Analysis of *Plasmodium falciparum* differentially expressed gene transcripts

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Malaria is the most debilitating infectious disease worldwide. It is a blood disease caused by *Plasmodium* parasites and transmitted by the *Anopheles* mosquito. The life cycle of the parasite is complex, and requires a coordinated control of gene expression as it switches from the asexual pathogenic stages to the sexual transmissible stage. In this research Reverse Transcription Polymerase Chain Reaction Differential Display was used to compare the gene expression profile of the asexual blood stages and the gametocyte (sexual) stages of the parasite to gain a better understanding of the unique functional requirements of these two developmental stages. 22 fragments were differentially expressed and the corresponding genes were identified by BLASTN and BLASTX similarity searches. These were placed into categories consisting of single genes, gene families and non protein-coding genes based on the confidence with which their identities could be ascertained. Genes such as PfEMP1 involved in antigenic variation, metabolic enzymes such as HPRT and genes coding for structural proteins were amongst the genes identified. A third of the genes are annotated only as hypothetical proteins. Of specific interest are five transcripts representing two ribosomal RNA genes that showed a distinct pattern of asexual stage-specific expression. These are known to play an important role in gene regulation at the protein translational level, but their specific function with regard to sexual development is not known. A greater understanding of this process will facilitate the development of a malaria transmission blocking vaccine.