

The insignificance of MBL2 protein levels in conferring resistance to malaria infection in Uyo Metropolis, Akwa Ibom State, Nigeria

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Abstract

Mannose binding lectin (MBL2) is an innate immune system pattern recognition molecule that serves to identify pathogens through their surface antigen-pathogen associated molecular patterns and bind to particular sugar molecules on the surface of pathogens to activate their destruction by the immune system. The levels of the immune protein- mannose binding lectin- correlate with the resistance of an individual to disease infections. Samples for this study were recruited from the Uyo metropolis of Akwa Ibom State in Nigeria. The levels of MBL2 were measured by enzyme-linked immunosorbent assay in 60 malaria patients and 60 healthy individuals for determination of resistance or protection against malaria infection. MBL2 levels in malaria patients and healthy controls were 14.40ng/ml \pm 13.04 and 19.90ng/ml \pm 18.5 2, respectively. The results from the study showed that there was no association in MBL2 levels between malaria and controls (p=0.129) as well as between the different sub-groups. Therefore, levels of MBL2 are not a contributory factor in resistance against malaria in the population under study.

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1.0 Introduction

Despite the intense, positive-result-yielding malaria control and elimination effort of the World Health Organization, which saw the decline of malaria endemic countries from 108 to 84 in the last two decades, malaria has continued to be among the leading causes of death from infectious diseases, with Nigeria alone accounting for 31% of the 14.8 global malaria mortality rate (deaths per 100,000 population at risk) in 2021 (WHO, 2022a). The burden of malaria in the WHO African region and particularly Nigeria is attributable to the transmission of Plasmodium falciparum by Anopheles gambiae and a recently detected Anopheles stephensi, which is prevalent in urban areas and considered to pose an extra challenge to control measures due to its resistance to insecticides (Sinka et al., 2020; WHO, 2019, 2022b). Therefore, high morbidity and mortality attributed to malaria, particularly among pregnant women and children under the age of five, remain sustained.

Considering vector and parasite resistances to measures like insecticide-treated control nets(ITNs) and artemisinin combined therapies (ACTs), respectively, the last resort for the control, elimination, or eradication of malaria is the development of a vaccine for the parasite (Crompton et al., 2010). However, this venture is strongly hampered by the complex life cycle and ever evolving nature of the parasite (Florens et al., 2002; Gardner et al., 2002). The immediate goals of malaria vaccine research were to induce robust immune responses, identify protective antigens, and combine candidate immunogens successfully to elicit adaptive immunity. А major breakthrough in malaria vaccination came with the WHO's recommendation of RTS,S (MosquirixTM) vaccine. This vaccine which has a pre-erythrocytic activity for the vaccination of children in malaria endemic regions (Zavala, 2022) was assigned the name RTS, since it was obtained from a combination of the repeat (R) and T-cell epitope (T) of the pre-erythrocytic circumsporozoite protein (CSP) of *Plasmodium falciparum* genes and a surface antigen (S) of the hepatitis B virus and additional hepatitis B surface antigen (S) (Egbewande, 2022). Intense effort has been made in this direction as several vaccine candidates, such as Blood Stage Vaccines (BSVs), Placental Malaria Vaccines (PMVs) and Transmission Blocking Vaccines (TBVs), have gone through several stages of development already (Duffy & Patrick Gorres, 2020).

Pivotal to the malaria vaccine development technology is the knowledge of the parasite surface molecules that play major roles in infection and susceptibility to infectious diseases (Macola & Fauci, 2020). These molecules encompass immunogens and surface proteins that the pathogens express, which aid in inducing immune responses against these invading pathogens. These molecules are recognized through their associated molecular patterns (PAMPs) by immune proteins. A typical immune protein that plays a key role in the recognition and initiation of immune activity against infectious pathogens is the mannose binding lectin.

Mannose binding lectin (MBL), also referred to as mannan-binding protein or core specific lectin (Turner, 1996), expressed by the human MBL gene -MBL2 which is mapped to the human chromosome 10 (10q11.2-q21) (Sastry et al., 1989) is an innate immune system pattern recognition molecule (PRM) that recognizes pathogens through their pathogen associated molecular patterns (PAMPs) and initiates, regulates, and amplifies innate immune response against such pathogens (Boldt et al., 2006). The C-type liver serum (Eisen & Minchinton, 2003), acute phase protein (Ezekowitz et al., 1991), is a 32 KDa polypeptide consisting of 248 amino acids with a cysteine-rich N-terminal, a collagen-like domain, a helical neck, and a Cterminal (Ezekowitz & Stahl, 1988) which is the recognition domain; hence, it is classified



among the collectin protein family (Auriti *et al.*, 2017).

MBL plays a vital role in innate immunity through specific binding to sugar moieties expressed on the surfaces of a variety of microorganisms (bacteria, viruses, fungi and thereby parasites) activating the lectin complement pathway and enhancing opsonophagocytosis (Ezekowitz et al., 1989; Neth et al., 2002; Neth et al., 2000; Townsend et al., 2001; Ying et al., 2004). The mode of operation of the complement pathways at the different stages of the life cycle of the Plasmodium falciparum has been studied (Rathnayake et al., 2021). In its action against invading microbes, including P. falciparum, MBL binds MBL-associated serine proteases such as MASP -1,-2 and -3 to initiate immune response through the activation and coordination complement-mediated of phagocytosis, membrane attack complex, and proinflammatory cytokines release (Garred et al., 2003; Jack & Turner, 2003; Larsen et al., 2004). Susceptibility or resistance to infectious diseases have been linked to MBL levels, particularly in children and in adults with underlying autoimmuno deficiency diseases (Bak-Romaniszyn et al., 2020; Cosar et al., 2008; Eisen & Minchinton, 2003; Garcia-Laorden et al., 2006; Petersen et al., 2001; Takahashi & Ezekowitz, 2005).

There is a differential expression of MBL among individuals and populations. This differences in MBL levels is as a result of structural (point) mutations at codon 52, 54 and 57 of exon 1 of the MBL-2 and promoter gene polymorphisms at the 5' flanking region of the MBL-2 at -550 and -221 positions (Lipscombe *et al.*, 1993; Minchinton *et al.*, 2002; Sumiya *et al.*, 1991). The point mutations, some of which are of high frequency in sub-Saharan Africa have been associated with low MBL levels particularly among individuals who are homozygous for the mutant allele; these individuals have been observed to be of increased susceptibility to infectious diseases (Lambourne *et al.*, 2009; Luty *et al.*, 1998; Mombo *et al.*, 2003; Peterslund *et al.*, 2001; Shen *et al.*, 2020; Tong *et al.*, 2019).

Several association studies between MBL-2 variants/levels and clinical malaria presentations or other diseases have been conducted. However, the results of these studies are contradictory for different (African) populations: while reported some no associations, such as in tuberculosis (Udosen et al., 2021), as well as in some polymorphisms of another immune protein, such as toll-like receptor 2 (Udosen, 2019 and Udosen 2020) majority concludes findings of association between the MBL and clinical malaria presentations (Bellamy et al., 1998; Boldt et al., 2009; Boldt et al., 2006; Futagbi et al., 2022; Garred et al., 2003; Holmberg et al., 2008; Luty et al., 1998) and tuberculosis (Udosen and Nya, 2017). It is on the basis of this discrepancy that Denholm and Co-Workers(2010) suggested that the best approach to revealing the association between MBL deficiency and susceptibility to infections may be the direct assessment of the protein by measuring serum MBL levels in individuals. Moreover, despite a handful of studies on the association of MBL and malaria in African populations, to the best of our knowledge, there is no such study on a Nigerian population.

We therefore, set out to investigate the association between mannose binding lectin levels and malaria infection among individuals in the Uyo Metropolis of Akwa Ibom State, Nigeria, through a direct measurement of serum MBL levels among recruited subjects.

2.0 Materials and Methods

We recruited a total of 120 individuals from St. Luke's Hospital, Anua, Uyo, and the University of Uyo Teaching Hospital (UUTH), Uyo in line with the institution's Ethical Regulations. The



participants comprised 60 individuals who were diagnosed with symptomatic malaria as cases and 60 healthy individuals as controls. On a gender basis, the study population was made up of 21 males and 39 females for healthy controls, with 37 females and 23 males for malaria cases.

Laboratory analysis was carried out at UUTH medical laboratory. Ethical approval for the study was sought for and obtained from the hospitals study samples were gotten from. The blood samples were collected from cases and controls in accordance with ethical guidelines.

The presence of malaria parasites in samples was detected by microscopy using whole blood. To obtain serum/plasma for subsequent Enzymelinked Immunosorbent Assay (ELISA) analysis, whole blood was centrifuged at 1500 rpm to obtain serum/plasma. Measurement of serum/plasma MBL2 concentrations was carried out by ELISA technique following manufacturer's (OriGene Technologies) protocols. Final analysis was performed excluding samples with outlier values.

To determine the level of association of MBL2 concentrations with susceptibility to malaria, the data obtained was subjected to statistical analysis. The T-test and one way analysis of variance (ANOVA) were employed in assessing the level of association between groups, with the level of significance set at $p \le 0.05$.

3.0 Results

The result of the assay indicated the mean MBL2 levels in malaria cases were 14.41 ± 13.04 ng/ml, while those of healthy subjects were 19.90 ± 18.52 ng/ml (Table 1). There was no significant difference between the MBL2 levels of malaria cases and healthy controls when the two groups were subjected to statistical testing (p = 0.129)

Table 1: Mean MBL2 levels of study subjects by gender

Population	Malaria Cases (ng/ml)	Healthy Controls (ng/ml)
Total Population	14.41 ± 13.04	19.90 ± 18.52
Male	16.98 ± 13.90	15.50 ± 15.90
Female	22.09 ± 15.20	20.90 ± 18.80

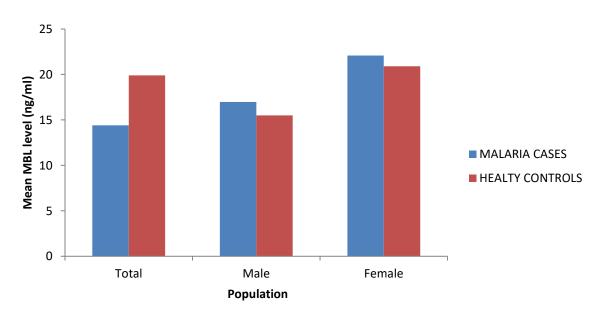


Fig.1: Mean MBL2 levels in malaria cases and healthy controls across study populations



Gender based analysis showed the mean MBL2 level for male malaria cases was 16.98 ± 13.90 ng/ml and that for male healthy controls to be 15.50 ± 15.90 ng/ml. The mean MBL2 levels for female malaria cases were 22.09 ± 15.20 ng/ml while those of female healthy controls were 20.90 ± 18.80 ng/ml. The MBL levels between male and female patients were not significantly different (p = 0.458).

Further stratification of the study population was based on age grouping. The mean MBL2 levels of the malaria cases and healthy controls are shown in table 2 and figure 2. ANOVA analysis of MBL2 levels between age groups 0-17, 18-35, 36-50, 51-65, and 65-80 showed no significant difference between the age groups (p = 0.282).

Age Group	Malaria Cases	Healthy Controls
0-17	12.49 ± 11.76	21.40 ± 19.59
18-35	23.74 ± 20.91	14.00 ± 18.34
36-50	5.44 ± 2.31	12.80 ± 15.36
51-65	20.29 ± 13.73	18.90 ± 9.61
66-80	18.81 ± 15.4	37.01 ± 10.80

Table 2: MBL2 levels of study subjects according to age groups

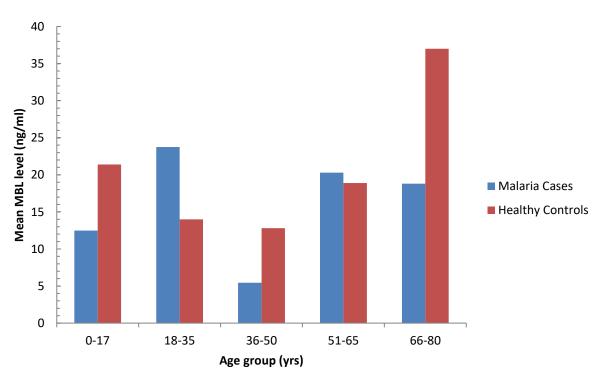


Fig. 2: Age-based mean MBL2 levels in malaria cases and healthy controls

4.0 Discussion

Mannose-binding lectin, a C-type, acute phase liver serum protein, is a major pathogen associated molecular pattern (PAMP) recognition molecule that plays an outstanding role in first line defense by binding to sugar moieties on the surface of microbes to activate the lectin complement pathway and aid opsonophagocytosis (Neth *et al.*, 2002; Townsend *et al.*, 2001; Ying *et al.*, 2004).

The immune response of the protein is exhibited during acute phase response through an increase in its serum concentration (Ezekowitz *et al.*, 1991; Thiel *etal.*, 1992). The protein binds to



specific surface proteases on microbial surfaces to cause their destruction through the lectin complement pathway.

However, humans exhibit differential expression of MBL levels basically due to mutations in exon one and the promoter region of the MBL-2 gene (Eisen & Minchinton, 2003; Sumiya *et al.*, 1991). Individuals, who have two copies of the wild type allele have been reported to have a mean serum level of approximately 1400 μ g/l while those who have a normal allele and the codon 54 mutant allele in conjunction with a particular promoter polymorphism exhibit mean MBL levels of between 26 and 396 μ g/l (Madsen *et al.*, 1995).

Boldt and Co-Workers (2006) suggested that malaria infection has a role to play in the evolution of MBL2 polymorphism among African populations due to their observed association between increased MBL protein levels and MBL2 variants among Gabonese children. The association of the MBL2 variants that result in low MBL plasma level and malaria susceptibility has also been established in other African and Indian populations(Holmberg *et al.*, 2008; Jha *et al.*, 2014; Luty *et al.*, 1998).

The above premises informed our investigation into a relationship between MBL levels and malaria symptoms among a Nigerian population resident in a Plasmodium falciparum haloendemic region (Edet et al., 2016). We obtained MBL serum levels of 14.41 ±13.04 ng/ml in malaria cases and 19.90 ± 18.52 mJ in healthy subjects. Grouping by age also shows differential serum MBL levels between cases and controls (table 2). Low MBL levels, occasioned by polymorphisms in the MBL2 gene that brings about deficiency in innate immunity, have been suggested to be a contributing factor to childhood malaria morbidity (Boldt et al., 2006; Eisen & Minchinton, 2003; Holmberg et al., 2008; Luty et al., 1998). However, there was no statistically significant difference in MBL levels between our case and control groups; hence, there is no association between MBL levels and malaria in our study population. This result indicates that mannose binding lectin levels do not confer resistance to malaria among our study population.

5.0 Conclusion

The study showed that mannose binding lectin protein did not give protection against malaria in the population under study because variations in its level did not confer resistance against the disease.

Conflict Of Interest

The authors hereby declare that there is no conflict of interest in relation to this article.

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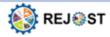


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