

Public Abstract

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Title:Piecing Together the *Plasmodium falciparum* Genome Puzzle: Characterization of Genes/Protein, PFE0565w and PF11_0394

Malaria is a mosquito-borne disease caused by a protozoan parasite of the genus *Plasmodium* and affects millions of people worldwide. Therefore, there is a need for better control methods. A key stage in the *Plasmodium* life cycle is the sporozoite because it exhibits dual infectivity in both the mosquito vector and vertebrate host. Thus, it is a promising target for discovering effective ways of controlling malaria. The *P. falciparum* genes, *PFE0565w* and *PF11_0394*, were selected based on data from PlasmoDB, the *Plasmodium* database, indicating that these genes are expressed both at the transcriptional and protein level in sporozoites and are likely surface proteins. Additional sequence analysis shows that these genes have orthologs in other *Plasmodium* species and that *PF11_0394* also has orthologs in other Apicomplexans. *PFE0565w* and *PF11_0394* have transcript present during both the sporozoite and erythrocytic stages of the parasite life cycle, as demonstrated by RT-PCR. However, both of their proteins are only present during the salivary gland sporozoite stage, as indicated by immunofluorescent assays and/or GFP-trafficking studies. Even though an exact function of *PFE0565w* and *PF11_0394* in *Plasmodium* biology has not been determined, both of these proteins are good candidates for a vaccine since they are expressed by sporozoites and do not have homology with any human proteins. Lastly, in addition to studies conducted with *P. falciparum*, a preliminary comparative study between the *P. berghei* orthologs of *PFE0565w* and *PF11_0394*, PBANKA_111090 and PBANKA_091050, respectively, was conducted.