P32

IDENTIFICATION OF T CELL EPITOPES ON *PLASMODIUM FALCIPARUM* HYPOXANTHINE-GAUNINE-XANTHINE PHOSPHORIBOSYLTRANSFERASE (PfHGXPRT) IN MICE

Chakrit Hirunpetcharat[1], Morris O. Makobongo[2], Huji Xu[2], and Michael F. Good[2]
[1]Department of Microbiology, Faculty of Public Health, Mahidol University, Bangkon, Thailand;
[2]Molecular Immunology Laboratory, Queensland Institute of Medical Research Queensland, Australia.

The enzyme, hypoxanthine-gaunine-xanthine phosphoribosyltransferase (HGXPRT) involves in purine synthesis by salvage pathway mechanism in malaria parasites. Recently we have defined the blood-stage antigens and demonstrated that HGXPRT can induce protective immunity against *P. yoelii* infection. In this report, we have identified the T cell epitopes of *P. falciparum* HGXPRT in four different stains of two different MHC genetic background mice. Peptides 20 amino acids in length, spanning the sequence of HGXPRT and overlapping each other by 10 amino acids, were analyzed for their ability to induce T cell proliferation in immunized mice. Multiple-epitopes were recognized in mice. Peptides CS-3, -16, and 21 were strongly recognized in H-2^k BALB/K and B10.BR mice, whereas peptides CS-7, -11, and 17 were strongly recognized both in H-2d BALB/c and B10.D2 mice. These results indicate that PfHGXPRT T cell epitopes are recognized differently by different MHC genetic backgrounds. The effector functions of the dominant epitopes are under investigation.

P33

PROFILES OF IGG AND IGM ANTIBODIES TO PV66/AMA-1 IN INDIVIDUALS NATURALLY INFECTED WITH *PLASMODIUM VIVAX* FROM SRI LANKA

W.T.A. Wickramarachchi[1, 2], H.P. Premarathne[1], K.L.R.L. Perera[2], S. Bandara[2], A. Thomas[3], S.M. Handunnetti[2] and P.V. Udagama-Randeniya[1]
[1]Department of Zoology, Faculty of Science, University of Colombo, Sri Lanka; [2]Malaria Research Unit, Department of Parasitology, Faculty of Medicine, University of Colombo, Sri Lanka;
[3]Department of Parasitology, Biomedical Primate Research Centre, The Netherlands.

An understanding of the natural immune response to vaccine candidates is important in vaccine development. Recombinant protein, PV66/AMA-1, representing native Apical Membrane Antigen-1 of *Plasmodium vivax*, was used in an antibody sandwich ELISA to assess the IgG1-4 and IgM isotype responses of acute *P. vivax* malaria patients from two malaria endemic areas of the island, Anuradhapura ($n=40$) and Kataragama ($n=46$), and from a non-endemic area Colombo ($n=47$). A significantly ($P<0.05$) higher magnitude and prevalence of the IgM response was observed in non-endemic individuals than in residents from both endemic areas. The prevalence and magnitude of cytophilic IgG1 and IgG3 antibodies to PV66/AMA-1 in endemic residents were significantly higher ($P<0.05$) than the corresponding non-cytophilic IgG2 and IgG4 isotypes. Although the responding proportions of IgG1 and IgG3 within each test area were not significantly different ($P>0.05$), most individuals showed a bias towards the IgG1 response in magnitude compared to their IgG3 response. In the endemic areas, prevalence of IgM markedly diminished with increasing exposure and was minimal in those with more than five past infections. In parallel, their prevalence of IgG1 and IgG3 antibodies increased after experiencing the first malaria infection. This isotype switch was not evident in the non-endemic individuals. Thus, under unstable malaria conditions prevalent in the endemic areas of the island, it is apparent that with increasing exposure to malaria, the bias of the anti-PV66/AMA-1 antibody response was towards the functionally important cytophilic IgG1 isotype.