

Public Abstract

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Title:Insights to Understanding Malaria Parasite Biology: Characterization of the Plasmodium Protein, MAL13P1.319

Malaria is responsible for approximately 250 million human infections and about a million deaths annually. Efforts to control malaria are increasingly demanding and therefore, the development of additional malaria control methods are crucial. Human malaria is caused by five species of the protozoan parasite Plasmodium, with *P. falciparum* the most pathogenic. There are many critical parasite stages that are essential for host-parasite interactions. Surface antigens and secreted proteins from these parasite stages are likely to be involved in infectivity and invasion of host tissues and therefore can be effective targets for control by vaccines, drugs, or novel mosquito control methods.

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 using specific criteria. The PfMAL13P1.319 protein demonstrates significant similarity with orthologs in other Plasmodium spp. and has no orthologs in humans. The PfMAL13P1.319 transcript was present during the erythrocytic stages, oocyst sporozoites, and salivary gland sporozoites via DNA microarray analyses and reverse-transcriptase PCR. To assess protein presence, immunofluorescence assays, western blot analyses and PfMAL13P1.319-GFP studies were performed. The PfMAL13P1.319 protein was present during the late erythrocytic stages and no protein was detected in the sporozoite stages. Additional mosquito parasite stages not previously observed or reported, such as zygotes, hemolymph sporozoites, and oocyst sporozoites, were analyzed however PfMAL13P1.319 was not present within these stages.

In assessing the functional role of PfMAL13P1.319, multiple attempts at disrupting the gene failed to produce a clonal population, thereby suggesting 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 that was predicted to encode a signal peptide and to be either a surface/secreted antigen. PbMAL13P1.319 transcript expression was detected during the erythrocytic stages but was not detected in oocyst sporozoites and salivary gland sporozoites of the mosquito stages, suggesting a different role of PbMAL13P1.319. Overall, this dissertation describes the characteristics of MAL13P1.319 in parasite biology.