

Resource Summary Report

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Full-Malaria: Malaria Full-Length cDNA Database

RRID:SCR_002348

Type: Tool

Proper Citation

Full-Malaria: Malaria Full-Length cDNA Database (RRID:SCR_002348)

Resource Information

URL: http://fullmal.hgc.jp/index_ajax.html

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Description: FULL-malaria is a database for a full-length-enriched cDNA library from the human malaria parasite *Plasmodium falciparum*. Because of its medical importance, this organism is the first target for genome sequencing of a eukaryotic pathogen; the sequences of two of its 14 chromosomes have already been determined. However, for the full exploitation of this rapidly accumulating information, correct identification of the genes and study of their expression are essential. Using the oligo-capping method, this database has produced a full-length-enriched cDNA library from erythrocytic stage parasites and performed one-pass reading. The database consists of nucleotide sequences of 2490 random clones that include 390 (16%) known malaria genes according to BLASTN analysis of the nr-nt database in GenBank; these represent 98 genes, and the clones for 48 of these genes contain the complete protein-coding sequence (49%). On the other hand, comparisons with the complete chromosome 2 sequence revealed that 35 of 210 predicted genes are expressed, and in addition led to detection of three new gene candidates that were not previously known. In total, 19 of these 38 clones (50%) were full-length. From these observations, it is expected that the database contains approximately 1000 genes, including 500 full-length clones. It should be an invaluable resource for the development of vaccines and novel drugs. Full-malaria has been updated in at least three points. (i) 8934 sequences generated from the addition of new libraries added so that the database collection of 11,424 full-length cDNAs covers 1375 (25%) of the estimated number of the entire 5409 parasite genes. (ii) All of its full-length cDNAs and GenBank EST sequences were mapped to genomic sequences together with publicly available annotated genes and other predictions. This precisely determined the gene structures and positions of the transcriptional start sites, which are indispensable for the identification of the promoter regions. (iii) A total of 4257 cDNA sequences were newly generated from murine malaria parasites, *Plasmodium yoelii yoelii*. The genome/cDNA sequences were compared at both nucleotide and amino acid levels, with those of *P.falciparum*, and the sequence alignment for each gene is presented graphically. This part of the database serves as a versatile platform to elucidate the function(s) of malaria genes by a

comparative genomic approach. It should also be noted that all of the cDNAs represented in this database are supported by physical cDNA clones, which are publicly and freely available, and should serve as indispensable resources to explore functional analyses of malaria genomes. Sponsors: This database has been constructed and maintained by a Grant-in-Aid for Publication of Scientific Research Results from the Japan Society for the Promotion of Science (JSPS). This work was also supported by a Special Coordination Funds for Promoting Science and Technology from the Science and Technology Agency of Japan (STA) and a Grant-in-Aid for Scientific Research on Priority Areas from the Ministry of Education, Science, Sports and Culture of Japan.

Synonyms: Full-Malaria

Resource Type: database, data or information resource

Defining Citation: [PMID:18987005](#), [PMID:14681428](#)

Keywords: drug, eukaryotic, expression, function, gene, alignment, amino acid, cdna, chromosome, clone, coding, comparative, genome, genomic, human, malaria, medical, nucleotide, oligo-capping, organism, parasite, pathogen, physical, plasmodium falciparum, promoter, protein, region, sequence, sequencing, unicellular eukaryote genome databases, vaccine

Resource Name: Full-Malaria: Malaria Full-Length cDNA Database

Resource ID: SCR_002348

Alternate IDs: nif-0000-21157

Record Creation Time: 20220129T080212+0000

Record Last Update: 20260805T044038+0000

Ratings and Alerts

No rating or validation information has been found for Full-Malaria: Malaria Full-Length cDNA Database.

No alerts have been found for Full-Malaria: Malaria Full-Length cDNA Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#).

Swann J, et al. (2015) Systems analysis of host-parasite interactions. Wiley interdisciplinary reviews. Systems biology and medicine, 7(6), 381.

Yamagishi J, et al. (2014) Interactive transcriptome analysis of malaria patients and infecting *Plasmodium falciparum*. Genome research, 24(9), 1433.