5. DISCUSSION

5.1. CLINICAL ASPECTS

5.1.1. SURVEY OF MALARIA INFECTED INDIVIDUALS

The most important disease of the coastal marshes, must have been Malaria. Though nowadays associated with the subtropics, indigenous Malaria has been present (Chwatt and Zulueta, 1980). The effect of gender on Malaria susceptibility varied from area to area and from season to season (Giha et al., 2000).

In this context, statistically significant difference in infection rate between Males and Females was observed. Females had lower infection rate than that of Males. This is likely to be due to the fact that women in this area as part of their traditional and social practice apply local cosmetic ointments on their skins and they have a tendency to expose their bodies to smoke for cosmetic purposes and cover their bodies before sleeping, in contrast to areas where Malaria endemic city is seasonal and unstable where the disease affects all age groups (Macdonald, 1957).
5.1.2. HAEMATOLOGICAL PARAMETERS OF INFECTED INDIVIDUALS

A definite diagnosis of malaria depends on finding parasites in the blood. This is because the symptoms of malaria, particularly fever, are shared with numerous ailments. The thick smears permit examination of a greater number of red blood cells. The thin smear is useful for identifying the species of the parasites, that’s a major tool in malarial field works.

The white blood cells formed in the bone marrow especially the granulocytes are stored within the marrow until they are needed in the circulatory system. The most important function of white blood cells that invade the pathogenic infection and various injurious agents, and mediate immune system in host. The total and differential white blood cells were increased in many pathogenic infections and inflammations.

Erythrocyte sedimentation rate is one of the hematological indicators of the systemic diseases. The growth of malaria parasites on the red cells is dependent on the catabolism of the hemoglobin in the red cells, (Philips, 1983). In its human host, heme detoxification is one of the haemostasis process, performed by combination of protein like hemopexin and heme oxygenase, (Kikuchi et al., 2005) whose homologs have not been found in the parasite genome.
5.1.3. BIOCHEMICAL PARAMETERS IN THE SERUM SAMPLES OF MALARIAL INFECTED INDIVIDUALS

Protein Level in Malarial Infected Individuals

Total protein was significantly lower in the malarial of patients compared with the normal similar to the finding reported by Schelp et al. (1977). The uptake of proteins and degradation of human serum albumin by *Plasmodium falciparum* infected human erythrocytes was reported by Tahir *et al.* (2003). Due to the profile of protein, showed the number of protein’s has been existed. By the changes occurs in the profile proteins probably due to protein formed against infection, (Warrell and Gilles, 2002). They also describe heme detoxification protein (HDP), a parasite protein which is a potent produced of hemozoin (HZ) and demonstrate that it reaches its intracellular destination utilizing a novel trafficking rut that has not been seen for any of the known of malaria proteins (Egan *et al.*, 2002).

**Aspartate transaminase and alanine transaminase ratio in malarial infected individuals**

The normal values for serum AST /ALT as reported by Pratt and Kaplan (2000). The AST / ALT ratio in acute malarial infection having to be higher. The possible reason for such variations includes
environmental, nutritional status, and anthropometric indices (Selvam and Mathew 1992). In malarial infection period that cause to invade red blood cells and multiply in pronounced amoeboid activity. The penetration of an erythrocyte by sporozoite which, differentiate after invading liver. The AST/ ALT ratio slightly higher in malarial infection and consequently male population highly affected compare with female (Sherman, 1998). Further more the interpretation of AST/ALT ratio’s are slightly higher except in alcoholic liver diseases.

**Alkaline Phosphatase Activities**

In terms of pathogenesis, the host liver is among the organs affected by malarial infection (Miller et al., 2002) leading to significant alterations in host hepatitis physiology and morphology. The observed elevation of serum alkaline phosphatase activities is an indication that the hepatic stage of the parasite’s Life cycle in its host and is accompanied by significant perturbation in the hepatocytes membrane leading to leakage of this enzyme out of all liver cells (Maegraith, 1981). The significantly higher serum alkaline phosphatase activity among the patients is evidence of the favour that changes in serum alkaline phosphatase activity can be used as a potential biomarker in malarial infection. The higher serum alkaline phosphatase activity in female patients relative to their male
counterparts is not unexpected finding. This is because sex related changes in serum alkaline phosphatase activity are not uncommon. In the present study, patient sex is not a significant factor with regards to the pattern of result obtained.

5.2. PROTEIN PROFILE

5.2.1. ELECTROPHORETIC PROTEIN PATTERN IN SERUM SAMPLES OF MALARIAL INFECTED INDIVIDUALS

Electrophoresis in polyacrylamide gel is the most widely used technique for analysis and characterization of proteins and nucleic acids. SDS was particularly used for monitoring protein purification and because the method is based on the separation of proteins according to size. The method was widely used to determine the native molecular mass of proteins. Due to the molecular weight of the proteins can be determined by comparing its mobility with those the number standard protein of known molecular weight that is run on the same gel.

5.2.2. SEQUENCING AND STRUCTURAL ANALYSIS OF 51 KDA PROTEIN *PLASMODIUM FALCIPARUM*

The built model was evaluated using comparison of SOPMA and Ramachandran Plot. The comparison modeling is a protein data bank (PDB) for 3D structural prediction and sequence analysis. By
the self optimized method (SOPMA) was used to predict 3D structure and correctly sequencing about 69.5 % of 3 D Structural proteins 82.2 % of amino acid residues. Evaluation of the model using Ramachandra Plot showed that the number of residues present in the favoured region allowed and outside regions. William et al. (1996) reported the similar 22 kDa protein associated with the Plasmodium falciparum merozoite surface protein-1 complex. Truccoa et al. (2001) also reported the 36 kDa protein associated with the Plasmodium falciparum merozoite surface protein-1 complex. Kumar et al. (2007) designed the three-dimensional structure of heat shock protein 90 from Plasmodium falciparum using molecular modelling approach to rational drug design against malaria. Zheng et al. (2009) reported the sequence and structural analysis of 4SNc-Tudor domain protein from Takifugu Rubripes.