

## Studies on comparative modeling of 51kda protein from *Plasmodium falciparum*

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### Abstract

The main aim of the present work was concern with protein sequencing and structural analysis of *Plasmodium falciparum*. The 120 samples of malarial infected individuals were collected in Thanjavur, Nagapattinam and Cudallore districts of Tamil Nadu, India. The 51 kDa sequence was isolated by using electroblotting method. The structural prediction and sequence analysis of 51 kDa parasitic protein were made by using SOPMA and Ramachandran Plot. Finally that predicts the enzymatic protein such as acetyl co-enzyme A carboxylase, propionyl COA Carboxylase and methyl transferase A. © 2010 IJRSR. All rights reserved.

**Key words:** Modeling, *Plasmodium falciparum*, 51kDa protein, sequence analysis.

### 1. Introduction

Malaria is a vector borne infectious disease caused by plasmodium. The clinical symptoms include fever, shivering, headache, joint pain and vomiting. In severe cases, patients can have jaundice, kidney failure, anemia and can lapse in to coma. Malaria has reemerged as a major public health problem in India during the Past few years (Perlin and Cohen, 1970). Proteins are essential for biological process they are responsible for catalyzing and regulating biochemical reactions then also transporting of various molecules (Chan and Dill, 1993). By the protein function can be understood it terms of its structure. In deed the 3D structure of proteins (Bohr *et al.*,1990) are closely related to biological functions and then proteins that perform similar functions tend to show a significant degree of structural homology (Voet and Voet, 1990) . There are several reports about the kDa proteins of *plasmodium falciparum* (Rees-Channera *et al.*,2006) and can also reported that 45 kDa Protein detected in membrane klefts of erythrocytes infected with *plasmodium falciparum* (Goldberg, 1991; Camus, 1985).

They also suggest that the synthesis of enzymes can having 51 kDa that can cleave to other enzymes (Banerjee *et al.*, 2002).

Acetyl COA Carboxylase is required to convert acetyl COA to Malonyl coA (Mabrouk *et al.*, 1990) and in important step by allosteric modifiers, induction, repression and covalent modification reactions. In gluconeogenesis Pathway was regulated by propionyl COA carboxylase the tool SOPMA and Ramachandran Plot used secondary structural Prediction (Ramachandran *et al.*, 1963). The investigation was mainly concern with comparison modeling of structural prediction and sequence analysis of 51 kDa protein from *Plasmodium falciparum*.

### 2. Materials and methods

#### 2.1. Samples

Totally 120 samples were collected from both male and female (age range of 20 to 50 years) of during the period of monsoon (from September 2006 to November 2009) in Thanjavur, Nagapattinam and Cudallore districts of Tamil Nadu, India. 72 malarial

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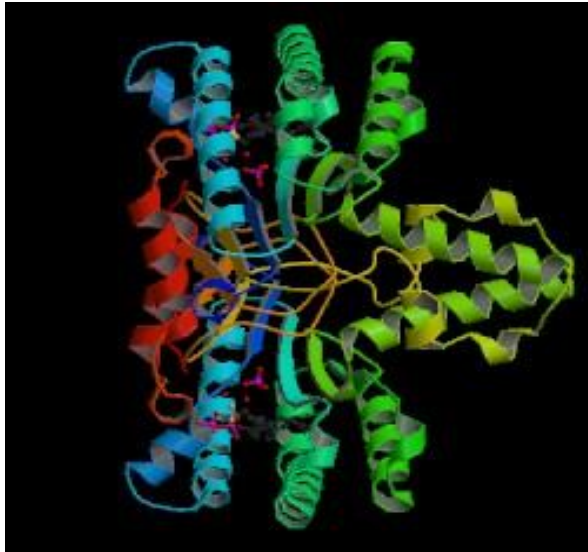


Fig. 1: Acetyl co – enzyme A cerboxylase (accD3)

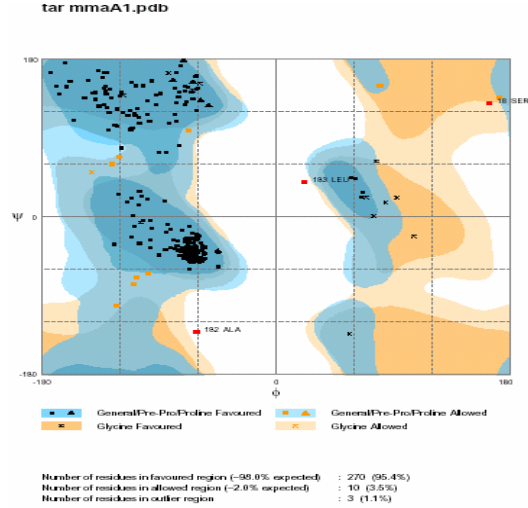


Fig. 3 Propionyl COA carboxylase (accD4)



Fig.2. Propionyl COA carboxylase (accD4)

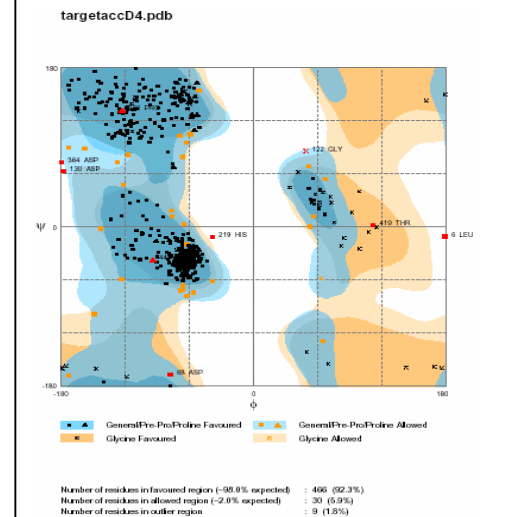


Fig. 4 Methyl Transeferase A1

infected individuals were identified by Giemsa staining method.

**2.2. Serum**

5 ml venous blood was obtained from each of the patient by venepuncture of the antecubital vein by using a sterile needle and syringe. The blood samples were then transferred to clean sterile centrifuge tube and allowed to clot for few minutes. Each clotted samples were centrifuged at 3000 rpm for 10 minutes to obtain sera. 5 ml venous blood was obtained from each of the patient by venepuncture of the antecubital vein by using a sterile needle and syringe. The blood samples were then transferred to clean sterile centrifuge tube and allowed to clot for few minutes. Each clotted samples were centrifuged at 3000 rpm for 10 minutes to obtain sera. Protein profile and elution of protein from gel were made in *plasmodium falciparum* infected serum samples. Bands are visualized on the slab gel after destaining.

**2.3. Isolation**

By the sequence of target 51 k Da protein was isolated by using electro blotting method (Bodhe *et al.*, 1982) and the protein data bank (PDB) was used for obtaining the secondary structure (Kabsch, 1983; Qian and Sejnowski, 1988; Wilox, 1990) with enough sequence similarity of target 51 kDa Protein selected and using the alignment the co-ordinates of matching residues in the known structure was predict and sequence analysis by SOPMA and Ramachandran plot (Ramachandran *et al.*, 1963).

**3.4 Structural prediction and sequencings by SOPMA**

Recently a novel tool such as self optimized prediction method ( SOPM) and the modified as (SOPMA) has been described (Sali and Blundell, 1993) to improve the success in the prediction of secondary structure of 51 kDa proteins . By this report improvements brought about by predicting all the sequenced correctly Predicts (Kissinger and Brunk 2002) about 69.5% of secondary structure of 3 dimensional proteins SOPMA correctly predict 82.2% of aminoacid residues and 74 % of co –predicted monoacids in sequence analysis by the total length of 2 helix, extended strand, turn and random coil were analysed (King-Haw *et al.*,2002).

**3.5. Structural prediction by Ramachandran plot**

A bioinformatics tool MODELLER was used for homology modeling of protein 3D structure. By the target 51 kDa Protein structure with enough sequence similarity and amino acid residues (Luc Nicolas, 1993) using the alignments the coordinates of the matching residues in the known structure were copied to the

unknown protein and the resulting model was evaluated by using Ramachandran Plot (1963).

**3. Result and discussion**

**3.1. Structural prediction of accD3 and accD4 by SOPMA method**

By the structural prediction of acetyl coenzyme – A carbo xylase was retrieved by 3D Structural prediction method. A suitable homology was built by using the software MODELLER to retrieve the 3 D structure of the target protein that was given as input. The best method at minimum energy level obtained the best 3 D structure was viewed as shows ( Fig. 1 and 2) with the help of SOPMA method were predicted. SOPMA Correctly Predicts 82.2 % of amino acid residues and 74 % of Co – predicted amino aids, in β – subunit structural protein.

**3.2. Sequencing analysis of accD3 and accD4**

The total sequence length having about 495, by the total length include α-helix β turn, extended strand and random coiling sequence. There are about 220α-helix (Hh) sequence 35 Beta turn (Tt) Sequence, 85 extended strand (Ee) and 155 random coiled (CC) sequences were analyzed

**SOPMA RESULT**

**accD3**

10 20 30 40 50 60

70

```

| | | | |
MSRITTDQLRHAVLDRGSFVSWDSEPLA
VPVADSYARELAAARAATGADESQVGTGE
GRVFGRRVAVVACE

hhhccchhhhhhheecttceeeetccccchhhhhhhhhh
hhhhhtcchheecttccceetceeeehh

FDFLGGSIGVAAAERITAAVERATAERLP
LLASPSSGGTRMQEGTVAFLQMVKIAAAI
QLHNQARLPYL V

hecccccehhhhhhhhhhhhhhhhhhhtcccccccccccc
chhhhhhhhhhhhhhhhhhhhhhhhhhhhhhtccccce

YLRHPTTGGVFASWGLGHLTVAEPGAL
IGFLGPRVYELLYGDPFPGSVQTAENLRR
HGIIDGVVALDRL

eccccccccceehhtttceeeccctceeeccccheeeeeccc
ccccchhhhhhhhhhhhttcctheeehhhh
```

RPMLDRALTVLIDAPEPLPAPQTPAPVPD  
VPTWDSVVASRRPDRPGVRQLLRHGATD  
RVLLSGTDQGEAA

hhhhhhhhheeeccccccccccccccccchheeeccc  
ccccchhhhhhhhhheettccccch

TLLALARFGGQPTVVLGQQRVGGGGG  
TVGPAALREARRGMALAAELCLPLVVI  
DAAGPALSAAAEQG

hhhhhhhhtttceeeeeecehhecccccccchhhhhhhh  
hhhhhhhtceeeeeeccccchhhhhhh

GLAGQIAHCLAELVTLDTPTVSILLGQGS  
GGPALAMLPA DRVLAALHGWLAPLPPEG  
ASAIVFRDTAAHA

chhhhhhhhhhhhtccccceeeeeeccccceeeecch  
hhhhhhhhheeccttcheeeecchhhhh

ELAAAQGIRSADLLKSGIVDTIVPEYPPDA  
ADEPIEFALRLSNAIAAEVHALRKIPAPER  
LATRLQRYRRI

hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh  
hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh

GLPRD

tcctt

Sequence length : 495

SOPMA :

Alpha helix (Hh) : 220 is 44.44%

Extended strand (Ee) : 85 is 17.17%

Beta turn (Tt) : 35 is 7.07%

Random coil (Cc) : 155 is 31.31%

accD4

10 20 30 40 50 60  
70

| | | | | | |

MTVTEPVLHTTAEKLAELRERLELAKEP  
GGEKAAAKRDKKGI PSARARIYELVDPG  
SFMEIGALCRTPGD

eecccchhhhhhhhhhhhhhhhhhhhhhhhhhhcttchhhhhhhct  
tcccchhhhhheeccttceeehhhhcccc

PNALYGDGVVTGHGLINGRPVGVFSDHQ  
TVFGGTGEMFGRKVARLMEWCAMVG  
CPIVGINDSGGARIQD

ccccceeeeeecccccttceeeeeeccccctccccchhhhh  
hhhhhhhhcttceeeeccttcccchhh

AVTSLAWYAELGRRHELLSGLVPQISILG  
KCAGGAVYSPIQTDLVAVRDQGYMFV  
TGPDVIKDVTEG

hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh  
hheeeetttceeeeeeceehhcccc

VSLDELGGADHQASYGNIHQVVESEAAA  
YQYVRDFLSFLPSNCFDKPPVVNPGLEPEI  
TGHDLELDSIVP

chhhcecccchhhcttchhhhhhhhhhhhhhhhhhhhhhhcc  
ccccccccccccccccccccchhhhhccc

DSDNMAYDMHEVLLRIFDDGDFLDVAA  
QAGQAITGYARVDGR TVGVVANQPMH  
MSGIDNEASDKAARF

cccccccchhhhhhhhhcttchhhhhhhchheeeehct  
tceeeeeecccccttcccchhhhhhhhh

IRFSDAFDIPLV FVVDTPGFLPGVEQEKN  
IIRGGRFLYAVVEADV PKVTITIRKSYG  
GAYAVMGSKQL

eehhhccccceeeeccttccccchhhhhhhhhhhhhhh  
hhtccccceeeeccttceeecccc

TADLNFAWPTARIAVIGADGAAQLLMKR  
FPDPNAPEAQAIRKSFVENYNLMAIPWI  
AAERGFIDAVIDP

cccccecccchheeeecttchhhhehhhhhhhhhhhhhhhh  
hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh

HETRLLLRKSMHLLRDKQLWWRVGRKH  
GLIPV

cccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh

Sequence length : 522

SOPMA :

Alpha helix (Hh) : 213 is 40.80%

Extended strand (Ee) : 90 is 17.24%

Beta turn (Tt) : 38 is 7.28%

Bend region (Ss) : 0 is 0.00%

Random coil (Cc) : 181 is 34.67%

Total carboxylase length having about 522. In this total length of the Propionyl CoA carboxylase having 213  $\alpha$  helix (Hh) Sequences, 90 extended (Ee) and then included 38 beta turn (Tt) Sequence, 181 random coil (Cc) Sequences were analysed.

### 3.3. Structural prediction of *accD4* and *mmA1* by Ramachandran Plot method

Ramachandran Plot showed that the number of aminoacids residues present in the favored region. In this propionyl co A carboxylase *accD4* (Fig. 3) having 466 residues (92.3 %) Present in favoured region. By the allowed region contain (5.9%) of residues and in the outside region contain only (1.8%) of residue were found (i.e – 9 residues) suggesting that a good model. Among that favoured and allowed region contain rich amount preproline and glycogen residues region contain rich amount of preproline and glycogen residues

### 3.4. Methy transfereas A1 (*mmA1*)

Only 270 residues were found (95.4 %) in the favoured region. In Methy transfereas A (Fig. 4), contain much amount of preproline and glycine residues in favored and allowed region. By the residues (3.5%) found in allowed region and lesser amount such as (1.1 %) of residues found in outside region.

The built model was evaluated using comparison of SOPMA and Ramachandran Plot. The comparison modeling is a protein data bank (PDB) for 3 D structural prediction and sequence analysis. By the self optimized method (SOPMA) was used to predict 3D structure and correctly sequencing about 69.5 % of 3D Structural proteins 82.2 % of amonocid residues. Evaluation of the model using Ramachandra Plot showed that the number of residues present in the favoured region allowed and outside regions.

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