Sporozoite transcriptome

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The protozoan parasite Plasmodium causes malaria, the most serious parasitic disease in humans. The identification of proteins expressed at the infectious sporozoite stage is important for the selection of potential vaccine candidates. In the August 14 Proceedings of the National Academy of Sciences, Stefan Kappe and colleagues from the New York University School of Medicine describe attempts to characterize the sporozoite transcriptome (*Proc Natl Acad Sci USA* 2001, **98**:9895-9900). They constructed a high-quality cDNA library from salivary gland sporozoites of the rodent malaria parasite Plasmodium yoelii, using PCR amplification to overcome the limited material resource. They then generated almost two thousand expressed sequence tags (ESTs), corresponding to 1,547 unique sequences. About one third of the predicted proteins are of unknown function, while others are likely to be kinases, phosphatases and secreted or transmembrane proteins. The latter may be involved in host-cell invasion and are therefore potential vaccine targets. Kappe *et al.* characterized three of these sporozoite sequences: MAEBL, SPATR (secreted protein with altered thrombospondin repeat) and Py52, a member of the six-cysteine superfamily. The identification of sporozoite-specific genes will contribute to understanding of the complex malaria life cycle and should help attempts to develop effective vaccination strategies.

References

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