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New Interventions for Malaria: Mining the Human and Parasite Genomes

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Abstract. Malaria has been the greatest scourge of humankind for many millennia, and as a consequence has had more impact than any other pathogen in shaping the human genome. The sequencing of the human genome provides a new opportunity to determine the genetic traits that confer resistance to infection or disease. The identification of these traits can reveal immune responses, or host–parasite interactions, which may be useful for designing vaccines or new drugs. Similarly, the parasite genome sequence is being exploited to accelerate the development of new ant malarial interventions, for example by identifying parasite metabolic pathways that may be targeted by drugs. The malaria parasites are well known for their ability to undergo antigenic variation and in parallel to cause a diverse array of disease syndromes, including the severe syndromes that commonly cause death. Genome-based technologies are being har- nessed to relate gene and protein expression levels, or genetic variation, to the parasite forms that are targets of protective immunity. Well-conducted clinical studies are required to relate host or parasite diversity with disease. However, genomics studies of human populations raise important ethical issues, such as the disposition of data related to disease susceptibility or paternity, and the ability of communities to understand the nature of the research.