

In silico prediction of the T-cell and IgE-binding epitopes of Per a 6 and Bla g 6 allergens in cockroaches

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Abstract. Per a 6 and Bla g 6 are cockroach allergens found in *Periplaneta americana* and *Blattella germanica*, respectively. The objective of the present study was to predict the B- and T-cell epitopes of the Per a 6 and Bla g 6 allergens. Three immunoinformatics tools, the DNASTar Protean system, the Bioinformatics Predicted Antigenic Peptides system and the BepiPred 1.0 server, were used to predict the potential B-cell epitopes, while Net-MHCIIpan-2.0 and NetMHCII-2.2 were used to predict the T-cell epitopes of the two allergens. As a result, seven peptides were predicted in the Per a 6 allergen and seven peptides were predicted in the Bla g 6 allergen in the B-cell epitope predictions. In the T-cell prediction, the Per a 6 allergen was predicted to have nine strongly binding nonamer core epitope sequences ($IC_{50} < 50$ nm) and 28 weakly binding sequences ($50 \text{ nm} < IC_{50} < 500$ nm), while the Bla g 6 allergen was predicted to have nine strong binders and 25 weak binders. These results may be useful for peptide-based vaccine designs.

Introduction

Cockroach allergies are type I hypersensitivities mediated by immunoglobulin E (IgE) and have been recognized as

such since 1964 (1). Cockroach allergies are associated with the development of asthma and have been shown to put patients with asthma at risk of requiring emergency medical aid. This is a particular issue for asthmatic children in less affluent urban households, where cockroach infestations are more prevalent (2). Several proteins from cockroaches are potent environmental aeroallergens. Skin prick tests in China revealed that 25.7% of patients with allergies reacted positively to the American cockroach *Periplaneta americana* (Per a allergens) and 18.7% exhibited positive responses to the German cockroach *Blattella germanica* (Bla g allergens) (3). Among the indoor cockroaches, the American cockroach is the dominant species and is responsible for a large proportion of the cockroach-induced allergic reactions worldwide. Seven allergens from *Periplaneta americana* have been characterized: Per a 1 (4), Per a 2 (5), Per a 4 (6), Per a 6 (7), Per a 7 (8), Per a 9 (9) and Per a 10 (10). Per a 6 is a troponin C protein identified in the American cockroach. It was found that native Per a 6-bound IgE was present in the sera of 17% of Thai individuals with cockroach allergies, indicating that Per a 6 is a minor cockroach allergen (11).

To date, the use of cockroach immunotherapy has been rare and there are few reports on its efficacy (12,13). Elucidation of the B- and T-cell epitopes of allergens may enhance the understanding of the structure-function relationship and predict the basis of cross-reactivity. Cross-reactive epitopes may be useful in reducing the number of allergens without compromising the efficacy of therapy (14). B-cell epitopes can be applied in the diagnosis, therapy and development of effective vaccines for immunotherapy. Numerous techniques can be utilized in the identification of B-cell epitopes; in particular, computational tools have been suggested to represent a promising and rapid approach. Following identification, the allergenicity of an allergen can be reduced by modifying the predicted B-cell epitopes (15). In the last decade, T-cell epitopes were successfully identified based on computer simulation. To stimulate T-lymphocyte responses, extracellular peptides bind to major histocompatibility complex (MHC) class II molecules (16). Therefore, T-cell epitopes were indirectly predicted by the identification of MHC-binding molecules (17). In the present study, the B- and T-cell epitopes of the Per a 6 allergen and its analog in the German cockroach, the Bla g 6.01 allergen, were identified by an *in silico* approach. The results indicated the

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potential utility of the B- and T-cell epitopes in a peptide-based vaccine design for cockroach allergy.

Materials and methods

Sequence retrieval. The primary sequence of the Per a 6 allergen was acquired from the nucleotide database of the National Center for Biotechnology Information (NCBI; <http://www.ncbi.nlm.nih.gov/>) with the accession number AY792950.1. The Basic Local Alignment Search Tool (BLAST; <http://blast.ncbi.nlm.nih.gov/Blast.cgi>) was used to obtain the homologous sequences.

Physicochemical analysis. Physicochemical analysis of the Per a 6 allergen and its homologous sequences, including analysis of the molecular weight, theoretical isoelectric point (pI), amino acid composition, instability index, aliphatic index and grand average of hydropathicity (GRAVY), was performed using the ProtParam tool (<http://web.expasy.org/protparam/>).

Phylogenetic analysis. The complete amino acid sequences of the Per a 6 allergen and its homologs were aligned using Clustalx 2.1 (18). The phylogenetic tree was obtained using the neighbor-joining (NJ) method on the basis of the Jones-Taylor-Thornton amino acid sequence distance implemented in the Molecular Evolutionary Genetics Analysis 5 software (19). The reliability was evaluated by the bootstrap method with 1,000 replications.

In silico prediction of B-cell epitopes. In the Protean™ system (DNASar, Inc., Madison, WI, USA), four properties (hydrophilicity, flexibility, accessibility and antigenicity) of the amino acid sequences were selected as parameters for the prediction of epitopes. The hydrophilicity prediction was performed by the methods of Hopp and Woods (20) and Kyte and Doolittle (21). Flexibility was analyzed by the strategies of Karplus and Schulz (22), while the surface accessibility and antigenicity were analyzed by the strategies of Emini *et al.* (23) and Jameson and Wolf (24). The peptide regions with good hydrophilicity, high flexibility, surface accessibility and a high antigenic index were selected as candidate epitopes for further investigation. In order to enhance the veracity of prediction towards the B-cell epitopes, the amino acid sequences were analyzed by the Protean system.

The Bioinformatics Predicted Antigenic Peptides (BPAP) system (<http://imed.med.ucm.es/Tools/antigenic.pl>) and BepiPred 1.0 server (<http://www.cbs.dtu.dk/services/BepiPred/>) were additionally used to predict B-cell epitopes. The BPAP system follows the prediction method by Kolaskar and Tongaonkar (25), while the BepiPred 1.0 server follows a combination of a hidden Markov model and a propensity scale method (26). The two servers only require the amino acid sequence and provide more straightforward results, which are combined with the physicochemical properties of the amino acids, including hydrophilicity, flexibility, accessibility, turns and an exposed surface (27). The ultimate consensus epitope results were obtained by combining the results of the three immunoinformatics tools with the previously published method (28). If all three methods concluded that the sequence was not an epitope, the consensus result was 0% epitope.

However, if only one or none of the methods predicted that the sequence was not an epitope, the consensus result was 67% or 100% epitope, respectively. The regions whose consensus epitope result was 67 or 100% were selected as the final potential epitope regions.

In silico prediction of T-cell epitopes. T-cell epitopes are principally predicted indirectly by identifying the binding of peptide fragments to the MHC complexes. However, the binding grooves of MCH-II molecules are open at both ends, allowing various lengths of peptides to bind, and the same MHC molecule can accommodate various different binding sequences. These two properties make the development of accurate predictive algorithms for MHC-class II binding complicated. It has been reported that a sequence nine amino acids in length (9-mer), known as a core peptide, is essential for MHC-class II binding (29). For human leukocyte antigen (HLA)-DR-based T-cell epitope prediction, the artificial neural network-based alignment (NN-align) method NetMHCIIpan-2.0 (<http://www.cbs.dtu.dk/services/NetMHCIIpan/>) was applied. NetMHCIIpan-2.0 provides predictions only for a selection of the most commonly found HLA-DR alleles. For HLA-DQ alleles, NetMHCII-2.2 (<http://www.cbs.dtu.dk/services/NetMHCII/>) was used (30). Although the predicted results provided limited binding-affinity data, it was recently reported to provide the best performance in predicting this locus (31). For the T-cell prediction process, the peptides predicted to be significant binders by at least one allele were examined. The binding significance of each peptide to the given MHC molecule was based on the estimated strength of binding exhibited by a predicted nested core peptide at a set threshold level. Based on the estimated strength of binding, the peptides were characterized as significant (weak or strong) or non-significant. Each predicted core 9-mer sequence represented the predicted putative T-cell epitope within each peptide examined (32).

Results

Physicochemical analysis and phylogenetic analysis. The amino acid sequence of the Per a 6 allergen was obtained from the nucleotide database of the NCBI. The primary structure contained 151 amino acids. A search with BLAST obtained 16 homologous sequences of the allergen. The accession numbers of these homologs were DQ279092.1 (*Blattella germanica* allergen Bla g 6.01), DQ279093.1 (*Blattella germanica* allergen Bla g 6.02), XM_001987063 (*Drosophila grimshawi* GH21731), XM_002049988 (*Drosophila virilis* troponinC41C), XM_002106068.1 (*Drosophila simulans* GD16679), XM_002086000 (*Drosophila yakuba* GE11315), GQ396705.1 (*Bombyx mori* troponin CIII), XM_001688761.1 (*Anopheles gambiae* str. PEST), AY075534.1 (*Drosophila melanogaster* RH0783), NM_078895.4 (*Drosophila melanogaster* troponin C), X76043.1 (*Drosophila melanogaster* troponin C), XM_002063468.1 (*Drosophila willistoni* GK21371), AB180453.1 (*Plutella xylostella* troponin C), XM_001867954.1 (*Culex quinquefasciatus* troponin C), AF432912.1 (*Solenopsis invicta* troponin C), and NM_001205104

Table I. Physicochemical properties of the Per a 6 allergen and its homologous sequences.

Accession no.	MW	NCR (n)	PCR (n)	TP	II	AI	G
AY792950.1	17130.9	44	11	3.84	24.97	87.22	-0.377
DQ279092.1	17216.2	43	13	3.96	35.44	86.56	-0.388
DQ279093.1	17095.1	43	13	3.96	31.48	87.22	-0.269
XM_001987063	16989.7	40	10	3.84	32.11	86.05	-0.324
XM_002049988	17557.4	40	10	3.84	29.52	81.58	-0.317
XM_002106068.1	17155.9	40	10	3.83	31.63	83.05	-0.325
XM_002086000	16937.6	40	10	3.83	29.02	84.14	-0.336
GQ396705.1	17275.3	42	13	4.03	34.45	86.01	-0.291
XM_001688761.1	17609.5	42	12	3.90	27.87	85.00	-0.384
AY075534.1	17155.9	40	10	3.83	31.63	83.05	-0.325
NM_078895.4	17155.9	40	10	3.83	31.63	83.05	-0.325
X76043.1	17125.9	39	11	3.90	31.77	82.94	-0.345
XM_002063468.1	17036.9	37	11	3.99	34.09	87.22	-0.220
AB180453.1	17262.2	42	13	4.05	37.38	84.12	-0.322
XM_001867954.1	18057.9	40	11	3.99	28.80	83.60	-0.343
AF432912.1	17304.2	42	13	4.01	38.57	84.84	-0.457
NM_001205104	17720.5	45	12	3.84	34.45	85.82	-0.394

MW, molecular weight; NCR, negatively charged residues; PCR, positively charged residues; TP, theoretical pI; II, instability index; AI, aliphatic index; G, gravity; AY792950.1, Per a 6 allergen; DQ279092.1, Bla g 6.01 allergen; DQ279093.1, Bla g 6.02 allergen.

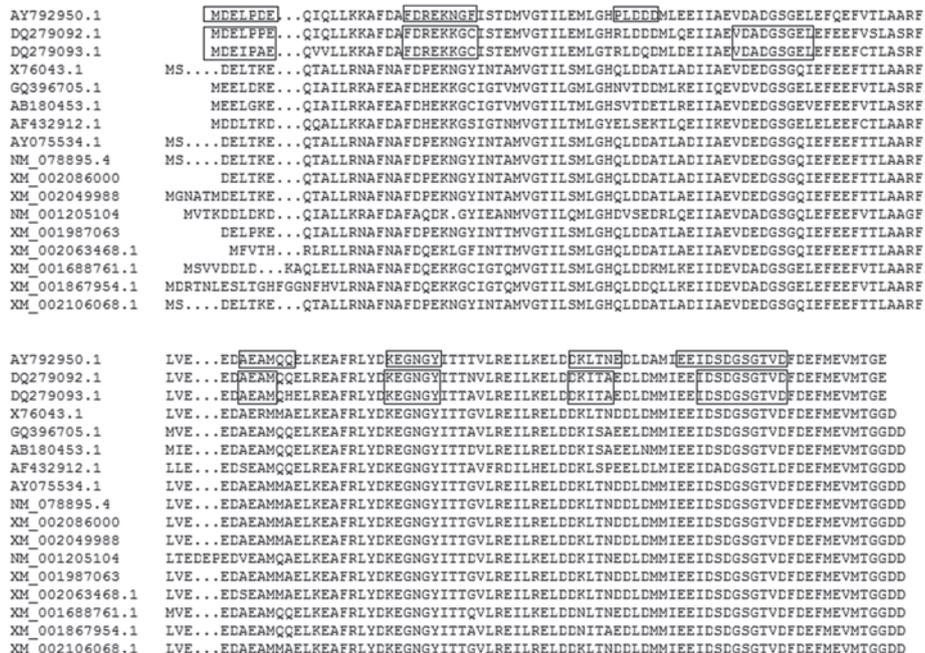


Figure 1. Alignment of the Per a 6 allergen and its homologs. The predicted peptides are displayed in gray boxes. AY792950.1, Per a 6 allergen; DQ279092.1, Bla g 6.01 allergen; DQ279093.1, Bla g 6.02 allergen.

(*Acyrtosiphon pisum* troponin C-like). Table I shows the details of the physicochemical analysis of these homologs. All homologs were stable (instability index ranging between 24.97 and 38.57) with theoretical pIs ranging between 3.83 and 4.05. The GRAVY values were found to be negative (-0.457 to -0.220) for complete sequences.

The alignment of the Per a 6 allergen and its homologs is shown in Fig. 1. The evolutionary tree (Fig. 2) was inferred by the NJ method. Phylogenetic analysis showed that Bla g 6.01 (DQ279092.1) and Bla g 6.02 (DQ279093.1) were two related sequences that were similar to the Per a 6 allergen. Bla g 6.01 and Bla g 6.02 are two cockroach isoallergens identified from

Table II. Location of the B-cell epitopes of the Per a 6 allergen predicted by three immunoinformatics tools.

Tools	Location of the prediction results
DNASStar Protean	1-7, 17-27, 42-48, 81-89, 96-102, 114-123, 129-140
BPAP	5-16, 32-41, 49-55, 64-78, 103-113
BepiPred 1.0 server	1-7, 19-26, 42-46, 81-86, 97-103, 117-122, 131-140
BPAP, Bioinformatics Predicted Antigenic Peptides.	

Table III. Location of the B-cell epitopes of the Bla g 6.01 allergen predicted by three immunoinformatics tools.

Tools	Location of the prediction results
DNASStar Protean	1-7, 17-27, 42-47, 55-65, 81-91, 95-102, 113-122, 129-140
BPAP	5-15, 23-29, 32-41, 48-54, 65-78, 107-113
BepiPred 1.0 server	1-7, 19-26, 55-63, 81-84, 97-103, 117-121, 131-140
BPAP, Bioinformatics Predicted Antigenic Peptides.	

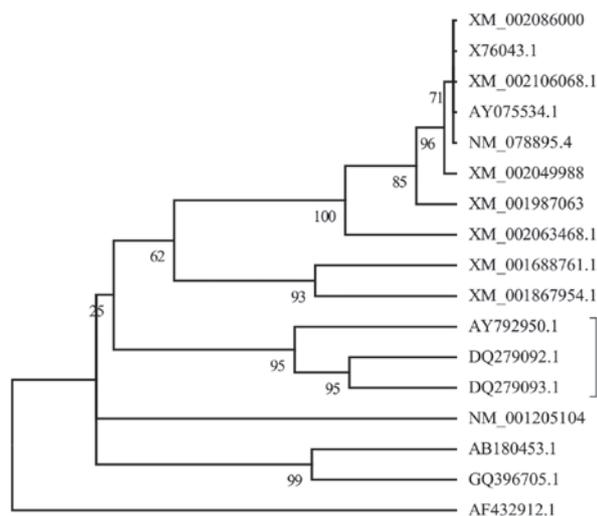


Figure 2. Phylogenetic association of the Per a 6 allergen amino acid sequence with other homologs. Bla g 6.01 and Bla g 6.02 are two related sequences similar to Per a 6. AY792950.1, Per a 6 allergen; DQ279092.1, Bla g 6.01 allergen; DQ279093.1, Bla g 6.02 allergen.

Blattella germanica, with Bla g 6.01 exhibiting 93% amino acid identity to Bla g 6.02. In the present study, the B- and T-cell epitopes of the Per a 6 and Bla g 6.01 allergens were investigated.

Epitope prediction

B-cell epitope prediction. Surface accessibility and fragment flexibility are important features for predicting antigenic

Table IV. B-cell epitopes of the Per a 6 allergen predicted by combined immunoinformatics methods.

Number	Position	Length of sequence (amino acids)	Sequence
Peptide 1	1-7	7	MDELPDE
Peptide 2	19-26	8	FDREKNGF
Peptide 3	42-46	5	PLDDD
Peptide 4	81-86	6	AEAMQQ
Peptide 5	97-102	6	KEGNGY
Peptide 6	117-122	6	DKLTNE
Peptide 7	129-140	12	EEIDSDGSGTVD

Table V. B-cell epitopes of the Bla g 6 allergen predicted by combined immunoinformatics methods.

Number	Position	Length of sequence (amino acids)	Sequence
Peptide 1	1-7	7	MDELPDE
Peptide 2	19-26	8	FDREKKGK
Peptide 3	55-63	9	VDADGSGEL
Peptide 4	81-84	4	AEAM
Peptide 5	97-102	6	KEGNGY
Peptide 6	117-121	5	DKITA
Peptide 7	131-140	10	IDSDGSGTVD

epitopes. In addition, the existence of regions with high hydrophobicity provides strong evidence for epitope identification. As shown in Figs. 3 and 4, the hydrophilic regions occupied most of the sequence, indicating high hydrophilicity of the Per a 6 and Bla g 6.01 allergens. Furthermore, the frequent appearance of the surface and flexibility regions indicated that the Per a 6 and Bla g 6.01 sequences were flexible, stretched and easily exposed to the outside. The stretched structure was further validated by the results of the flexibility and surface accessibility analysis. The antigenic index directly showed the epitope-forming capacity of the Per a 6 and Bla g 6.01 sequences. Most of the sequences exhibited a high antigenic index, suggesting a high tendency of Per a 6 and Bla g 6.01 to form epitopes. Based on these sequence properties, the final regions predicted by DNASStar Protean were obtained as shown in Tables II and III. Tables II and III also show the predicted results obtained using the BPAP system and the BepiPred 1.0 server. The final potential epitopes of the Per a 6 and Bla g 6.01 allergens were selected on the basis of the results from these two tools and those from the DNASStar Protean system. The ultimate results of the three immunoinformatics tools predicted seven peptides (1-7, 19-26, 42-46, 81-86, 97-102, 117-122 and 129-140) to be the potential linear B-cell epitopes of the Per a 6 allergen, and seven peptides, 1-7, 19-26, 55-63, 81-84, 97-102, 117-121 and 131-140, were predicted as

Table VI. Location of the T-cell epitopes of the Per a 6 allergen predicted by Net-MHCIIpan-2.0 and NetMHCII-2.2.

Per a 6 allergen	
Strong-binding core peptides	7-15, 35-43, 65-73, 66-74, 68-76, 102-110, 121-129, 123-131, 142-150
Weak-binding core peptides	9-17, 12-20, 26-34, 27-35, 28-36, 31-39, 32-40, 33-41, 36-44, 47-55, 48-56, 51-59, 63-71, 64-72, 69-77, 75-83, 84-92, 86-94, 87-95, 88-96, 94-102, 95-103, 100-108, 103-111, 107-115, 111-119, 120-128, 140-148
Strong-binding, $IC_{50} < 50$ nm; weak-binding, 50 nm $< IC_{50} < 500$ nm.	

Table VII. Location of the T-cell epitopes of the Bla g 6 allergen predicted by Net-MHCIIpan-2.0 and NetMHCII-2.2.

Bla g 6.01 allergen	
Strong-binding core peptides	8-16, 35-43, 50-58, 68-76, 75-83, 84-92, 88-96, 89-97, 142-150
Weak-binding core peptides	4-12, 10-18, 12-20, 28-36, 24-32, 26-34, 41-49, 45-53, 48-56, 51-59, 65-73, 69-77, 70-78, 73-81, 76-84, 77-85, 86-94, 95-103, 100-108, 102-110, 107-114, 108-116, 111-119, 119-127, 139-147
Strong-binding, $IC_{50} < 50$ nm; weak-binding, 50 nm $< IC_{50} < 500$ nm.	

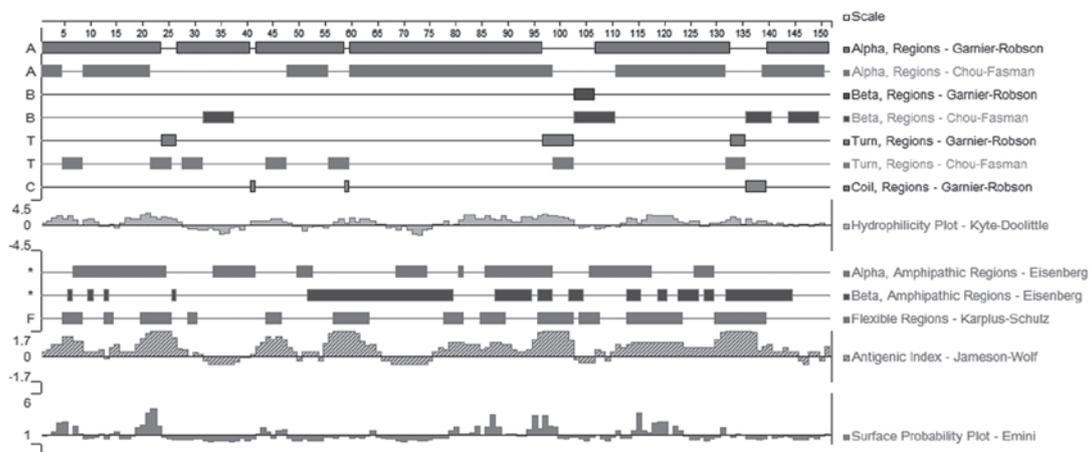


Figure 3. Analysis results of the amino acid sequence of the Per a 6 allergen using the DNASTar Protean system.

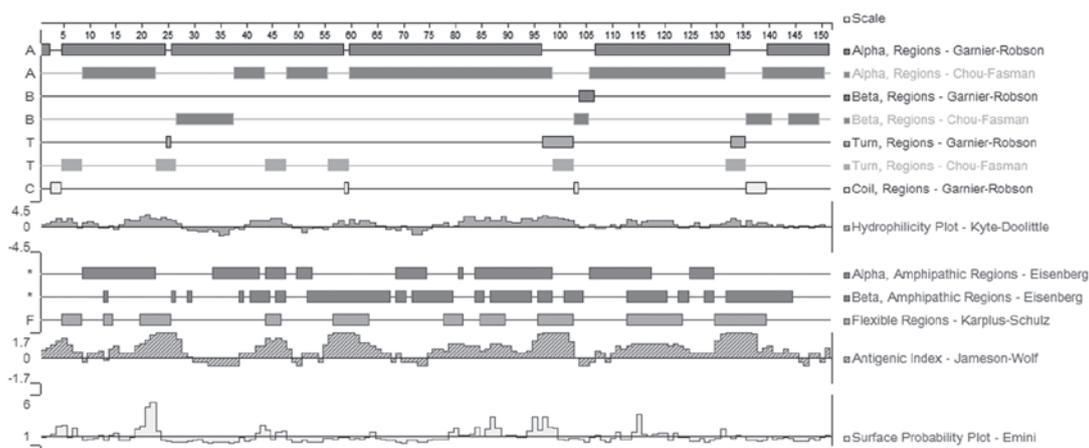


Figure 4. Analysis results of the amino acid sequence of the Bla g 6 allergen using the DNASTar Protean system.

potential linear B-cell epitopes of the Bla g 6.01 allergen. The amino acid sequences are shown in Tables IV and V.

T-cell epitope prediction. Net-MHCIIpan-2.0 and NetMHCII-2.2 were used to identify significant core 9-mer peptides in the Per a 6 and Bla g 6.01 allergens. All estimations were based on the HLA-DRB1 alleles found in the study cohort. For HLA-DQ alleles, only DQB1 0201, 0402, 0501 and 0602 were used for epitope prediction. In the overall analysis using Net-MHCIIpan-2.0 and NetMHCII-2.2, Per a 6 was predicted to have nine strongly binding 9-mer core epitope sequences ($IC_{50} < 50$ nM): Peptides 7-15, 35-43, 65-73, 66-74, 68-76, 102-110, 121-129, 123-131, 142-150 (Table VI). The Per a 6 allergen was also predicted to have 28 weakly binding 9-mer core epitope sequences ($50 \text{ nm} < IC_{50} < 500 \text{ nm}$) (Table VI). The Bla g 6.01 allergen was predicted to have 34 significant nonamer core epitope sequences. Nine of them were strong binders and comprised peptides 8-16, 35-43, 50-58, 68-76, 75-83, 84-92, 88-96, 89-97 and 142-150 (Table VII). The remaining peptides were weak binders and are shown in Table VII.

Discussion

The prevalence and morbidity of allergies, such as asthma, rhinitis and eczema, in children have been increasing over recent decades. This is currently a major concern for the international medical community and cannot solely be attributed to the improved diagnosis of these diseases (33). Conventional immunotherapy for allergies using crude allergen extracts has been shown to have a high risk of anaphylaxis. One alternative approach is the use of peptide fragments corresponding to the B- and T-cell epitopes of the allergen (34). In a previous study, overlapping synthetic peptides were used to validate the IgE-binding capacity. Although this method decreases the possibility of missed epitopes, it requires the synthesis of large numbers of peptides, which is time-consuming and costly (35). *In silico* prediction has become a common and useful tool for selecting epitopes from immunologically relevant proteins, and can save the time and cost of peptide synthesis (36).

Per a 6 is a minor cockroach allergen from *Periplaneta americana*, while Bla g 6 is an allergen from *Blattella germanica* with a sensitization prevalence of 14% among patients with cockroach allergy. Bla g 6 consists of three isoallergens: Bla g 6.01, 6.02 and 6.03. Bla g 6.01 shows 93% amino acid identity to Bla g 6.02 and 68% identity to Bla g 6.03. The evolutionary tree in the present study (Fig. 2) showed that Bla g 6.01 and 6.02 are homologs of Per a 6 (11). To the best of our knowledge, the present study is the first to predict B- and T-cell epitopes from the Per a 6 and Bla g 6.01 allergens. A previous study showed that the prediction of B-cell epitopes using the bioinformatics approach correlated well with the experimental approach (37). The prediction of B-cell epitopes among protein sequences has been enabled by the development of numerous algorithms that are based on certain amino acid properties, including hydrophilicity, antigenicity, segmental mobility, flexibility and accessibility (38). In the present study, the linear B-cell epitopes of the Per a 6 and Bla g 6.01 allergens were predicted using three sequence-based tools (the DNASTar Protean system, BPAP and the BepiPred

1.0 server). Seven B-cell epitopes of Per a 6 and seven epitopes of Bla g 6 were investigated. The alignment results (Fig. 1) showed that all the peptides of Per a 6 and Bla g 6 were located in similar positions, with exception of peptide three. This indicated that Per a 6 shares a cross-reactive epitope with Bla g 6. Peptide three of Per a 6 was located at position 42-46, while that of Bla g 6 was located at 55-63, indicating that peptide three may represent a distinction between the epitopes of these two cockroach allergens.

In recent years, certain algorithms have substantially improved in their accuracy to predict T-cell epitopes. However, most algorithms have targeted HLA-DR molecules, not HLA-DP or HLA-DQ molecules, despite the importance of HLA-DP and HLA-DQ molecules for antigen presentation. NetMHCpan-2.0 was recently shown to have a per-allele mean accuracy of 0.854 (1.0 being 100% accurate and 0.5 of no significance) (39). In another study, the per-allele mean accuracy of the NN-align method was 0.882 (31). In the present study, Net-MHCIIpan-2.0 and NetMHCII-2.2 were used to predict the core 9-mer T-cell epitopes in the Per a 6 and Bla g 6 allergens. Combining the results obtained with Net-MHCIIpan-2.0 and NetMHCII-2.2, a total of 37 and 34 epitopes were predicted for the Per a 6 and Bla g 6 allergens, respectively. Nine epitopes from the Per a 6 allergen and nine from Bla g 6 allergen were strongly binding, with an $IC_{50} < 50$ nm.

In conclusion, the present study predicted B- and T-cell epitopes of the Per a 6 allergen and its homolog, the Bla g 6.01 allergen in *Blattella germanica*, using an *in silico* method. The results may be used to benefit allergen immunotherapies and reduce the frequency of allergic reactions. However, the accuracy of these epitopes requires confirmation in further experiments.

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