Analyzing the Biochemistry of the *Plasmodium* BEM46-like Protein (PBLP)

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Malaria is a febrile illness transmitted through Anopheline mosquitoes, causing approximately 241 million annual cases worldwide. After infected mosquitoes take a blood meal, *Plasmodium* parasites (sporozoites) proliferate to high numbers in the liver before infiltrating the bloodstream (merozoites), where they initiate the infection's symptomatic and diagnostic stage. The *Plasmodium* BEM46-like protein (PBLP) is continually expressed throughout the parasitic life cycle and plays a role in the development of infectivity, making it an ideal target for antimalarial drugs. Using a predictive protein model, we identified the putative PBLP active site, which contains a catalytic triad (S153, D229, H258) commonly seen in members of the α/β hydrolase superfamily. To gain insight into PBLP's catalytic function, we are generating a mutant panel that consists of three-single amino acid substitutions (S153N, D229K, H258F) in PBLP's active site, as well as a triple mutant, which will be analyzed alongside the wild-type (WT) protein. Our objective is to subclone these mutant *pblp* protein-coding regions into a bacterial expression plasmid using molecular cloning techniques. Afterwards, the soluble proteins can be isolated and analyzed to characterize the catalytic function of PBLP. Thus far, protein isolation using standard column chromatography methods has been unsuccessful. We are currently diagnosing issues using two different induction parameters, the incubation temperature and duration of the induction phase. Samples will be analyzed on a Western blot to determine which parameters increase protein yield. A greater understanding of PBLP function allows for further exploration of this potential drug target and the development of novel therapies.