Progress in understanding the malarial parasite

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About 2 million people die of malaria every year, of which more than a million are children in sub-Saharan Africa. Malaria is caused by a protozoan parasite belonging to the genus Plasmodium, and Plasmodium falciparum is responsible for the most severe form of malaria. Due to the increasing incidence of resistance to existing drugs, there is a growing need to discover new and more effective drugs against malaria.

In a new study publishing in *PLoS Computational Biology* on September 14, 2007, Dr. Tatu and colleagues from the Indian Institute of Science have constructed a chaperone interaction network for the parasite which provides, for the first time, a rational basis for the anti-malarial effect of known drugs and highlights new proteins that can potentially be used in the fight against malaria.

Recent reports from several labs point to a critical role played by a group of proteins termed molecular chaperones. These chaperones participate in the maintenance and growth of cells and are implicated in parasite survival and growth. Although a vast body of information is available regarding individual chaperones, few studies have attempted a systems level analysis of chaperone function. The researchers' systems-level approach provides information on 95 different chaperones in the parasite and also provides insights into their business partners and cellular processes that they might regulate.

Analysis of the network reveals the broad range of functions regulated by chaperones. The network predicts involvement of chaperones in

chromatin remodeling, protein trafficking, and cytoadherence. Importantly, it allows making predictions regarding the functions of hypothetical proteins based on their interactions. Analysis of the network provides a rational basis for the anti-malarial activity of geldanamycin, a well-known Hsp90 inhibitor, and provides a theoretical basis for further experiments designed toward understanding the involvement of this important class of molecules in parasite biology.

Source: Public Library of Science