



Category: Bioinformatics

Comparative Genome analysis of *Plasmodium sp.* and identification of unique signature with Next Generation Sequencing Technology

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Abstract

Malaria is a malignant disease which is growing all over the world and its causative agent. *Plasmodium* species easily develops resistant to commonly used antimalarial drugs easily. These empower different strains of *Plasmodium* e.g. *Plasmodium falciparum* and *Plasmodium vivax* to infect humans with malaria. To get the deeper molecular insights, next generation sequencing data were used for further analysis as it has shifted the paradigm of genomics to address biological questions with high confidence and in timely manner. The short reads for above mentioned parasites were retrieved from SRA (Sequence read archive) and *de novo* assembly was performed. Several novel genes along with known genes were predicted from assembled contigs, Functional annotation followed by gene ontology and pathway analysis. Comparison between species gave structural and functional diversity of the specific genes responsible for disease condition which further can be studied for disease biology.

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