Mutagenesis and Isolation of the *Plasmodium* BEM46-like Protein (PBLP)

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The *Plasmodium* BEM46-like protein (PBLP) plays a key role in conferring infectivity throughout the malaria life cycle, making it an exciting target for pharmaceutical development. While PBLP is predicted to have an α/β-hydrolase domain at its C-terminus, its exact crystal structure and function remain unknown. To identify the function, a catalytically inactive triple mutant (S153N, D229K, and H258F) was engineered into a protein expression plasmid using MegaWhop PCR. Additionally, wild-type (WT) PBLP was purified under native conditions, but initial results were inconclusive. A modified version of the protein induction protocol evaluated PBLP expression under different temperature (room temperature vs. 37°C) and incubation (1, 3, 5, and 8 hours post-induction) conditions. WT PBLP samples were analyzed via Western blot, which showed a very faint band at the expected size for monomeric confirmation (30 kDa) when PBLP is expressed at room temperature. This project is ongoing as we continue optimizing protein isolation conditions to characterize the exact crystal structure of PBLP and begin understanding its function. Malaria is a public health concern in many tropical and subtropical countries worldwide, and while there is a viable vaccine available, the rise in antimalarial drug resistance has yet to be addressed. The findings from this research will inform the development of new therapeutics directed against a protein expressed at all stages of the parasitic life cycle. New therapeutics will be crucial as developed nations are expected to see more vector-borne diseases when the range of mosquito vectors expands due to climate change.