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IN-SILICO APPROACH FOR PREDICTION OF VACCINE POTENTIAL ANTIGENIC PEPTIDES FROM 23-kDa TRANSMEMBRANE ANTIGEN PROTEIN OF *Schistosoma haematobium*

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Abstract- Urogenital schistosomiasis is frequently occurring parasitic disease in tropical countries, *S. haematobium* is main causative agent responcible for urogenital schistosomiasis; till date no effective invention made to against urogenital schistosomiasis. In this analysis we a have predicted suitable antigenic peptides from *Schistosoma haematobium* 23-kDa transmembrane protein for peptide vaccine design against urogenital schistosomiasis based on cross protection phenomenon as, an ample immune response can be generated with a single protein subunit. We found MHC class II binding peptides of *S. haematobium* 23-kDa are important determinant against the diseased condition. The analysis shows *S. haematobium* 23-kDa transmembrane protein having 218 amino acids, which shows 210 nonamers. In this assay, we have predicted MHC-I binding peptides for 8mer_H2_Db allele (optimal score is 14.128), 9mer_H2_Db allele (optimal score is 20.065), 10mer_H2_Db allele (optimal score is 13.776), 11mer_H2_Db allele (optimal score is 31.213). We also predicted the SVM based MHCII-IAb peptide regions, 152-DYGPNIPAS, 51-WQAAPIAII, 50-VWQAAPIAI, 142-FHCCGAKGP, 97-AELAAAIVA (optimal score is 14.911); MHCII-IAd peptide regions, 100-AAAIVAVVY, 71-LGCCGAIKE, 192-FGVCFFQLL, 186-IVACVAFGV (optimal score is 13.112); and MHCII-IAg7 peptide regions 42-QYGDNLHKV, 101-AAIVAVVYK, 28-VLIGAGAYV, 103-IVAVVYKDR, 203-VIACCLGRQ (optimal score is 11.605) which shows potential binders from *S. haematobium* 23-kDa transmembrane protein. The method integrates prediction of MHC class I binding proteasomal C- terminal cleavage peptides and Six potential antigenic peptides at average propensity 1.094 having highest local hydrophilicity. Thus a small antigen fragment can induce immune response against whole antigen. This approach can be applied for designing subunit and synthetic peptide vaccines.

Keywords- Urogenital schistosomiasis, parasitic disease, Antigenic peptides, MHC-Binders, Nonamers, synthetic peptide vaccines

Abbreviations- MHC-Major Histocompatibility Complex, SVM-Support Vector Machine, APC- Antigen Presenting Cell

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Introduction

Schistosomiasis is one of the neglected tropical disease caused by a parasitic worm of *Schistosoma* spp. that primarily lives in the blood. The parasite is transmitted to humans by penetration of the skin in fresh water and cause severe damage including bleeding and cancer, which may cause the death of an individual. Schistosomiasis infection estimated in ~240 million people in the world. The classic sign of urogenital schistosomiasis is haematuria. Fibrosis of the bladder and ureter and kidney damage are common findings. *S. haematobium* is one the major causative agents of urogenital schistosomiasis in tropical and sub-tropical countries [1].

Pathogenesis

The free living cercarial form of the *S. haematobium* penetrates human skin in fresh water. The cercariae travel through the tissue to the blood stream. Mature male and female worms over mating in the veins of the liver before moving to their final destination, the veins that drain to the bladder. The female adult worm produces 200-2000 eggs per day. Eggs circulate in the blood vessels until they become lodged in various organs. The accumulation of eggs in the various tissues and organs of the body can cause severe damage including bleeding and cancer. An accumulated damage caused by the eggs rather than the parasites themselves that caus-

es the majority of mortality and morbidity associated with the disease [2].

Strategy

This approach is based on the phenomenon of cross-protection [3] hereby an individual infected with a mild strain of pathogen possess immunity against more severe strain of the same pathogen. Body proteins are necessary for production of immunity in or on all food commodities. Relief from the requirement of a tolerance is established for residues of the drugs or chemicals.

MHC Class Binding Peptides

The new paradigm in vaccine design is emerging, following essential discoveries in immunology and development of new MHC class I binding peptides prediction tools [4-6]. MHC molecules are cell surface glycoproteins, which take active part in host immune reactions. The involvement of MHC class I in response to almost all antigens and the variable length of interacting peptides make the study of MHC class I molecules very interesting. MHC molecules have been well characterized in terms of their role in immune reactions. They bind to some of the peptide fragments generated after proteolytic cleavage of antigen [7]. This binding act like red flags for specific antigen and to generate immune response against the parent antigen, thus an antigen subunit can induce immune response against whole antigen. Antigenic peptides are most suitable for subunit vaccine development because with single epitope, the immune response can be generated in large population. MHC-Peptide complexes will be translocated on the surface of antigen presenting cells (APCs). This theme is implemented in designing subunit and synthetic peptide vaccines [8-11]. One of the important problems in subunit vaccine design is to search for antigenic regions in an antigen protein [12] that can stimulate T-cells called T-cell epitopes. Fortunately, in literature a large amount of data about such peptides is available. Pastly and presently, a number of databases have been developed to provide comprehensive information related to T-cell epitopes [13-17].

Materials and Methods

Protein Sequence Analysis

The antigenic protein sequence of *Schistosoma haematobium* 23-kDa transmembrane protein was analyzed to study the antigenicity [18], solvent accessible regions and MHC class binding peptides, which allows potential drug targets to identify active sites against lymphatic filariasis.

Antigenicity Prediction

Antigenicity prediction program results those segments from *Schistosoma haematobium* 23-kDa transmembrane protein that are likely to be antigenic by eliciting an antibody response. Antigenic epitopes are determined using the Gomase (2007), Hopp and Woods (1981), Welling (1985), Parker (1986), BepiPred Server (2006) and Kolaskar and Tongaonkar Antigenicity (1990) methods [19-24].

Protein Secondary Structure Prediction

The important concepts in secondary structure prediction are identified as: residue conformational propensities, sequence edge effects, moments of hydrophobicity, position of insertions and deletions in aligned homologous sequence, moments of conservation, auto-correlation, residue ratios, secondary structure feedback effects and filtering [25, 26].

MHC Binding Peptide Prediction

The MHC binding peptides are predicted by using neural networks trained on C terminals of known epitopes. In this work predicted MHC-Peptide binding is a log-transformed value related to the IC50 values in nM units. RankPep predicts peptide binders to MHC-I and MHC-II molecules from protein sequences or sequence alignments using Position Specific Scoring Matrices (PSSMs). Support Vector Machine (SVM) based method has been used for prediction of promiscuous MHC class II binding peptides. The average accuracy of SVM based method for 42 alleles is ~80%. For determination of potential MHC binders, an elegant machine learning technique SVM has been applied. SVM has been trained on the binary input of single amino acid sequence. In addition, we predicts those MHC -I ligands whose C-terminal end is likely to be the result of proteosomal cleavage [27-33].

Result and Interpretation

A *Schistosoma haematobium* 23-kDa antigenic sequence (gi-2501225) is 218 residues long as-

MATLGTGMRCLKSCVFVLNIICLLCSLVLIGAGAYVEVKFSQYG-
DNLHKVWQAAPIAIIVVGVIILIVSFLGCCGAIKENVCMLYMYAFFLI
ILLIAELAAAIVAVVYKDRIDSEIDALMTGALDKPTPEITEFMDLIQS
SFHCCGAKGPQDYGPNIPASCRGETTVYHEGCVPVFGAFLKRNL
VIVACVAFGVCFFQLLSIVIACCLGRQIKEYENV

Antigenic Peptides Prediction

In this assay we predicted the antigenic determinants by finding the area of highest local hydrophilicity. We studied methods BepiPred Server, Kolaskar and Tongaonkar antigenicity, Parker, Emini Surface Accessibility methods [Fig-1], [Fig-2], [Fig-3], [Fig-4], [Table-1] and Hopp & Woods hydrophobicity method which predict the locations of antigenic determinants in antigen protein, assuming that the antigenic determinants would be exposed on the protein surface and thus would be located in hydrophilic regions [Fig-5], its values are derived from the transfer-free energies for amino acid side chains between ethanol and water.

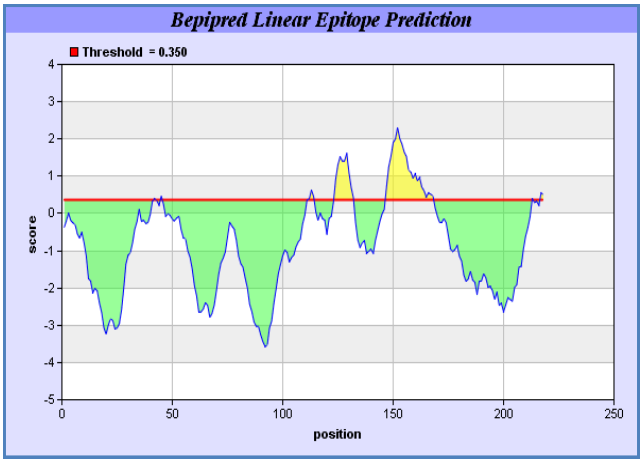

Fig. 1- Bepipred Linear Epitope Prediction plot showing antibody recognized B-cell epitopes of the *S. haematobium* 23-kDa

Welling hydrophobicity plot gives value as the log of the quotient between percentage in a sample of known antigenic regions and percentage in average proteins [Fig-6]. The predicted antigenic fragments can bind to MHC molecule is the first bottlenecks in vaccine design.

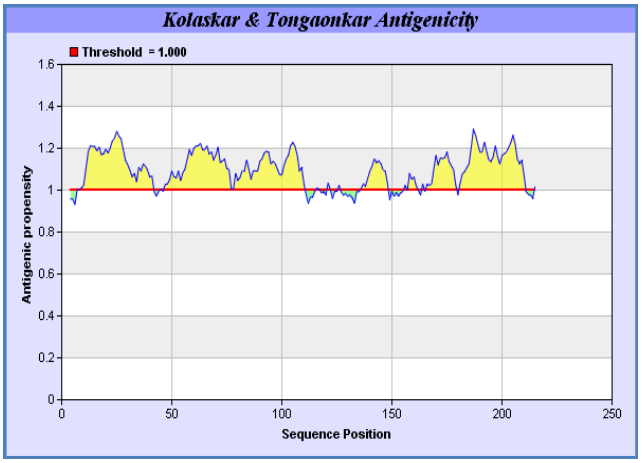

Fig. 2- Kolaskar and Tongaonkar antigenicity plot showing antibody recognized antigenicity for the *S. haematobium* 23-kDa.

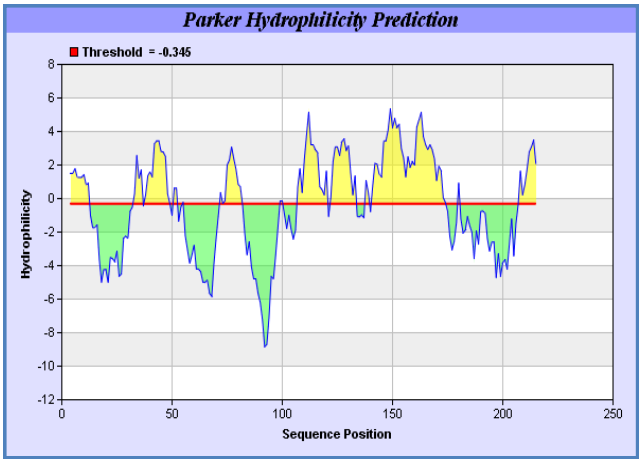

Fig. 3- HPLC / Parker et al. (1986) hydrophobicity plot of *S. haematobium* 23-kDa

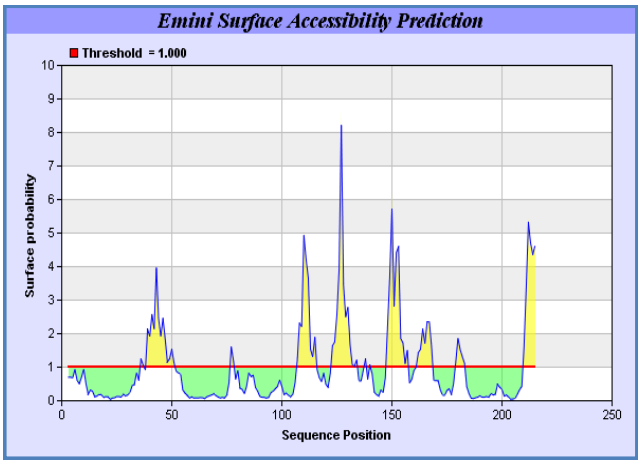

Fig. 4- Emini Surface Accessibility Prediction plot of *S. haematobium* 23-kDa

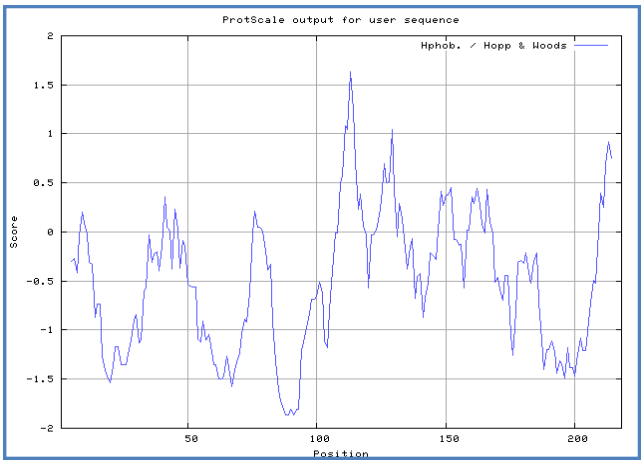

Fig. 5- Hopp and Woods (1981) hydrophobicity plot of *S. haematobium* 23-kDa

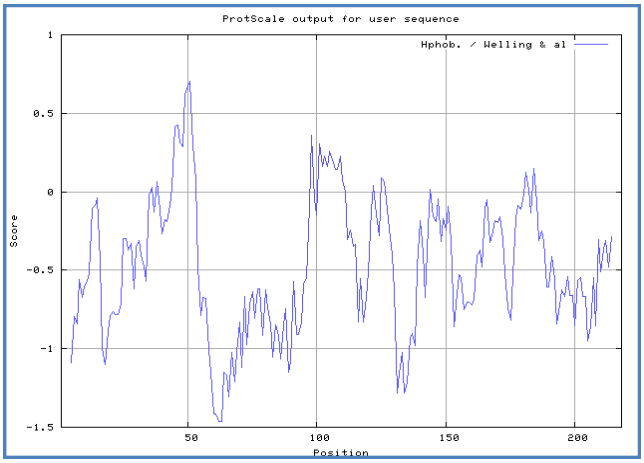

Fig. 6- Welling et al. (1985) hydrophobicity plot of *S. haematobium* 23-kDa

Secondary Alignment

The Robson and Garnier method has been applied for the prediction of *Schistosoma haematobium* 23-kDa transmembrane protein secondary structure. Each residue is assigned values for alpha helix (*Shown in Red*), beta sheet (*Shown in Blue*) and coils (*Shown in Pink*) using a window of 7 residues [Fig-7]. Using these information parameters, the likelihood of a given residue assuming each of the four possible conformations alpha, beta, reverse turn, or coils calculated, and the conformation with the largest likelihood is assigned to the residue.

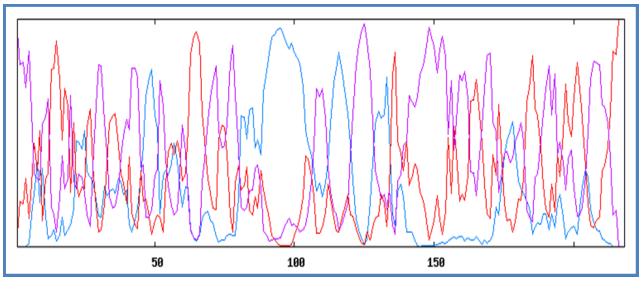

Fig. 7- Secondary structure plot of the *S. haematobium* 23-kDa *transmembrane protein.*

**Red: helix, Blue: Sheet, Pink: Coil*

Table 1- Antigenic epitopes of S. haematobium 23-kDa transmembrane protein

No.	Start Position	End Position	Peptide	Peptide Length
1	7	41	GMRCLKSCVFVLNIICLLCSLVLIGAGAYVEVKFS	35
2	47	110	LHKVWQAAPIAIIVVGVIILIVSFLGCCGAIKENVCMLYMYAFFLIILLIAELAAAIVAVVYKD	64
3	136	148	DLIQSSFHCCGAK	13
4	156	161	NIPASC	6
5	166	179	TVYHEGCVPVFGAF	14
6	181	210	KRNLVIVACVAFGVCFFQLLSIVIACCLGR	30

Prediction of MHC Binding Peptides

These MHC binding peptides are sufficient for producing the desired immune response. The prediction is based on support vector machine, using amino acids sequence. In this test, we found the MHC-I and MHC-II binding regions [Table-2], [Table-3]. MHC molecules are cell surface glycoproteins, which actively take part in host immune reactions and involvement of MHC-I and MHC-II in response to almost all antigens. In this study we predicted the binding affinity of *Schistosoma haematobium* 23-kDa protein, having 218 amino acids, which show several potential nonamers [Table-2], [Table-3]. For development of MHC binding prediction method, an elegant machine learning technique Support Vector Machine (SVM) has been used. SVM has been trained on the binary input of single amino acid sequence. In this assay we predicted the binding affinity of *S. haematobium* 23-kDa protein sequence having 218 amino acids, which shows 210 nonamers.

Table 2- Prediction of MHC class I peptides, from S. haematobium 23-kDa transmembrane protein having C-terminal ends are proteosomal cleavage sites

MHC-I Allele	POS.	N	SEQUENCE	C	MW (Da)	SCORE	% OPT.
8mer_H2_Db	150	AKG	PQDYGPNI	PAS	884.95	14.128	26.91%
8mer_H2_Db	124	TGA	LDKPTPEI	TEF	894.04	11.679	22.25%
8mer_H2_Db	52	KVW	QAAPIAII	VVG	777.97	9.638	18.36%
8mer_H2_Db	51	HKV	WQAAPIAI	IVV	828.02	8.25	15.72%
8mer_H2_Db	60	AII	VVGVIILI	VSF	807.08	6.37	12.13%
8mer_H2_Db	173	EGC	VPVFGAFL	KRN	831.03	6.357	12.11%
8mer_H2_Db	78	GAI	KENVCMLY	MYA	981.19	6.245	11.90%
8mer_H2_Db	29	SLV	LIGAGAYV	EVK	744.89	6.162	11.74%
8mer_H2_Db	49	NLH	KVWQAAPI	AII	871.08	5.716	10.89%
8mer_H2_Db	190	VAC	VAFGVCFF	QLL	871.07	5.676	10.81%
8mer_H2_Db	146	HCC	GAKGPQDY	GPN	816.87	5.4	10.29%
8mer_H2_Db	31	VLI	GAGAYVEV	KFS	746.82	4.94	9.41%
8mer_H2_Db	77	CGA	IKENVCML	YMY	931.17	4.036	7.69%
8mer_H2_Db	54	WQA	APIAIIVV	GVI	777.02	3.746	7.14%
8mer_H2_Db	85	CML	YMYAFFLI	ILL	1049.31	3.215	6.12%
8mer_H2_Db	205	IVI	ACCLGRQI	KEY	845.05	2.062	3.93%
8mer_H2_Db	36	GAY	VEVKFSQY	GDN	981.12	1.98	3.77%
8mer_H2_Db	185	RNL	VIVACVAF	GVC	803.03	1.535	2.92%
8mer_H2_Db	18	VFV	LNIICLLC	SLV	886.18	1.467	2.79%
8mer_H2_Db	193	VAF	GVCFFQLL	SIV	908.13	1.134	2.16%
8mer_H2_Db	17	CVF	VLNIICLL	CSL	882.17	1.044	1.99%
8mer_H2_Db	70	IVS	FLGCCGAI	KEN	764.96	0.48	0.91%
9mer_H2_Db	192	CVA	FGVCFFQLL	SIV	1055.31	20.065	39.84%
9mer_H2_Db	172	HEG	CVPVFGAFL	KRN	934.17	13.666	27.13%
9mer_H2_Db	16	SCV	FVLNIICLL	CSL	1029.35	12.346	24.51%
9mer_H2_Db	70	IVS	FLGCCGAIK	ENV	893.13	10.577	21.00%
9mer_H2_Db	179	FGA	FLKRNLVIV	ACV	1083.38	10.175	20.20%
9mer_H2_Db	22	NII	CLLCSLVLI	GAG	958.29	10.086	20.03%
9mer_H2_Db	3	MA	TLGTGMRCL	KSC	933.14	9.834	19.53%
9mer_H2_Db	19	FVL	NIICLLCSL	VLI	973.26	9.563	18.99%
9mer_H2_Db	191	ACV	AFGVCFFQL	LSI	1013.23	9.532	18.93%
9mer_H2_Db	189	IVA	CVAFGVCFF	QLL	974.21	9.521	18.90%
9mer_H2_Db	76	CCG	AIKENVCML	YMY	1002.25	9.469	18.80%
9mer_H2_Db	10	GMR	CLKSCVFVL	NII	993.29	9.12	18.11%

Table 2- Continue

MHC-I Allele	POS.	N	SEQUENCE	C	MW (Da)	SCORE	% OPT.
9mer_H2_Db	140	LIQ	SSFHCCGAK	GPQ	921.06	7.709	15.31%
9mer_H2_Db	15	KSC	VFVLNIICL	LCS	1015.32	7.326	14.55%
9mer_H2_Db	82	ENV	CMLYMYAFF	LII	1170.48	6.696	13.29%
9mer_H2_Db	200	FQL	LSIVIACCL	GRQ	916.21	6.17	12.25%
9mer_H2_Db	69	LIV	SFLGCCGAI	KEN	852.04	5.707	11.33%
9mer_H2_Db	28	CSL	VLIGAGAYV	EVK	844.02	5.508	10.94%
9mer_H2_Db	204	SIV	IACCLGRQI	KEY	958.21	3.66	7.27%
9mer_H2_Db	21	LNI	ICLLCSLVL	IGA	958.29	3.505	6.96%
9mer_H2_Db	184	KRN	LVIVACVAF	GVC	916.19	3.465	6.88%
9mer_H2_Db	12	RCL	KSCVFVLNI	ICL	1004.25	3.421	6.79%
9mer_H2_Db	87	LYM	YAFFLIILL	IAE	1094.42	3.365	6.68%
9mer_H2_Db	84	VCM	LYMYAFFLI	ILL	1162.47	2.922	5.80%
9mer_H2_Db	168	TTV	YHEGCVPVF	GAF	1032.19	2.69	5.34%
9mer_H2_Db	171	YHE	GCVPVFGAF	LKR	878.06	2.561	5.08%
9mer_H2_Db	62	IVV	GVIILIVSF	LGC	942.21	2.295	4.56%
9mer_H2_Db	83	NVC	MLYMYAFFL	IIL	1180.5	2.292	4.55%
9mer_H2_Db	176	VPV	FGAFLKRNL	VIV	1047.27	1.085	2.15%
9mer_H2_Db	13	CLK	SCVFVLNII	CLL	989.24	1.021	2.03%
9mer_H2_Db	48	DNL	HKVWQAAPI	AII	1008.22	0.67	1.33%
9mer_H2_Db	73	FLG	CCGAIKENV	CML	918.09	0.638	1.27%
9mer_H2_Db	111	YKD	RIDSEIDAL	MTG	1013.13	0.582	1.16%
10mer_H2_Db	148	CGA	KGPQDYGPNI	PAS	1070.17	13.776	23.41%
10mer_H2_Db	153	PQD	YGPNIPASCR	GET	1059.22	5.726	9.73%
10mer_H2_Db	82	ENV	CMLYMYAFFL	IIL	1283.64	5.404	9.18%
10mer_H2_Db	125	GAL	DKPTPEITEF	MDL	1158.28	4.829	8.20%
10mer_H2_Db	2	M	ATLGTGMRCL	KSC	1004.22	4.647	7.90%
10mer_H2_Db	122	LMT	GALDKPTPEI	TEF	1022.17	4.57	7.76%
10mer_H2_Db	110	VYK	DRIDSEIDAL	MTG	1128.22	4.038	6.86%
10mer_H2_Db	41	VKF	SQYGDNLHKV	WQA	1142.23	3.966	6.74%
10mer_H2_Db	38	YVE	VKFSQYGDNL	HKV	1152.27	1.785	3.03%
10mer_H2_Db	170	VYH	EGCVPVFGAF	LKR	1007.18	0.568	0.97%
11mer_H2_Db	74	LGC	CGAIKENVCML	YMY	1162.44	31.213	39.26%
11mer_H2_Db	187	LVI	VACVAFGVCFF	QLL	1144.42	21.342	26.85%
11mer_H2_Db	14	LKS	CVFVLNIICLL	CSL	1231.62	13.338	16.78%
11mer_H2_Db	82	ENV	CMLYMYAFFLI	ILL	1396.8	12.78	16.08%
11mer_H2_Db	25	CLL	CSLVLIGAGAY	VEV	1048.27	11.875	14.94%
11mer_H2_Db	15	KSC	VFVLNIICLLC	SLV	1231.62	7.887	9.92%
11mer_H2_Db	13	CLK	SCVFVLNIICL	LCS	1205.54	6.595	8.30%
11mer_H2_Db	189	IVA	CVAFGVCFFQL	LSI	1215.5	5.816	7.32%
11mer_H2_Db	192	CVA	FGVCFFQLLSI	VIA	1255.55	5.771	7.26%
11mer_H2_Db	1		MATLGTGMRCL	KSC	1135.41	5.508	6.93%
11mer_H2_Db	56	AAP	IAIIVVGVIIL	IVS	1104.48	4.487	5.64%
11mer_H2_Db	81	KEN	VCMLYMYAFFL	IIL	1382.77	3.235	4.07%
11mer_H2_Db	121	ALM	TGALDKPTPEI	TEF	1123.27	2.928	3.68%
11mer_H2_Db	147	CCG	AKGPQDYGPNI	PAS	1141.25	2.278	2.87%
11mer_H2_Db	61	IIV	VGVIILIVSFL	GCC	1154.5	1.969	2.48%
11mer_H2_Db	84	VCM	LYMYAFFLIIL	LIA	1388.79	1.612	2.03%
11mer_H2_Db	198	CFF	QLLSIVIACCL	GRQ	1157.5	1.505	1.89%
11mer_H2_Db	176	VPV	FGAFLKRNLVI	VAC	1259.56	1.473	1.85%

**Optimal Score for given MHC binder in Mouse*

We Predicted the SVM based MHCII-IAb peptide regions, 152-DYGPNIPAS, 51-WQAAPIAII, 50-VWQAAPIAI, 142-FHCCGAKGP, 97-AELAAAIVA (optimal score is 14.911); MHCII-IAd peptide regions, 100-AAAIVAVVY, 71-LGCCGAIKE, 192-FGVCFFQLL, 186-

IVACVAFGV (optimal score is 13.112); and MHCII-IAg7 peptide regions 42-QYGDNLHKV, 101-AAIVAVVYK, 28-VLIGAGAYV, 103-IVAVVYKDR, 203-VIACCLGRQ (optimal score is 11.605); which represents predicted binders from *S. haematobium* 23-kDa transmembrane protein [Table-3]. The predicted binding affinity is normalized by the 1% fractil. The MHC-Peptide binding is predicted using neural networks trained on C terminals of known epitopes. In this analysis predicted MHC-Peptide binding is a log-transformed value related to the IC50 values in nM units. These MHC binding peptides can decently elicit the desired immune response. Predicted MHC binding regions in an antigen sequence and these are directly associated with immune reactions, in analysis we found the MHC-I and MHC-II binding region.

Table 3- Peptide binders to MHCII molecules of S. haematobium 23-kDa transmembrane protein

MHC-II Allele	POS.	N	SEQUENCE	C	MW (Da)	SCORE	% OPT.
I_Ab	152	GPQ	DYGPNIPAS	CRG	914.98	14.911	41.85%
I_Ab	51	HKV	WQAAPIAII	VVG	941.18	13.831	38.82%
I_Ab	50	LHK	VWQAAPIAI	IVV	927.15	12.589	35.33%
I_Ab	142	QSS	FHCCGAKGP	QDY	901.07	10.703	30.04%
I_Ab	97	LLI	AELAAAIVA	VVY	809.97	10.117	28.39%
I_Ad	100	AEL	AAAIVAVVY	KDR	858.05	13.112	24.67%
I_Ad	71	VSF	LGCCGAIKE	NVC	875.07	9.244	17.39%
I_Ad	192	CVA	FGVCFFQLL	SIV	1055.31	8.643	16.26%
I_Ad	186	NLV	IVACVAFGV	CFF	860.08	7.5	14.11%
I_Ag7	42	KFS	QYGDNLHKV	WQA	1055.15	11.605	28.39%
I_Ag7	101	ELA	AAIVAVVYK	DRI	915.14	11.112	27.19%
I_Ag7	28	CSL	VLIGAGAYV	EVK	844.02	9.385	22.96%
I_Ag7	103	AAA	IVAVVYKDR	IDS	1044.26	8.49	20.77%
I_Ag7	203	LSI	VIACCLGRQ	IKE	944.18	8.458	20.69%

**Optimal Score for given MHC II peptide binder in Mouse.*

Discussion and Conclusion

Gomase method (2007), BepiPred Server, Hopp and Woods, Welling, Parker, Kolaskar and Tongaonkar antigenicity scales were designed to predict the locations of antigenic determinants in *S. haematobium* 23-kDa transmembrane protein. It shows beta sheets regions, which have higher antigenic response than helical region of this peptide and shows high antigenicity [Fig-1], [Fig-2], [Fig-3], [Fig-4], [Fig-5], [Fig-6]. In this assay we predicted the binding affinity of *S. haematobium* 23-kDa transmembrane protein having 218 amino acids, which shows 210 nonamers. We predicted MHC-I binding peptides for 8mer_H2_Db allele (optimal score is 14.128), 9mer_H2_Db allele (optimal score is 20.065), 10mer_H2_Db allele (optimal score is 13.776), 11mer_H2_Db allele (optimal score is 31.213) [Table-2]. MHC molecules are cell surface glycoproteins, which take active part in host immune reactions and involvement of MHC I and MHC II in response to almost all antigens [Table-2], [Table-3]. Kolaskar and Tongaonkar antigenicity predicted epitopes are the sites of molecules those are recognized by the immune system antibodies for the *S. haematobium* 23-kDa protein, analysis shows epitopes present in the *S. haematobium* 23-kDa protein are adequate to induce desired immune response. The region of maximal hydrophilicity is likely to be an antigenic site, having hydrophobic characteristics, because C- terminal regions of *S. haematobium* 23-kDa transmembrane protein are solvent accessible and unstructured; antibodies against those regions are also likely to recognize the native protein. During prediction of antigenic determinant site of *S. haematobium* 23-kDa protein, we found Six antigenic determinant sites in the sequence. The highest pick is recorded between sequence of amino acid in the region are 7-GMRCLKSCVFVLNIICLLCSLVLIGAGA YVEVKFS-41 (35AA) and 47-LHKVWQAAPIAIIVVGVIILIVSFLGCC GAIKENVCMLYMYAF-FLIILLIAELAAAIVAVVYKD-110 (64AA) [Table-1]. The average propensity for the *S. haematobium* 23-kDa *protein* found is 1.094 [Fig-2]. All residues having above 1.0 propensity are always potentially antigenic [Table-1]. The predicted segments in transmembrane protein are 7-GMRCLKSCVFVLNIIC LLCSLVLIGAGAYVEV-KFS-41, 47-LHKVWQAAPIAIIVVGVIILIVSF LGCCGAIKENVCML YMYAFFLIILLIAELAAAIVAVVYKD-110, 136-DLIQSSFHCCGAK-148, 156-NIPASC-161, 166-TVYHEGCVPVF GAF-179, 181-KRNLVIVACVAFGVCFFQLLSIVIACCLGR-210. Fragments identified through this approach seem to be high-efficiency binders, which is a much percentage of their atoms are directly involved in binding as compared to larger molecules.

Future Perspectives

This method will be applicable in cellular immunology, Vaccine design, immunodiagnostics, immunotherapeutics and molecular understanding of autoimmune susceptibility. *S. haematobium* 23-kDa transmembrane protein sequence contains multiple antigenic components to direct and empower the immune system to protect the host against lymphatic filariasis disease. MHC molecules are cell surface proteins, which take active part in host immune reactions and involvement of MHC class in response to almost all antigens and it give impacts on specific sites. Predicted MHC binding regions acts like red flags for specific antigen and generate immune response against the parent antigen. So a small fragment of antigen can induce immune response against complete antigen. The method integrates prediction of peptide MHC class binding; proteosomal C terminal cleavage and potential antigenic epitope prediction. This theme is implemented in designing subunit and synthetic peptide vaccines.

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