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SENSITIVE QUANTITATIVE PREDICTIONS OF MHC BINDING PEPTIDE FROM *SCHISTOSOMA MANSONI*

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Abstract- *Schistosoma mansoni* is a significant parasite of humans, a trematode that is one of the major agents of the disease intestinal schistosomiasis. Peptide fragments of antigen protein can be used to select nonamers for use in rational vaccine design and to increase the understanding of roles of the immune system in infectious diseases. Analysis shows MHC class II binding peptides of antigen protein from *Schistosoma mansoni* are important determinant for protection of host form parasitic infection. In this assay, we used PSSM and SVM algorithms for antigen design and predicted the binding affinity of antigen protein having 190 amino acids, which shows 182 nonamers. Binding ability prediction of antigen peptides to major histocompatibility complex (MHC) class I & II molecules is important in vaccine development from *Schistosoma mansoni*.

Keywords- antigen protein, epitope, PSSM, SVM, MHC, peptide vaccine

Abbreviations*: Goldman, Engelberg and Steitz, (GES); major histocompatibility complex, (MHC); Position Specific Scoring Matrices, (PSSMs); Support Vector Machine, (SVM)*

I. Introduction

Schistosoma mansoni is a significant parasite of humans, a trematode that is one of the major agents of the disease intestinal schistosomiasis [1, 2]. *Schistosoma mansoni* antigen peptides are most suitable for subunit vaccine development because with single epitope, the immune response can be generated in large population. This approach is based on the phenomenon of cross-protection, whereby a infected with a mild strain and is protected against a more severe strain of the same. The phenotype of the resistant transgenic hosts includes fewer centers of initial infection, a delay in symptom development, and low accumulation. Antigen protein from *Schistosoma mansoni* is necessary for new paradigm of synthetic vaccine development and target validation [3-5].

II. Methodology

In this research work antigenic epitopes of antigen protein from *Schistosoma mansoni* is determined using the Gomase in 2007, Hopp and Woods, Welling, Parker Chou & Fasman and Deleage & Roux antigenicity [6-8]. The major histocompatibility complex (MHC) peptide binding of antigen protein is predicted using neural networks trained on C terminals of known epitopes. In analysis predicted MHC/peptide binding of antigen protein is a log-transformed value related to the IC50 values in nM units. MHC2Pred predicts peptide binders to MHCI and MHCII molecules from protein sequences or sequence alignments using Position Specific Scoring Matrices (PSSMs). Support Vector Machine (SVM) based method for prediction of promiscuous MHC class II binding peptides. SVM has been trained on the binary input of single amino acid sequence [9-14]. In addition, we predict those MHC ligands from whose C-terminal end is likely to be the result of proteosomal cleavage [15].

III. Results and Interpretations

We found binding of peptides to a number of different alleles using Position Specific Scoring Matrix. An antigen protein sequence is 190 residues long, having antigenic MHC binding peptides. MHC molecules are cell surface glycoproteins, which take active part in host immune reactions and involvement of MHC class-I and MHC II in response to almost all antigens. PSSM based server predict the peptide binders to MHCI molecules of antigen protein sequence are as 11mer_H2_Db, 10mer_H2_Db, 9mer_H2_Db, 8mer_H2_Db and also peptide binders to MHCII molecules of antigen protein sequence as I_Ab.p, I_Ad.p, analysis found antigenic epitopes region in putative antigen protein (Table 1). We also found the SVM based MHCII-IAb peptide regions; MHCII-IAd peptide regions; MHCII-IAg7 peptide regions and MHCII- RT1.B peptide regions, which represented predicted binders from bacterial antigen protein (Table 2). The predicted binding affinity is normalized by the 1% fractil. We describe an improved method for predicting linear epitopes (Table 2). The region of maximal hydrophilicity is likely to be an antigenic site, having hydrophobic characteristics, because terminal regions of antigen protein is solvent accessible and unstructured, antibodies against those regions are also likely to recognize the native protein (Fig. 1, 2, 3). It was shown that a antigen protein is hydrophobic in nature and

contains segments of low complexity and high-predicted flexibility (Fig. 4, 5). Predicted antigenic fragments can bind to MHC molecule is the first bottlenecks in vaccine design.

IV. Conclusion

An antigen protein from *Schistosoma mansoni* peptide nonamers are from a set of aligned peptides known to bind to a given MHC molecule as the predictor of MHC-peptide binding. MHCII molecules bind peptides in similar yet different modes and alignments of MHCII-ligands were obtained to be consistent with the binding mode of the peptides to their MHC class, this means the increase in affinity of MHC binding peptides may result in enhancement of immunogenicity of antigen protein. These predicted of antigen protein antigenic peptides to MHC class molecules are important in vaccine development from *Schistosoma mansoni*

V. References

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Table 1- PSSM based prediction of MHC ligands, from whose C-terminal endare proteosomal cleavage sites

MHC-I	POS.	N	Sequence	C	MW (Da)	Score	% OPT.
8mer_H2_Db	166	MNF	SHEPFLSI	QFK	911.04	10.599	20.19 %
8mer_H2_Db	112	KTK	QYEICCQF	KEY	1015.18	8.465	16.13 %
8mer_H2_Db	129	TSR	TGNDMREV	ANK	902.97	8.141	15.51 %
8mer_H2_Db	183	YVC	LAWRTPSQ		917.07	5.601	10.67 %
9mer_H2_Db	175	SIQ	FKYNNYVCL	AWR	1145.34	29.945	59.46 %
9mer_H2_Db	95	KFP	KLPPNIEII	AAT	1018.27	18.14	36.02 %
9mer_H2_Db	155	WQV	VLLTGSYWM	NFS	1028.26	8.183	16.25 %
9mer_H2_Db	115	QYE	ICCQFKEYV	DNT	1114.35	6.116	12.14 %
10mer_H2_Db	178	FKY	NNYVCLAWRT	PSQ	1198.39	17.495	29.72 %
10mer_H2_Db	76	LKV	SEIRREKDEL	KKE	1256.4	12.259	20.83 %
10mer_H2_Db	174	LSI	QFKYNNYVCL	AWR	1273.47	12.048	20.47 %
10mer_H2_Db	142	KMK	SLLDNTYGRV	WQV	1119.24	11.439	19.43 %
11mer_H2_Db	174	LSI	QFKYNNYVCLA	WRT	1344.55	20.466	25.75 %
11mer_H2_Db	108	ATM	SKTKQYEICCQ	FKE	1312.52	12.393	15.59 %
11mer_H2_Db	30	MID	KQELIKYCQKY	RLD	1425.71	11.493	14.46 %
11mer_H2_Db	134	NDM	REVANKMKSLL	DNT	1270.55	9.737	12.25 %

Table 2- SVM based prediction of promiscuous MHC class II binding peptides from antigen protein

MHC ALLELE	Rank	Sequence	Residue No.	Peptide Score
I-Ab	1	RREKDELKK	79	0.938
I-Ab	2	VCLAWRTPS	181	0.848
I-Ab	3	AATMSKTKQ	104	0.793
I-Ab	4	IIAATMSKT	102	0.681
I-Ad	1	EEFCRGFGL	65	0.849
I-Ad	2	RAFLEIDAD	15	0.610
I-Ad	3	LSQMEEFIR	7	0.575
I-Ad	4	GSYWMNFSH	159	0.558
I-Ag7	1	EIIAATMSK	101	1.468
I-Ag7	2	EIRREKDEL	77	1.456
I-Ag7	3	LIDPWIARF	46	1.420
I-Ag7	4	YVCLAWRTP	180	1.416
RT1.B	1	ETKLSQMEE	4	1.102
RT1.B	2	TMSKTKQYE	106	0.597
RT1.B	3	TKQYEICCQ	110	0.582
RT1.B	4	TKLSQMEEF	5	0.539

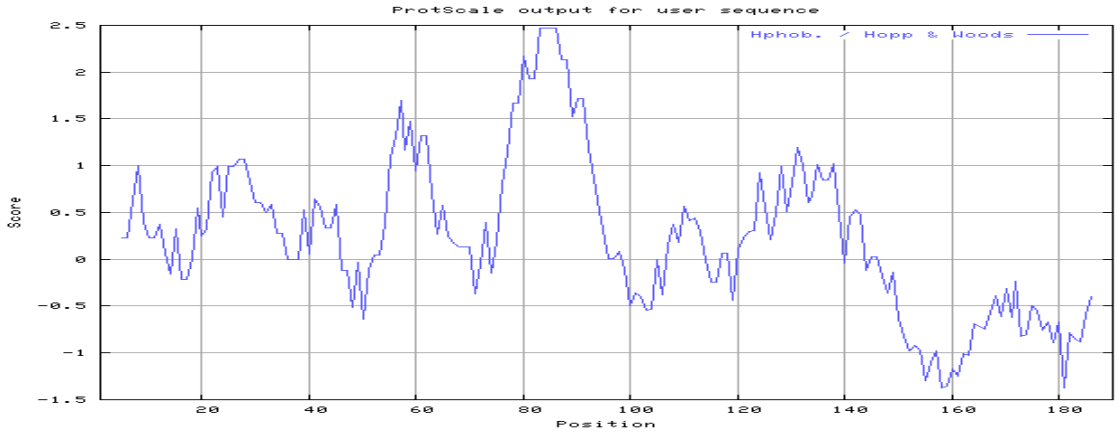

Fig. 1-Hydrophobicity plot of antigen protein by Hphob./ Hopp & Woods scale

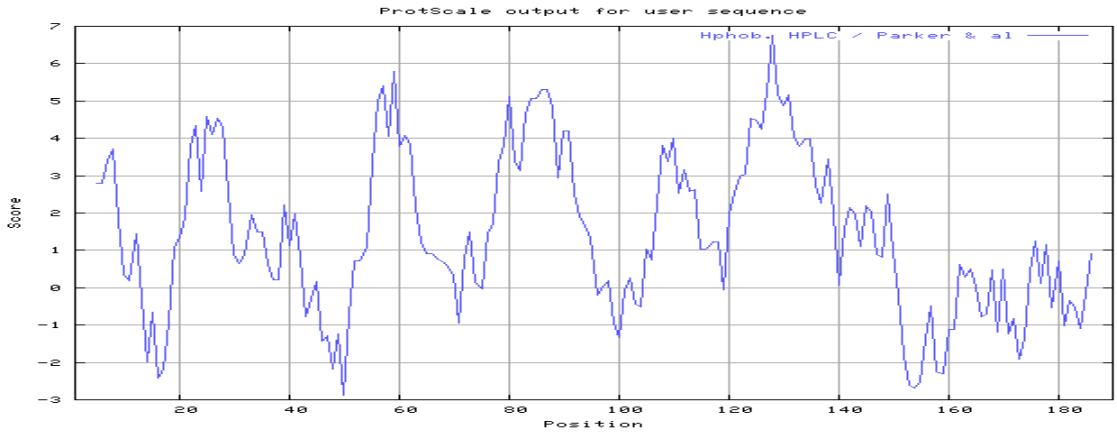

Fig. 2- Hydrophobicity plot of antigen protein by HPLC / Parker, et al., scale

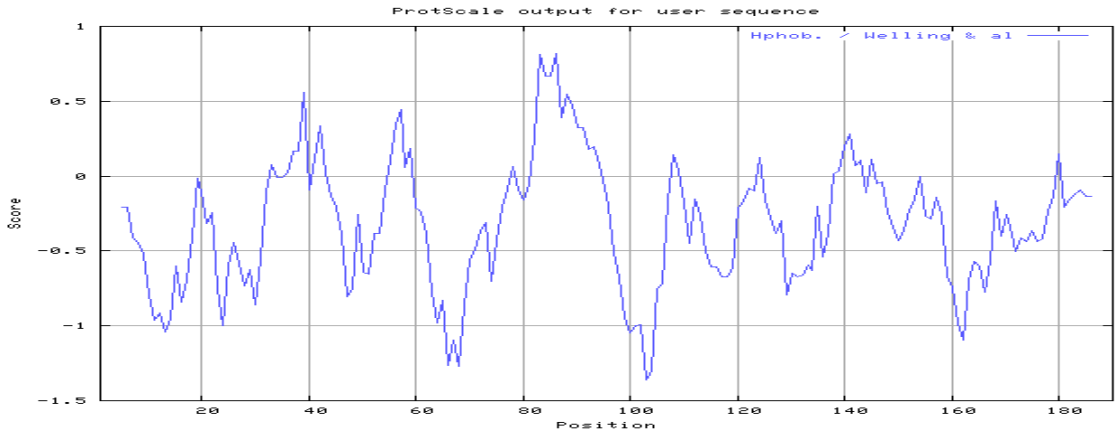

Fig. 3- Hydrophobicity plot of antigen protein by Welling, et al., scale

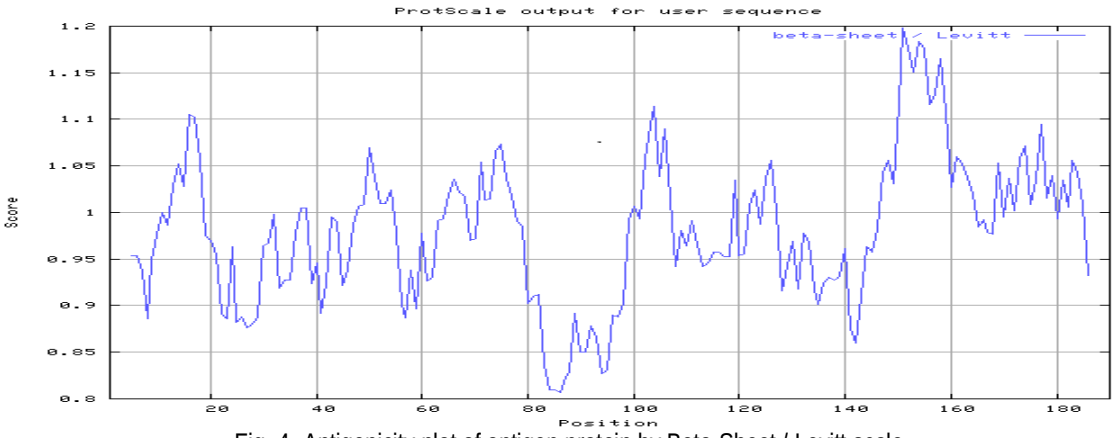

Fig. 4- Antigenicity plot of antigen protein by Beta-Sheet / Levitt scale

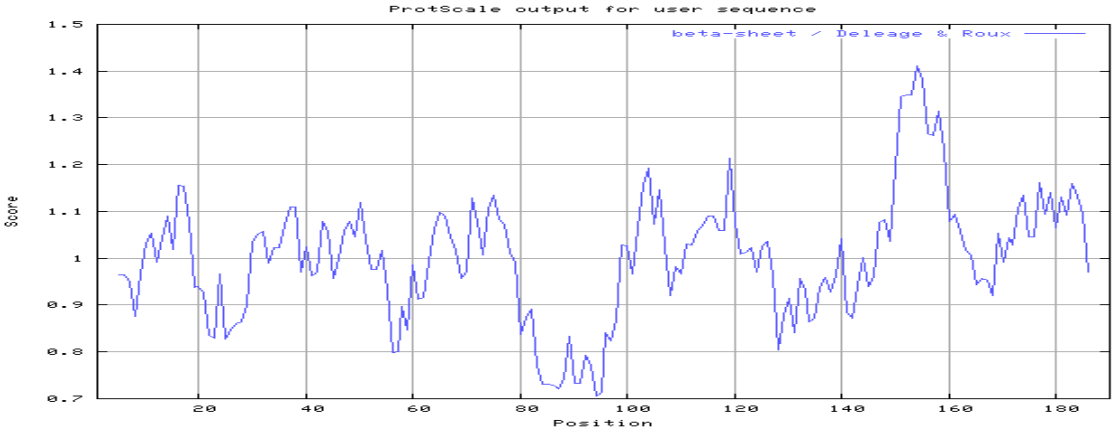

Fig. 5- Antigenicity plot of antigen protein by Beta-Sheet / Deleage & Roux , scale