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Understanding the expression and trafficking of Plasmodium falciparum Maurer's clefts proteins

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Abstract

Malaria is a potentially fatal disease caused by parasites in the genus *Plasmodium*. Of the five species that cause human malaria, *P. falciparum* causes an estimated 1 million deaths annually, particularly in young children in sub-Saharan Africa. *Plasmodium falciparum* is most commonly found in tropical and subtropical regions of the world. After invasion into human red blood cells, parasite induced transport structures known as Maurer's clefts, are formed within red cells. In previous studies, two Maurer's clefts proteins were identified; an approximately 130 kDa peripheral membrane protein and a 20-kDa integral membrane protein. Immunofluorescence and confocal microscopy identified both proteins within large cytoplasmic vesicles in the red cell cytoplasm. The 20 kDa protein, known as *P. falciparum* Maurer's cleft two transmembrane protein (PfMC2TM), is encoded by a family of genes identified using proteomic analysis of immune complexes (IC). The gene encoding the 130 kDa protein is unknown. Furthermore, the mechanism of protein trafficking after protein expression is also unknown. Our goal in this study was to prepare IC using schizont extracts for use in proteomic analysis to identify the gene encoding the 130 kDa protein, identify the pathway of protein traffic using Brefeldin A (BFA) in *P. falciparum* cultures and perform bioinformatics analysis of the *PfMC2TM* gene family using the database, PlasmoDB (plasmodb.org). The 110 kDa Rhop-3 rhoptry protein and PfMC2TM were identified using immunoprecipitation and western blotting analysis of parasite extracts prepared with Triton X-100 in stage specific and BFA treated parasites. PfMC2TM proteins encoded by family members in *P. falciparum* strains 3D7 and IT were compared to one another and across species in *P. reichenowi.* Among the proteins encoded by paralogs in *P. falciparum,* there were some differences found. However, there was no reported expression data annotated for *P. reichenowi* within PlasmoDB. Increasing knowledge of the Maurer's clefts proteins is crucial in understanding *P. falciparum* biology and the role of the clefts in malaria vaccine development.