

Novel Gene Discovery in *Plasmodium falciparum* Malaria

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Human malaria is a leading cause of death and disease worldwide. The most severe forms of malaria result from infection by the *Plasmodium falciparum* parasite. Resistance to existing anti-malarial medications is an emerging hurdle to the effective treatment of malaria. A molecular understanding of the fundamental biological process of *P. falciparum* replication will provide the necessary tools to develop new anti-malarial therapeutics. Although the genome of *P. falciparum* has been fully sequenced, the function of more than half of the 5,300 genes in the parasite remains unknown. Many of the genes with unknown function have little or no homology with characterized genes from other organisms. Therefore, existing molecular genetic and bioinformatics techniques cannot be used to efficiently determine the function of many of the genes in the parasite. Our goal is to discover essential genes in *P. falciparum*. We have generated a transgenic parasite strain that readily allows high throughput analysis of the growth and replication of individual parasite clones. Utilizing the automated liquid handling facilities at ICCB-Longwood, we are able to perform a forward-genetic screen for essential genes in *P. falciparum*. The long-term objectives of these studies are to identify novel targets for new anti-malarial therapeutics.