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The epidemiology of the human malaria, *Plasmodium falciparum*, has been vastly improved by the introduction of molecular biology techniques to study parasite biology, parasite genetics and parasite genetics. The development of molecular biological techniques has provided a new look at parasite biology that is critical for the continuing search for an effective malaria vaccine and the development of anti-malarial drugs. The level of parasite biomass is an important determinant of host-parasite interactions. To examine the dynamics of the parasite biomass with time, DNA samples obtained from peripheral blood at different time points, and from different geographic locations (East Asia, South America and Africa) are being examined for parasite genes. To obtain quantitative data on the parasite biomass with time, we are screening many of the samples using PCR primers for the repeat unit of the merozoite surface protein 2 gene. We are also attempting to identify the parasite genes that are expressed during erythrocyte invasion. Once we determine the time and location of parasite growth, we will correlate the levels of parasite biomass with the expression of variant surface antigens. Studies on parasite immunogenicity are being performed by three groups. The first examines immune response in *P. falciparum*-infected children from Ngorongoro District, Tanzania (Wright et al.). The second group examines immune response in infants in an endemic area (Gaur et al.) and in patients undergoing chloroquine treatment (Klur et al.). The third group has begun characterizing the cellular immune response of patients to the merozoite surface protein 1 (MSP1) following treatment with chloroquine or artemisinin derivatives. 82157476af

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