDT reliability to detect malaria in endemic regions in Chad. Data generated from this project will provide evidence to the local National Malaria Control Programme (NMCP) on programmatic decisions on *Pfhrp2*-based RDT deployment.