INSIGHTS TO UNDERSTANDING MALARIA PARASITE BIOLOGY: CHARACTERIZATION OF THE *PLASMODIUM* PROTEIN, MAL13P1.319

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ABSTRACT

Malaria is responsible for approximately 250 million human infections and about a million deaths annually and is caused by the protozoan parasite *Plasmodium*, with *P. falciparum* the most pathogenic form of human malaria. In an effort to discover molecules that aid in parasite invasion, *P. falciparum* MAL13P1.319 (PfMAL13P1.319) was identified by a search of the *Plasmodium* genome database and demonstrates significant similarity with orthologs in other *Plasmodium* spp. and no orthologs in humans. The PfMAL13P1.319 transcript was present during the erythrocytic stages, oocyst sporozoites, and salivary gland sporozoites and protein was detected only during the late erythrocytic stages. Additional mosquito parasite stages not previously observed or reported, such as zygotes, hemolymph sporozoites, and oocyst sporozoites, also were analyzed however displayed no detection of PfMAL13P1.319.

The functional role of PfMAL13P1.319 has yet to be determined, although multiple failed attempts at disrupting the gene would suggest that the PfMAL131.319 protein may have an important function for intraerythrocytic parasites. A comparative study of the *P. berghei* ortholog of MAL13P1.319 (PbMAL13P1.319) discovered a 2.0-kb gene predicted to encode a surface or secreted antigen and has transcript expression during the erythrocytic stages. Overall, this dissertation describes the characteristics of MAL13P1.319 in parasite biology.