PublisherInfo		
PublisherName	:	BioMed Central
PublisherLocation	:	London
PublisherImprintName	:	BioMed Central

Plasmodium proteomics

ArticleInfo		
ArticleID	:	4599
ArticleDOI	:	10.1186/gb-spotlight-20021004-01
ArticleCitationID	:	spotlight-20021004-01
ArticleSequenceNumber	:	265
ArticleCategory	:	Research news
ArticleFirstPage	:	1
ArticleLastPage	:	3
ArticleHistory	:	RegistrationDate : 2002–10–4 OnlineDate : 2002–10–4
ArticleCopyright	:	BioMed Central Ltd2002
ArticleGrants	:	
ArticleContext	:	130593311

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In the October 3 Nature, Laurence Florens and colleagues describe a large-scale proteomic study that complements the genome sequencing approach to understanding the malaria parasite Plasmodium falciparum (*Nature*, **419:**520-526, October 3, 2002).

The *Plasmodium* life cycle is extremely complex, as the parasite must adapt to both vertebrate and invertebrate hosts, invade different cell types and evade the immune system. As a consequence of this, not all the stages of the parasite life cycle are amenable to cultivation and characterization *in vitro*.

Florens *et al.* analyzed the proteome isolated from different stages; sporozoites (the human infectious form), merozoites (the invasive stage), trophozoites (the form multiplying in erythrocytes) and gametocytes (sexual stages). Using multidimensional protein identification technology (MudPIT) they were able to detect about half of the predicted *Plasmodium* genes in the four stages - only 6% of proteins were common to all four stages.

The sporozoite proteome was very different from the others with half of the proteins unique to this stage. The merozoite stage was characterized by the expression of surface proteins that mediate invasion and immune evasion. Serine proteases - important for the digestion of hemoglobin - are expressed at the trophozoite stage and gametocyte-specific proteins, ribonucleoproteins and transcription factors were identified in the gametocyte proteome.

When they mapped the expressed genes back on to the *Plasmodium* genome they found that co-expressed proteins were often located in chromosomal clusterssuggesting coordinated regulatory mechanisms.

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