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Functional annotation and pathway analysis of genes differentially expressed in different stages of *Plasmodium falciparum* using RNA-Seq Data

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Abstract

Plasmodium falciparum, the deadly protozoan parasite, causes malaria. Malaria remains one of the deadliest infectious diseases in the world. The RNA-Seq data sets were downloaded from NCBI Short Read Archive under accession number SRP009370 for our analysis. Differentially expressed genes (DEGs) between Ring (R) and early trophozoite (ET), late trophozoite (LT), schizont (Sc), gametocyte stages (GII), gametocyte stages (GV), ookinete (Oo) stages are 2442, 2796, 2935, 2807, 2180, 2895 respectively. There are total 4594 unique DEGs in the samples. DAVID was used to categorize enriched biological themes in the list of DEGs. It can be seen that main functions related to GO term 'Biological Process' are antigenic variation, pathogenesis, single organismal cell-cell adhesion, GO term 'Cellular Component' are host cell plasma membrane, infected host cell surface knob and GO term 'Molecular Function' are cell adhesion molecule binding, ATP-dependent RNA helicase activity. We found that PF3D7_1000400, PF3D7_1000600, PF3D7_0900500, PF3D7_0901500, PF3D7_0937400 were most up regulated and PF3D7_0632800, PF3D7_0711700, PF3D7_0712400, PF3D7_0712600, PF3D7_0712900, PF3D7_0808600 and PF3D7_0808700 were most down regulated genes involved in antigenic variation. Also PF3D7_0930300 was most up-regulated in Sc, LT and Oo stages and PF3D7_0936500 was most up-regulated in GV stage and PF3D7_0632800, PF3D7_0711700, PF3D7_0712400, PF3D7_0712600, PF3D7_0712900, PF3D7_0808600, PF3D7_0808700 were most down regulated genes involved in pathogenesis. A total of 300 pathways were predicted using KAAS server. Majority of the DEGs were found to be associated with important biological pathways such as metabolic pathways, biosynthesis of secondary metabolites, ribosome, spliceosome, biosynthesis of antibiotics, purine metabolism.

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