

PREFACE

Malaria remains one of the most serious and widespread causes of pathogen-specific mortality in humans. The disease affects between 350 and 500 million people globally each year. There are estimated to be between 1 and 2 million deaths annually, with over 90% of cases occurring in sub-Saharan Africa. Malaria is an expanding health problem in many developing countries (WHO, 2005). The escalating disease burden has significant implications for social development and economic performance. Malaria costs Africa approximately US\$12 billion in lost gross domestic product and about 40% of public health spending (WHO, 2005). Attempts to control the disease have failed due to increasing resistance of the parasite to drugs and the resistance of *Anopheles* mosquitoes to insecticides. Together with failing healthcare services in some countries and a climate conducive to vector survival, these factors highlight the need for new approaches in combating the disease. These include the identification of novel therapeutic agents and the development of vaccines targeted to various stages of the parasite life cycle (Ridley, 2002).

Malaria is caused by a group of infectious protozoan parasites (family: Haemosporidiidea; genus: *Plasmodium*) that alters the physiological functioning and cellular biology of erythrocytes. There are four generally recognised malaria protozoa that infect humans: *Plasmodium malariae*, *P. vivax*, *P. ovale* and *P. falciparum* (Bray and Garnham, 1982). *P. falciparum* is the best-studied species, which is highlighted by successful development of the continuous culture of *P. falciparum in vitro* (Trager and Jensen, 1976). This parasite is also the commonest, most virulent and principal cause of the majority of infections and deaths worldwide. Of particular pathophysiological importance, the sequestration of *P. falciparum* infected erythrocytes within the microvasculature of the brain is believed to be one of the principal events in the development of cerebral malaria (Newbold et al., 1999).

The completion of the *P. falciparum* genome sequence has provided a comprehensive blueprint for analysing gene expression and protein function in the malaria parasite (Gardner et al., 2002). The genome encodes approximately 5,300 genes and represents a major advance in our understanding of this species. However, biological profiling of the predicted genes has only resulted in the functional classification of around one third of the parasite's proteome. Assigning function to the remaining hypothetical proteins will therefore represent a major challenge to researchers in the new post-genomic era (Florens et al., 2002; Gardner et al., 2002).

To date, a wealth of knowledge has been generated through a number of genomic and proteomic studies. Methods for high-throughput screening have provided valuable insight into the transcriptome of *P. falciparum* (Bozdech et al., 2003; Le Roch et al., 2003). Studies utilising protein identification technology, such as mass spectrometry, have resulted in the identification and characterisation of predicted proteins (Carucci et al., 2002; Florens et al., 2002; Lasonder et al., 2002; Sowa et al., 2004). The application of gene knockout technology (Carvalho and Menard, 2005; Horrocks and Lanzer, 1998) and RNA interference (Dasaradhi et al., 2005; Gissot et al., 2005; Malhotra et al., 2002; Ullu et al., 2004) will assist further in deciphering the complex molecular processes governing the parasite's life cycle.