Optimizing the Isolation of Plasmodium BEM46-Like Protein, an Enzyme from Malarial Parasite ***Plasmodium yoelii***

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Malaria is an infectious disease caused by *Plasmodium* parasites and is transmitted between mammalian hosts and mosquitoes. *Plasmodium* BEM46-Like Protein (PBLP) is a conserved enzyme from the α/β-hydrolase superfamily found in *Plasmodium yoelii*. Deletion of PBLP has been shown to reduce parasitemia in rodents, indicating an important role of the protein in the invasive stages of the parasite despite its native substrate and biological function being unknown. In this project, we used computational tools to predict the catalytic function and substrate specificity of PBLP, optimized the experimental protocol to isolate PBLP from E. coli, and tested purified PBLP's activity against potential substrates. Ligand docking predictions suggested that PBLP had promising interactions with ester containing ligands. Initial expression and purification of wild type and mutant truncated PBLP resulted in the protein being retained in the cell pellet. To improve the cell lysis step for isolation of PBLP, we tested the effect of enzymatic lysis using lysozyme coupled with sonication. However, we saw a significantly lower protein yield with the new lysis procedure, indicating that further optimization is necessary. Enzyme assays with p-nitrophenyl acetate and p-nitrophenyl butyrate showed that wild-type PBLP had similar activity to a catalytically-dead mutant, raising questions about the viability of the construct we were using. Future work can focus on improving the isolation and purification methods, while further testing of enzymatic activity can aid in identification of the native substrate. These findings in the project can further our understanding of *Plasmodium* parasites and contribute to the development of antimalarial treatments.