Investigating the -ase:
Understanding the Catalytic Function of *Plasmodium* BEM46-like Protein (PBLP)

Jillian Sheppard, Asem Qusiem, Jack Vincent, and Anna Groat Carmona*

Plasmodium parasites cycle between a vertebrate host and their *Anopheles* mosquito vector, causing the disease malaria. Sporozoites released into the skin during a mosquito blood meal will travel through the bloodstream to the liver. They differentiate into liver-stage parasites before undergoing atypical mitotic division, massively amplifying before the onset of symptomatic disease. The *Plasmodium* BEM46-like protein (PBLP) is expressed throughout *Plasmodium* development, which is an atypical expression pattern for malaria proteins and previous research indicates that PBLP plays a role in modulating malaria infectivity. Our objective is to characterize the function of the PBLP catalytic domain by creating a panel of mutant PBLP expression plasmids that can be used to further discern its role in malaria infectivity. The wild type *pblp* gene was previously introduced into a protein expression plasmid and served as the template DNA to introduce mutations into the putative PBLP active site using PCR. We amplified a 300-500 bp segment of dsDNA to serve as a mutagenesis megaprimer. During MegaWHOP PCR, these megaprimers served as both a forward and reverse primer to generate a whole mutant PBLP expression plasmid. These PCRs were successful in introducing each of the three individual amino acid mutations into the putative active site (S153N, D229K, and H258F), generating the proposed panel of mutant PBLP expression plasmids. These constructs, and our proposed triple PBLP mutant, will be assessed in future biochemical analyses of PBLP to discern its role in modulating invasive-stage morphogenesis during malaria infection, aiding in the development of anti-malaria drug therapies.