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Original Article

Immunoinformatics Based Vaccine Design for Zea M 1 Pollen Allergen

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ABSTRACT

Objective: Zea m1 is one of the most common aeroallergens, causing allergy. This pollen allergen, present in maize, is responsible for type I hypersensitivity reaction. Despite having available X ray crystal structure of this pollen allergen, no definite vaccine has been developed for allergic disorder in humans. **Method:** In our present study, an epitope-based peptide vaccine against Zea m 1 pollen allergen, using a combination of B cell and T cell epitope predictions, followed by molecular docking and molecular dynamics simulation methods are carried out. Here, protein sequences of homologous pollen allergens of Zea m1 are collected and conserved regions present in them are investigated. **Result:** From the identified region of the allergenic protein, the peptide sequence KVPPGPNITTNY and the sequence AEWKPMKLSM are considered as the most potential B cell and T cell epitopes respectively. Furthermore, this predicted T cell epitope AEWKPMKLSM interacted with MHC allelic protein HLA-B*44:02 with the lowest IC_{50} value (7.94 nM). This epitope perfectly fitted into the epitope binding groove of alpha helix of MHC I molecule with lowest energy weighted score -620.0, showing stability in MHC binding. This epitope also showed a good conservancy of 69.75% in world population coverage. **Conclusion:** The epitopes KVPPGPNITTNY and AEWKPMKLSM may be considered as potential peptide for peptide vaccine for pollen allergen after further experimental study.

Key words: Immunoinformatics, Vaccine design, Zea m1 pollen allergen, B cell epitope, T cell epitope, Molecular docking, Molecular dynamics.

Key message: Immunoinformatic study shows that the predicted epitopes KVPPGPNITTNY and AEWKPMKLSM provide in long term and highly specific protective immunity against Zea m 1 pollen allergen during allergic reaction for whole world population.

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INTRODUCTION

Allergic diseases are one of the most prevalent health problem along the world. More than 25% of the world's population is affected by type I hypersensitivity reaction. Among the other causes of allergic reactions, pollen allergens are considered as potential source of hypersensitivity reaction. Aeroallergens, the most common causes of nasobronchial allergy due to contact with grass and tree pollen allergens.[1] Grass pollen allergens from *Zea mays* are responsible for the allergic reaction among susceptible individuals.[2] In the medical science different types of medicines e.g. mast cell stabilizers etc. are used to treat allergic reactions. But several other alternative methods e.g. hypo allergen production, allergen – specific immunotherapy, conversion of allergens into vaccines with reduced allergenic activity[3] etc. are recommended in post genomic era.

Zea m 1 has been crystalized and identified as group I pollen allergen from maize.[4] By the process of molecular allergen characterization, allergy vaccines can be achieved as recombinant allergens, peptides and genes of allergens. B-cell epitope mapping is a promising method to identifying the main antigenic determinants or epitopes of microorganisms. Epitope-based vaccines have outstanding approach compared to the conventional ones since they are specific in nature, able to avoid unwanted immune reactions, having power to generate long lasting immunity, and are practically cheaper in price. Epitope based peptide vaccine design method is to develop vaccines for various disorders, for example, malaria,[5] common krait toxin[6] and zika virus.[7]

MATERIALS AND METHODS

Retrieval of Zea m 1 and identification of conserved regions among homologous pollen allergen of Zea m 1

The protein sequence and 3D structure of Zea m1 allergenic protein were obtained from UniProt knowledgebase.[8] In SDAP allergen database,[9] FAO/WHO Allergenicity Rules based on sequence homology for full FASTA alignment for fasta sequence of 2HCZ showed 50 sequences of allergens with an E score higher than 0.01. Alignment was made with FAST 3.45.[10] Different protein sequences of pollen allergens were selected and retrieved from Swiss-prot[11] in FASTA format. To find conserved region, retrieved sequences were aligned using Muscle tool 3.8.31[12] where *k*-mer clustering was used. In the next step a tree was constructed by the method known as progressive alignment. The evolutionary divergence analysis for all 50 pollen allergens were completed by forming a phylogenetic tree using Phy ML 3.1/3.0 aLRT software.[13]

Potential T- cell epitope Identification

CD+8 T- cell epitope prediction

Linear T-cell epitopes for MHC-I binding for Zea m 1 allergenic protein are identified by consensus methods using Artificial neural network (ANN)[14] and Stabilized matrix method (SMM)[15] from tools for MHC -I binding prediction methods of Immune Epitope Database (IEDB) (www.iedb.org).[16] SMM algorithm of MHC-1 binding, transporter of antigenic peptides (TAP) transport efficiency and proteasomal cleavage efficiency

are considered to determine the IC_{50} values for processing prediction of epitopes by MHC-I molecules.[17] On the basis of low IC_{50} values, 5 best epitopes bind with specific MHC-1 molecules are designated for further evaluation.

CD+4 T- cell epitope prediction

CD4+ T-cell receptor responses against concerned allergen are done by using Peptide binding to MHC class II molecules software using MHC II binding prediction tool in IEDB analysis resource, including a consensus approach which combines NN-align, SMM-align[18] and Combinatorial library methods. For this prediction we chose thirty HLA class II alleles from the reference set. For the predicted T-cell epitopes with low percentile rank are identified and their IC50 values for respective alleles are determined by SMM-align method.[18]

Potential B cell epitope identification

The B cell epitope is the part of the antigenic polypeptide chain which interacts with immunoglobulin molecules. Various physico- chemical properties e.g. hydrophilicity, flexibility, accessibility, turns, exposed surface, polarity and antigenic propensity of polypeptides chains have been associated with the location of continuous epitopes of antigenic proteins.[19] Thus, different tools from IEDB (www.iedb.org), including the classical propensity scale methods such as Kolaskar and Tongaonkar antigenicity scale,[20] Emini surface accessibility prediction,[21] Parker hydrophilicity prediction,[22] Karplus and Schulz flexibilty prediction,[23] Bepipred linear epitope prediction[24] and Chou and Fashman beta turn prediction tool[25] are used to predict B cell epitopes of Zea m 1. From the prediction results most common findings are considered a probable B cell epitope.

Analysis of population coverage

Population coverage for identified T cell epitopes is assessed for world population with the help of IEDB population coverage calculation tool.[26] This tool computes the fraction of individuals predicted to reply to a given set of epitopes with recognized MHC restrictions.

Docking study of B cell and T cell epitopes

For docking studies, the T cell epitope AEWKPMKLSM and B cell epitope KVPPGPNITTNY are selected and subjected to PEP-FOLD server[27] for 3D structure formation. To identify the molecular interactions with specific HLA protein and immunoglobulin E for respective epitopes, docking studies are performed with ClusPro 2.2 web server.[28] Cluster scores for lowest binding energy prediction are calculated. Modified PDB ID 1M6O for HLA-B*44:02 is used as allelic protein for docking study of T cell epitope. Similarly, 3D structure (PDB ID 4J4P) for immunoglobulin E molecule is used as receptor molecule for B cell epitope docking analysis.

Molecular simulation study of predicted T cell epitope with HLA allelic protein

The entire molecular dynamics simulation study for HLA-epitope protein complex is accomplished with MDWeb i.e. Molecular dynamics on Web[29] a web server. A solvent box is added to minimize the energy of the system after equilibrating it using NAMD force field method. Then the solvent is heated to 300K and after that protein restraints are lowered. A multiple time step algorithm along with a simulation time step 2.0 fs has been chosen. Molecular dynamics simulations of 5ns long is performed at constant temperature and pressure. The MD trajectories are drawn for 0.1 ps for analysis. The trajectories are generated from the simulation study are evaluated for the stability by various parameters viz, B factor (atomic fluctuation), RMSD, radius of gyration.

RESULT

Homologous pollen allergenic sequences retrieval and identification of conserved regions

From SDAP allergen database,[9] 50 homologous allergens are identified using amino acid sequence of pollen allergen Zea m 1 as shown in Table 1, since sequences with E values < 0.01 are almost always homologous in nature. All 50 protein sequences are retrieved from SwissProt[11] and aligned to identify conserved sequences with varying length using Muscle tool 3.8.31[12] in Table 2.

A phylogenetic tree illustrating the evolutionary relationship among the 50 homologous allergens is depicted in Figure 1.

CD8+ T-cell epitope identification

IEDB recommended prediction method for MHC-I binding with CD8+ T cell epitope suggest that the lower the percentile rank the epitope would be good binder. The predicted percentile rank with consensus method and IC_{50} values with SMM method[15] are shown in Table 3.

CD4+ T-cell epitope identification

Peptide binding cleft in MHC -II molecule is wider than that of MHC- I molecule. So, 15mer epitopes are predicted by consensus method. IC_{50} values for predicted epitopes along with their MHC II alleles are displayed in Table 4.

Analysis of Population coverage

IEDB population coverage tool[26] is used to calculate the population coverage of the predicted epitopes. The result for combined method with both class I and II MHC restriction for the whole world and Indian population with the selected MHC I and MHC II alleles is shown in Table 5.

Prediction of B cell epitopes

Predicted scores for Emini surface accessibility,[21] Parker hydrophilicity,[22] Karplus and Schulz flexibility[23] and Chou and Fashman beta turn[25] along with their threshold values are exhibited in Table 6.

Prediction scores of above-mentioned parameters for each residue of peptide ^{28}KVPPGPNITTNYN^{40} reveals that this short stretch of antigenic protein can act as linear B cell epitope. Kolaskar and Tongaonkar antigenicity prediction scores[20] for each residue of that peptide chain confirms KVPPG as antigenic determinant of Zea m 1 allergenic protein. Residue N at position 40 is not present in sequence of conserved region.

Docking study of B cell and T cell epitopes

The T cell epitope ^{209}AEWKPMKLSW^{218} is selected on the basis of its interactions with large number of alleles and lowest IC_{50} value with HLA-B*44:02 MHC I allele. Similarly, ^{28}KVPPGPNITTNY^{39} is designated as most probable B cell epitope which is also present in conserved region of pollen allergen Zea m 1. Docking studies are performed with these two epitopes with human HLA-B*44:02 MHC I molecule and immunoglobulin protein E respectively.

Molecular simulation study of predicted T cell epitope with HLA allelic protein

The complex structure of predicted T cell epitope with HLA allelic protein is subjected for molecular dynamics study. The 5ns MD simulation of HLA-epitope (HLA-B*44:02-AEWKPMKLSW) complex is carried out using NAMD force field, following the energy minimization protocol. The stability of the HLA protein with T cell epitope complex with the help of B factor and RMSD value are calculated and shown in Figure 4a and 4c. From the figure, it can be concluded that the complex (HLA-B*44:02-AEWKPMKLSW) is stabilized after 0.5 ns simulation, is tended to remain in plateau phase thereafter for the rest of the period. The RMSD value of HLA-epitope complex is observed to grow up from 0.1 Å to 0.8 Å

Table 1: List of homologous allergens of Zea m 1.

No	Allergen	Sequence ID in SwissProt/NCBI/PIR	Sequence Length	E score
1	Zea m 1	P58738	269	9.0e-96
2	Pas n 1.0101	ACA23876	265	2.4e-81
3	Ory s 1	AAF72990	269	4.0e-74
4	Zea m 1	Q07154	191	1.6e-71
5	Ory s 1	AAF72983	267	2.2e-64
6	Ory s 1	AAF72991	267	9.3e-64
7	Phl p 1	P43213	263	4.3e-60
8	Phl p 1.0101	CAA81613	263	5.6e-60
9	Cyn d 1	O04701	246	1.6e-59
10	Hol l 1.0102	CAA93121	248	3.5e-59
11	Hol l 1	P43216	265	4.0e-59
12	Hol l 1	CAA10140	263	1.2e-58
13	Cyn d 1	AAL14078	262	3.3e-58
14	Cyn d 1.0203	AAL14079	262	4.9e-58
15	Cyn d 1.0202	AAL14077	262	4.9e-58
16	Poa p a	CAA10520	263	6.4e-58
17	Pha a 1	Q41260	269	7.4e-58
18	Cyn d 1.0204	AAF80379	244	9.4e-58
19	Cyn d 1.0201	AAK96255	244	1.8e-57
20	Lol p 1.0103	CAB63699	263	1.8e-57
21	Ory s 1	AAF72987	275	2.1e-57
22	Lol p 1.0102	AAA63278	252	3.5e-57
23	Lol p 1.0101	AAA63279	263	6.0e-57
24	Lol p 1	P14946	263	7.9e-57
25	Ory s 1	AAF72984	268	3.4e-56
26	Ory s 1	AAF72985	286	2.8e-55
27	Tri a ps93	AAD10496	271	1.8e-54
28	Ory s 1	AAB61710	261	2.0e-54
29	Ory s 1	Q40638	263	3.6e-53
30	Sor h 1.0101	ABC58726	239	6.9e-53
31	Ory s 1	AAF72989	271	3.4e-52
32	Ory s 1	AAF72988	327	1.5e-42
33	Gly m 2	AAA50175	277	2.3e-39
34	Ory s 1	AAF72986	275	2.2e-36
35	Arat expansin	CAB37496	265	5.3e-20
36	Ory s 1	AAG13596	275	6.1e-18
37	Ory s 1	BAA85432	284	3.0e-17
38	Cyn d 2	CAA10346	122	3.5e-09
39	Dac g 2	CAA10345	122	5.9e-09
40	Poa p 2	CAA10348	122	5.9e-09
41	Phl p 2	P43214	122	5.9e-09
42	Lol p 2	P14947	97	7.0e-08
43	Dac g 3	P93124	96	1.2e-07
44	Lol p 2	CAA51775	88	3.3e-07
45	Phl p 3.0101	2JNZ_A	108	1.5e-06
46	Dac g 1.0101	Q7M1X8	34	2.0e-06
47	Lol p 3	P14948	97	3.6e-06
48	Cyn d 15	AAP80171	112	3.7e-06
49	Ant o 1.0101	Q7M1X6	32	2.2e-05
50	Tri a 3	CAA90746	118	4.6e-05

Table 2: Conserved sequences of homologous pollen allergens with their positions.

Conserved sequences of pollen allergen	Position of the selected sequences
KVPPGPNITTNYN	28-40
TWYG	49-52
DNGGACG	61-67
CGNVPIFKDGKGCGSCYE	82-99
YHFDLSGKAFGSLAKP	123-138
FRRV	154-157
FHIEKGCNP	171-179

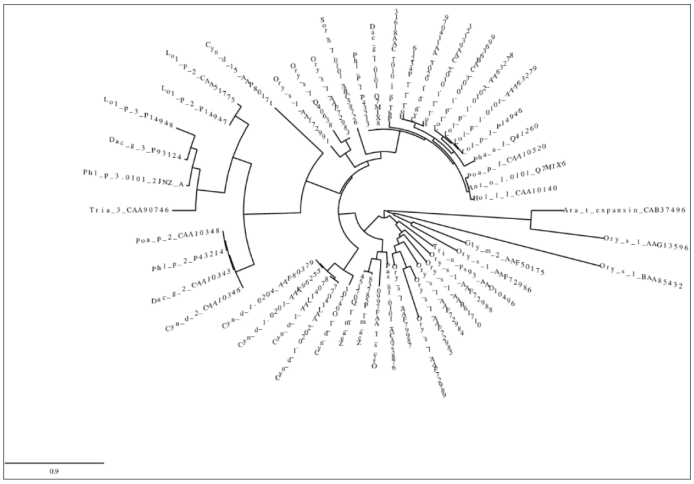

Figure 1: A phylogenetic tree with all fifty pollen allergens showing their phylogenetic relationship.

Potential T-cell epitope identification

Table 3: CD8+ T cell epitopes.

No. of epitope	Start position	End position	T cell epitopes	Interacting MHC-I alleles	Percentile rank	IC_{50}
1.	79	88	MTACGNVPIF	HLA-A*68:02	0.2	27.77
				HLA-A*26:01	0.15	391.81
				HLA-A*32:01	0.3	604.93
2.	121	130	NYEPIAPYHE	HLA-A*24:02	0.15	40.41
				HLA-A*23:01	0.3	10.85
3.	165	174	KYPAGQKIVF	HLA-A*24:02	0.15	72.19
				HLA-B*07:02	0.3	114.07
4.	209	218	AEWKPMKLSW	HLA-B*44:02	0.15	7.94
				HLA-B*44:03	0.15	14.40
5.	212	221	KPMKLSWGAI	HLA-B*07:02	0.15	6.39

Table 4: CD4+ t cell epitopes.

No. of epitope	Start position	End position	T cell epitopes	Interacting MHC-II alleles	Percentile rank	IC_{50}
1.	79	93	MTACGNVPIFKDGKG	HLA-DRB1*01:01	69.23	1759.00
2.	121	135	NYEPIAPYHEDLSGK	HLA-DRB5*01:01	6.33	403.00
				HLA-DQA1*01:01	6.94	749.00
				HLA-DRB3*01:01	14.85	
				HLA-DPA1*01:03	15.14	
				HLA-DRB1*15:01	18.96	1029.00
				HLA-DRB1*11:01	20.33	
3.	165	174	KYPAGQKIVFHIEKG	HLA-DRB1*11:01	15.51	3299.00
				HLA-DRB1*01:01	21.87	
4.	209	223	AEWKPMKLSWGAIWR	HLA-DRB1*12:01	30.1	74.88
				HLA-DRB1*03:01	10.35	379.8
				HLA-DRB1*08:02	27.81	1234.07
5.	212	226	KPMKLSWGAIWRMDT	HLA-DRB1*11:01	1.18	322.00
				HLA-DRB1*09:01	4.27	498.00
				HLA-DRB1*15:01	5.12	746.00
				HLA-DRB1*08:02	6.42	749.00
				HLA-DRB3*01:01	9.37	2170.00

Table 5: Population coverage for predicted T cell epitopes.

Predicted T cell epitopes	Interacting MHC I alleles	15 mer peptides	Interacting MHC II alleles	Population coverage	
				World	India
AEWKPMKLSW	HLA-B*44:02 HLA-B*44:03	AEWKPMKLSWGAIWR	HLA-DRB1*12:01 HLA-DRB1*03:01 HLA-DRB1*08:02 HLA-DRA1*01:03 HLA-DRB1*04:01 HLA-DRB1*11:01	69.75%	83.44%
KPMKLSWGAI	HLA-B*07:02	KPMKLSWGAIWRMDT	HLA-DRB1*11:01 HLA-DRB1*09:01 HLA-DRB1*15:01 HLA-DRB1*08:02 HLA-DRB3*01:01	12.78%	2.74%
NYEPIAPYHE	HLA-A*24:02 HLA-A*23:01	NYEPIAPYHEDLSGK	HLA-DPA1*01:03 HLA-DRB1*15:01 HLA-DRB1*11:01	5.43%	1.5%
KYPAGQKIVF	HLA-A*24:02 HLA-A*23:01 HLA-B*07:02	KYPAGQKIVFHIEKG	HLA-DRB1*11:01	5.43%	1.5%
MTACGNVPIF	HLA-A*68:02 HLA-A*26:01 HLA-A*32:01	MTACGNVPIFKDGKG	HLA-DRB1*01:01 HLA-DRB1*08:02	5.82%	3.5%

Table 6: Surface accessibility, hydrophilicity, flexibility, beta turn and antigenicity prediction score for each residue of B cell epitope.

B cell epitope	Emini surface accessibility score for each residue (threshold=1.000)	Parker hydrophilicity score for each residue (threshold=1.521)	Karplus and Schulz flexibility score for each residue (threshold=0.993)	Chou and Fashman beta turn score for each residue (threshold=1.035)	Kolaskar and Tongaonkar antigenicity score for each residue (threshold=1.030)
K	1.932	2.3	1.051	1.307	1.063
V	1.932	2.3	1.053	1.307	1.063
P	1.932	2.3	1.063	1.307	1.063
P	2.009	3.0	1.066	1.313	1.022
G	0.704	1.043	1.067	1.236	1.054
P	1.37	2.314	1.057	1.301	0.986
N	1.278	2.757	1.044	1.221	0.964
I	1.329	3.457	1.036	1.227	0.923
T	2.105	2.371	1.029	1.167	0.964
T	2.189	3.071	1.025	1.173	0.923
N	1.347	2.886	1.024	1.173	0.937
Y	3.843	4.843	1.028	1.25	0.905
N	2.8	2.671	1.031	1.25	0.903

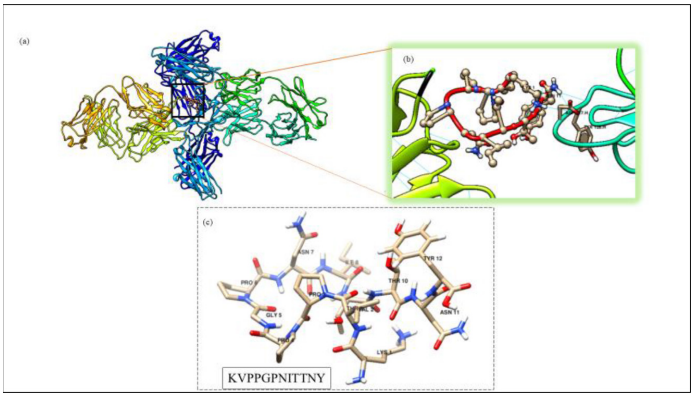

Figure 2: (a) Bound structure of B cell epitope with IgE (b) H bonding between epitope and CDR region of heavy chain of IgE (c) 3D structure of B cell epitope. B cell epitope [28]KVPPGPNITTNY[39] is bound with human immunoglobulin E with lowest energy weighted score -282.5. Hydrogen bonds are formed between side chains of Lys and Asn of epitope and Tyr, Asp of complementarity determining region (CDR) of heavy chain of immunoglobulin molecule (Figure (b)).

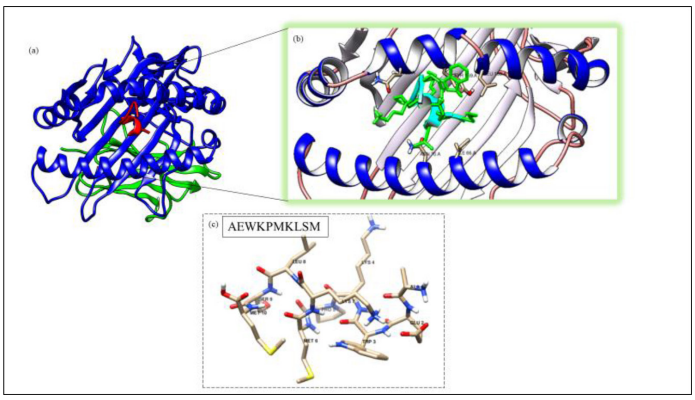

Figure 3:(a) Bound structure of T cell epitope with MHC I (b) Interacting residues of epitope and helical groove of alpha chain of MHC I molecule (c) 3D structure of T cell epitope.
T cell epitope [209]AEWKPMKLSW[218] in docking structure with HLA-B*44:02 MHC I molecule, perfectly fitted into the epitope binding groove of alpha helix of MHC I molecule with lowest energy weighted score -620.0 as shown in Figure 3.

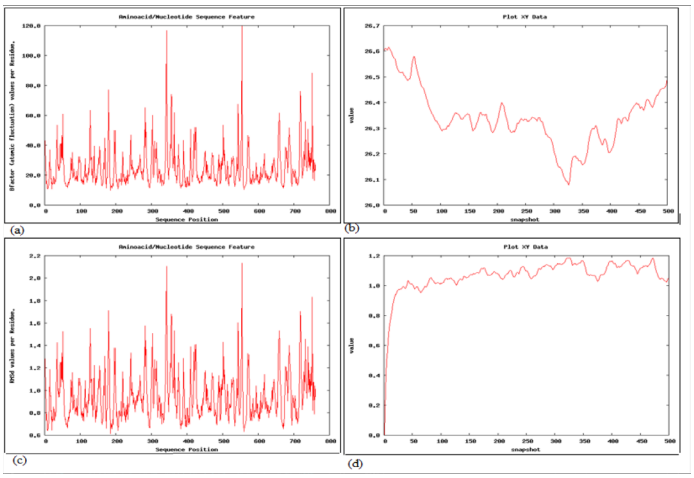

Figure 4: (a) B factor values for individual residues (b) Radius of Gyration for the complex for 5ns (c) RMSD values for individual residues (d) RMSD along trajectory.

and remained stable in the range of 1.0 Å to 1.2 Å. As seen in Figure 4a, highest B factor (atomic fluctuation) is observed for SER residue at the position of 342 in HLA-epitope complex, while lowest B factor observed for TRP 237. Similarly, the 342 residue also shows the highest RMSD of 0.915458 Å. The plot for radius of gyration of the HLA-epitope complex shows its compactness. The radius of gyration value during 5ns simulation slightly varies from 26.1 to 26.6. This means that the HLA-epitope complex is stably folded during simulation study. Hence, all analyses lead to the conclusion that AEWKPMKLSM is the most suitable T cell epitope for peptide-based vaccine design.

DISCUSSION

In present days, the primary focus of vaccine development mainly depends on peptide-based vaccine design. Here, computational method-based epitope mapping is very efficient method for drug design where the total process is safe, rapid and cost effective. This study incorporates various immunoinformatic, molecular docking and molecular simulation techniques to identify potential epitopes present in Zea m 1 pollen allergen.

First of all, fifty homologous allergens from SDAP allergen database[9] are identified and aligned to identify conserved sequences present in them. Moreover, a phylogenetic analysis shows a closed evolutionary relationship among the homologous allergens. So, it is believed that targeting Zea m 1 pollen allergen for vaccine design against pollinosis, could provide cross reactive reaction data for all homologous allergens.

At the beginning five potent 10mer $CD8^+$ T cell epitopes for MHC-I binding have been predicted from IEDB recommended prediction method. The percentile rank and IC_{50} values with SMM method, covering all 12 MHC class I supertypes are also predicted. The five most potent epitopes are represented in Table 3 along with their IC_{50} values.

For MHC I binding prediction, peptides with the lower percentile rank and IC_{50} values are considered higher affinity for those interacting MHC-I alleles. Therefore, we select AEWKPMKLSW T cell epitope as it binds with HLA-B*44:02 with the lowest percentile rank 0.15 and having lowering IC_{50} value 7.94 for this interacting MHC-I allele. Not only that, AEWKPMKLSW epitope interacting MHC-I allele represents highest population coverage in world as well as in India and henceforth is considered as epitope of choice.

Similarly, due to wider peptide binding cleft in MHC-II molecule than that of MHC-I, 15 mer epitopes are searched by consensus method with their IC_{50} values and shown in Table 4. For MHC-II binding prediction a 15 mer T cell epitope AEWKPMKLSWGAIWR, starts from 209 position and ends in 223 of allergic protein, shows percentile rank 30.1 with the lowest IC_{50} value 70.88 during interaction with HLA-BRB1*12:01 MHC-II allele. This result confirms peptide AEWKPMPSW as most suitable T cell epitope for our antigenic protein.

In case of B cell epitope prediction, prediction scores of Emini surface accessibility,[21] Parker hydrophilicity,[22] Karplus and Schulz flexibility,[23] Chou and Fashman beta turn[25] for each residue of peptide KVPPGPNITTNY starting from 28 position and ending in 39 positions of Zea m 1 protein sequence, reveals that this is the most potential B cell epitope present in this pollen allergen. Furthermore, Kolarskar and Tangaonkar antigenicity prediction scores, confirm our prediction. Lastly, this predicted B cell epitope sequence is also conserved among the fifty homologous allergenic protein sequences.

We also validate our predicted B cell epitope and T cell epitope by molecular docking analysis. In Docking study, the B cell epitope KVPPGPNITTNY with protein human immunoglobulin E, forms a stable complex. Similarly, the most suitable T cell epitope is perfectly fitted with the epitope binding groove of a helix of HLA-B*44:02 MHC-I molecule.

To study the stability of MHC-I protein with peptide AEWKPMKLSW, with the complex is undergone MD simulation study for 5ns. Plot of radius of gyration shows compactness in MHC-epitope complex. Similarly, the RMSD value during simulation, reaches maxima after 0.5ns and remains almost constant during remaining time interval. So, these simulation results evidently demonstrate that the binding complex of T cell epitope with allelic protein HLA-B*44:02, forms a stable complex in thermodynamic environment (Figure 4).

It is one of the important factors in vaccine design that the distribution of HLA allelic protein varies according to the population in different geographic regions of the world. Our selected T cell epitope AEWKPMKLSW is present in 69.75% of world population and 83.44% of Indian population. This result indicates that the selected T cell epitope will specifically bind with the prevalent HLA molecules in the target population in India as well as whole world.

CONCLUSION

Earlier days, most peptide vaccines have been developed on B cell immunity, however our current study considers both B cell and Tcell epitopes in Zea m 1 pollen allergen. These two epitopes stimulate human immunity during type I hypersensitivity reaction when susceptible individual comes in contact with allergens. These two selected peptides i.e. KVPPGPNITTNY and AEWKPMKLSW show B cell and T cell selectivity, better conservancy among the homologous allergens, highest population coverage of interacting MHC allelic protein. The second epitope depicts significant interaction with MHC-I allele with good affinity. Above all, the predicted epitopes are participated in long term and high protective immunity in peptide vaccine design against Zea m 1 pollen allergen.

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CONFLICT OF INTEREST

The authors report no conflicts of interest in this work.

ABBREVIATIONS

MHC-I: Major histocompatibity complex I; **MHC-II:** Major histocompatibity complex II; **HLA:** Human leukocyte antigen complex; **MD:** Molecular dynamics; **NAMD:** Nanoscale molecular dynamics; **CD8:** Cluster of differentiation 8; **CD4:** Cluster of differentiation 4.

SUMMARY

Computer based epitope mapping, a state-of-art method is used for vaccine design against Zea m 1 pollen allergen from maize. One of the selected epitope for Zea m 1 , is present in the conserved region of other fifty homologous allergenic proteins also. Not only for Zea m 1 pollen allergen, but also for these allergic proteins, the epitope KVPPGPNITTNY is selected as peptide based vaccine for clinical verification against disease pollinosis.

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