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POLLEN ALLERGENS AND BIOINFORMATIC ANALYSIS OF THE IMMUNE EPITOPES RELATED TO POLLEN ALLERGY

Dzhemal Moten, Plamen Stoyanov, Ivanka Teneva, Balik Dzhambazov*

Faculty of Biology, Plovdiv University „Paisii Hilendarski“, 24 Tsar Assen Str., 4000 Plovdiv, Bulgaria
****Corresponding author. E-mail: balik@uni-plovdiv.bg***

ABSTRACT

Pollen allergy is one of the most common allergies worldwide and it has been attributed to cross-reactive IgE. It may be also responsible for the development of plant food allergy inducing primary sensitization of susceptible individuals, which results secondary allergy to plant foods via cross-reactivity. The aim of this study was to compare the known pollen T-cell and B-cell epitopes and to analyze their cross-reactivity. Using bioinformatic approaches, we have identified the most abundant pollen epitope sequences. We have selected 16 often-repeated sequences within the investigated T- and B-cell epitopes and 11 of them contained MHC class-II binding regions. Some of the sequences had high percent of identity with sequences of other proteins found in pathogens suggesting that previous infections with some of these pathogens could be responsible for the initial priming of the T-cells and production of antibodies cross-reacting with pollen allergens.

KEY WORDS: pollen allergens, immune epitopes, sequences, cross-reactivity.

INTRODUCTION

In order to reproduce, many plants form microscopic grains called „pollen". Pollen grains are produced in the microsporangium and have a wide variety of shapes (most often round or oval), sizes, and surface markings characteristic of the species. For fertilization in some anemophilous plants, pollen must be transferred by the wind from one plant to another plant of the same species. Such plants produce large quantities of lightweight pollen grains, which can be carried for great distances and are easily inhaled, bringing them into contact with the sensitive nasal passages. Pollen can act as a source of allergens that induce primary sensitization in the susceptible individuals. The appearance of respiratory symptoms (rhinoconjunctivitis and/or bronchial asthma) as a result of the inhalation of pollen to which some individuals are sensitized is defined as pollinosis.

It is well known that the allergic rhinitis and asthma are a global problem that affects up to 40 % of the European population and may vary according to the patient age and geographical distribution (Bousquet et al., 2001). Since more and more people are developing allergic diseases and it is estimated that, by 2015, one in two Europeans is likely to suffer from at least one form of allergy, the research in this field is ranked with highest priority. Major efforts are still needed in research to understand pollen allergy and its complex mechanisms. Thus, identification, isolation and characterization of the pollen allergens are necessary tasks to improve the diagnosis and treatment of these clinical disorders and to explain the relationship between biological function, protein structure and allergenic activity (Aalberse, 2000).

So far, about 50 plant species are registered in the official allergen list of the International Union of Immunological Societies (IUIS) Allergen Nomenclature Subcommittee (http://www.allergen.org) as potential inducers of pollen allergy in susceptible individuals (Mothes et al., 2004). Hauser et al. (2010) divided these pollinosis-associated plants into three groups: (I) trees (*Fagales, Pinales, Rosales, Arecales, Scrophulariales, Junglandales, Salicales* and *Myrtales*), (II) grasses (*Bambusioideae, Arundinoideae, Chloridoideae, Panicoideae* and *Poideae*), and (III) weeds (*Asteraceae*, *Chenopodiaceae* and *Urticaceae*).

Current *in vivo* and *in vitro* diagnostics for pollen allergy are usually performed with pollen extracts from different species. Allergenic pollen is

a complex mixture of several molecules including major and minor allergens. Defining the composition of pollen extracts, each consisting of many different glycoproteins and polysaccharides, is an almost impossible task. The trend in allergen standardization is moving from biological standardization toward the measurement of major allergens (Van Ree, 1997). Major allergens represent components to which the majority of allergic individuals (>50 %) reacting to a given allergen source is sensitized.

Based on the all known plant allergen sequences from the Allergome database, Radauer and Breiteneder (2005) have been classified the pollen allergens into 29 of a total of 7868 protein families. The major pollen allergen families are expansins, profilins and polcalcins (calcium-binding proteins).

Expansins are a family of proteins (≈ 30 kDa) that catalyse long-term extension of isolated plant cell walls due to an as yet unknown biochemical mechanism. Beta-expansins include grass group I allergens and their vegetative homologs. These grass group I allergens, to which more than 95 % of patients allergic to grass pollen possess IgE antibodies, are highly immunologically crossreactive glycoproteins exclusively expressed in pollen of all grasses.

Profilins are small (12–15 kDa) cytosolic proteins associated with the reorganization of cytoskeleton processes and cell motility (Hauser et al., 2010). They are highly conserved molecules sharing sequnce identities of more then 75 % even between members of distantly related organisms. Allergenic profilins were identified in pollen of trees, grasses, and weeds, in plant-derived foods, as well as in latex (Hauser et al., 2010). Therefore, profilin sensitization is a risk factor for allergic reactions to multiple pollen allergen sources.

Polcalcins are highly cross-reactive calcium-binding allergens sharing common domains termed EF-hands (helix-loop-helix motifs) that are specifically expressed in pollen tissues. The biologic function of polcalcins is still unclear. However, due to their pollen-specific localization and their ability to bind calcium, it has been proposed that polcalcins function in the control of intracellular calcium levels during pollen germination (Wopfner et al., 2007). Recent data indicate that the clinical relevance of polcalcin sensitization is linked to geographical factors and level of exposure to different allergenic sources (Wopfner et al., 2008).

After inhalation of the pollen, allergen particles are deposited in the nasal mucus, with subsequent elution of allergenic proteins and diffusion into nasal tissues. Protease activities of several common aeroallergens can facilitate allergen access to antigen-presenting cells by cleaving tight junctions in the airway epithelium and activation of protease-activated receptors on epithelial cells. Activated epithelial cells then produce cytokines, chemokines, and thymic stromal lymphopoietin, which interact with interepithelial and subepithelial dendritic cells to skew T-cell development and adaptive allergic sensitization (Dykewicz & Hamilos, 2010). In the nose allergens are processed by antigen-presenting cells (dendritic cells expressing CD1a and CD11c and macrophages) in the nasal epithelial mucosa, with subsequent presentation of allergenic peptides by MHC class II molecules to T-cell receptors on resting $CD4^+$ T lymphocytes in regional lymph nodes. With costimulatory signals, allergen-stimulated T cells proliferate into T_H2-biased cells that release IL-3, IL-4, IL-5, IL-13, and other cytokines. These cytokines then lead to a cascade of events that promote B-cell isotype switching with subsequent local and systemic production of allergen-specific IgE antibody, eosinophilic infiltration into the nasal epithelium and mucosa, and mast cell proliferation and infiltration of airway mucosa.

Within minutes of inhalation of allergen in sensitized individuals, deposited allergens are recognized by IgE antibody bound to mast cells and basophils, causing degranulation and release of preformed mediators (immediate response), such as histamine and tryptase, and the rapid de novo generation of mediators, including cysteinyl leukotrienes (leukotrienes C_4, D_4, and E_4) and prostaglandin D_2. Mediators and cytokines released during the immediate response set off a cascade of events over the ensuing 4 to 8 hours that lead to an inflammatory response called a late response.

The amount of allergen necessary to elicit an immediate response becomes less when allergen challenges are given repeatedly, a phenomenon called the priming effect (Wachs et al., 1989). During ongoing, prolonged allergen exposure and repeated late-phase/inflammatory responses, the nasal mucosa becomes progressively more inflamed and responsive to the allergen.

It has been shown that the regulatory $CD4^+$ $CD25^+$ $FoxP3^+$ T cells are functional in most allergic patients and their function is dependent on the

concentration and the type of the respective allergen with different thresholds for individual allergens and patients (Bellinghausen et al., 2005). Allergic diseases are linked to a Th2-skewed response to inhaled allergens (Larche et al., 2006), which may be a result of a defect in the regulation of allergen-stimulated T cells. Mittag et al. (2010) found that the expression of FoxP3 on the regulatory T cells is reduced in allergic patients and suggested that the cogeneration of FoxP3 regulatory T cells in response to allergen may be a mechanism for controlling allergic reactions in healthy individuals, which is impaired in those with allergies.

Most clinical allergists evaluate the humoral response to allergens by measuring the levels of specific IgE, but they are not able to investigate the T-cell response. Commercial allergen extracts used in the immunotherapy are complex mixtures of several proteins that may contain both T-cell and B-cell epitopes. These proteins have the ability to decrease allergic symptoms through regulatory T cells, but in the same time they may cause anaphylaxis if IgE binding B-cell epitopes are presented (Letz & Calabria, 2009). The aim of this study was to compare the known pollen T-cell and B-cell epitopes and to analyze their cross-reactivity.

METHODS

All known pollen T-cell and B-cell epitopes related to pollen allergy (single sequence per epitope) were extracted from the Immune Epitope Database (http://www.iedb.org/) and compared for similarity by using the CLC Sequence Viewer 6.5.3 software. Investigated epitopes were aligned with other sequences of allergenic as well as non-allergenic proteins using the BLAST program of the NCBI (http://blast.ncbi.nlm.nih.gov) with parameters optimized for short query sequences (E-value threshold, 100, low-complexity filter off, ungapped alignment for fragments shorter than 20 residues). To visualize relationships between the allergenic epitopes and other proteins a cluster analysis was performed. Neighbor-joining trees were generated and drawn by using the PHYLIP package (Felsenstein, 1989).

Most abundant pollen sequences (T-cell and B-cell epitopes) were analyzed for binding affinity to human MHC class-II molecules using the Pro-

Pred prediction (http://www.imtech.res.in/raghava/propred/) developed by Singh & Raghava (2001).

RESULTS AND DISCUSSION

Most B-cell epitopes (but not all) that are recognized by IgE molecules are usually three-dimensional structures, whereas T-cell epitopes are short linear peptides presented by the antigen-presenting cells. Thus, it should be possible to use short peptide fragments of natural pollen allergens to modulate T-cell immune response without risk developing an anaphylactic reaction. Still, these short peptides should be selected very carefully to avoid including B-cell epitopes in the sequence since many T- and B-cell pollen epitopes are overlapped. In addition, the homogeneity of pollen allergens in phylogenetically related plant species could generate high levels of cross-reactivity, both in terms of IgE and T-cell response.

In this study, we have performed multiple sequence alignments of 2309 T-cell epitopes and 1010 B-cell epitopes from completely or partially sequenced pollen allergens available in the public databases (Immune Epitope Database, Allergen Nomenclature, Allergen Database for Food Safety, AllergenOnline, Allergome, Structural Database of Allergenic Proteins, UniProt, National Center for Biotechnology Information) by using the CLC Sequence Viewer 6.5.3 software. Most repeated sequences (12 mers) within the investigated immune epitopes were selected and further analyzed (Table 1).

Table 1. *Characteristic of the most abundant sequences within the pollen immune epitopes. MHC class-II binding motifs are given in „bold“. Threshold setting – 3 %.*

№	Sequences	MHC class-II binding prediction	Range of highest score (%)
1.	SNE**IKIVATPDG**	DRB1*0301, DRB1*0305, DRB1*0309, DRB1*0402, DRB1*0404, DRB1*0405, DRB1*0408, DRB1*0421, DRB1*0423, DRB1*0801, DRB1*0806, DRB1*0817, DRB1*1101, DRB1*1104, DRB1*1106, DRB1*1107, DRB1*1128, DRB1*1305, DRB1*1307, DRB1*1311, DRB1*1321, DRB5*0101, DRB5*1105.	8.82 – 47.37
2.	KKISFPEGFPFK	–	–

3.	**LRAVESYLLAHS**	DRB1*0101, DRB1*0102, DRB1*0305, DRB1*0309, DRB1*0402, DRB1*0404, DRB1*0405, DRB1*0408, DRB1*0410, DRB1*0421, DRB1*0423, DRB1*0701, DRB1*0703, DRB1*0801, DRB1*0802, DRB1*0804, DRB1*0806, DRB1*0813, DRB1*0817, DRB1*1102, DRB1*1107, DRB1*1114, DRB1*1120, DRB1*1121, DRB1*1301, DRB1*1302, DRB1*1304, DRB1*1321, DRB1*1322, DRB1*1323, DRB1*1327, DRB1*1328, DRB1*1501, DRB1*1506, DRB5*0101, DRB5*1105.	10.63 – 67.24
4.	V**FEAALTKAI**TA	DRB1*0421	25.56
5.	**YLALLVKYV**DGD	DRB1*0101, DRB1*0421, DRB1*0426, DRB1*0801, DRB1*0802, DRB1*0806, DRB1*1101, DRB1*1114, DRB1*1120, DRB1*1128, DRB1*1302, DRB1*1304, DRB1*1305, DRB1*1307, DRB1*1321, DRB1*1506.	10.20 – 39.08
6.	P**YHFDLSGHA**FG	DRB1*0305, DRB1*0309, DRB1*0401, DRB1*0421, DRB1*0426, DRB1*1107.	17.05 – 42.86
7.	IDAA**FKIAATAA**	DRB1*0101, DRB1*0102, DRB1*0301, DRB1*0305, DRB1*0306, DRB1*0307, DRB1*0308, DRB1*0309, DRB1*0311, DRB1*0401, DRB1*0402, DRB1*0404, DRB1*0405, DRB1*0408, DRB1*0410, DRB1*0421, DRB1*0423, DRB1*0426, DRB1*0701, DRB1*0703, DRB1*0801, DRB1*0802, DRB1*0804, DRB1*0813, DRB1*0817, DRB1*1101, DRB1*1102, DRB1*1104, DRB1*1106, DRB1*1107, DRB1*1114, DRB1*1120, DRB1*1121, DRB1*1128, DRB1*1301, DRB1*1302, DRB1*1305, DRB1*1307, DRB1*1311, DRB1*1321, DRB1*1322, DRB1*1323, DRB1*1327, DRB1*1328, DRB1*1502, DRB5*0101, DRB5*1105	23.06 – 56.67
8.	IPSLEAAVKQAY	–	–
9.	ITAMSQAQKAAK	–	–
10.	**YKLAYKTAE**GAT	DRB1*0309, DRB1*0801, DRB1*0813, DRB1*0817, DRB1*1120, DRB1*1302, DRB1*1304, DRB1*1321	9.52 – 38.20
11.	QKM**IEKINVGFK**	DRB1*1107, DRB5*0101, DRB5*0105	17.58 – 24.49

12.	ITAEYGDKWLDA	–	–
13.	S**YKFIPALEA**AV	DRB1*0101, DRB1*0102, DRB1*0305, DRB1*0306, DRB1*0307, DRB1*0308, DRB1*0309, DRB1*0311, DRB1*0401, DRB1*0402, DRB1*0404, DRB1*0405, DRB1*0408, DRB1*0421, DRB1*0423, DRB1*0426, DRB1*0701, DRB1*0703, DRB1*0801, DRB1*0802, DRB1*0813, DRB1*0817, DRB1*1101, DRB1*1104, DRB1*1106, DRB1*1114, DRB1*1128, DRB1*1305, DRB1*1307, DRB1*1311, DRB1*1321, DRB1*1323, DRB1*1501, DRB1*1502, DRB1*1506, DRB5*0101, DRB5*1105.	10.47 – 51.81
14.	KVTVA**FNQFGPN**	DRB1*0101, DRB1*0102, DRB1*0401, DRB1*0402, DRB1*0405, DRB1*0408, DRB1*0421, DRB1*0426, DRB1*0813, DRB1*1114, DRB1*1120, DRB1*1302, DRB1*1323, DRB1*1502.	8.43 – 37.76
15.	RAE**VSYVHVNGA**	DRB1*0306, DRB1*0307, DRB1*0308, DRB1*0311, DRB1*0404, DRB1*0408, DRB1*0410, DRB1*0423.	8.75 – 29.55
16.	DVIPEGWKADTS	–	–

We found 16 often repeated sequences within the investigated T- and B-cell epitopes. These sequences were analyzed for binding to human MHC class-II molecules using the ProPred prediction server developed by Singh & Raghava (2001). Eleven of the selected sequences contained MHC class-II binding regions (Table 1, labeled in bold) and five among them were predicted to bind a number of HLA-DR molecules (>15) with different binding capacity ranged between 8.43 % and 67.24 % (Table 1). It has been shown that HLA-DR type of the MHC class-II alleles is almost exclusively associated with different pollen allergens and plant-derived food allergens (Huang & Marsh, 1993) although association of grass pollen allergy with HLA-DQ alleles was also observed (Boehncke et al., 1998).

Alignment of the first sequence containing an MHC class-II binding motif (SNE**IKIVATPDG**) with the available protein sequences in the public databases revealed that this is a part from the sequence of the major pollen allergen Bet-v1 isolated from different species of the genus *Betula*

(*B. pendula, B. platyphylla var. japonica, B. lenta, B. nigra, B. platyphylla, B. costata, B. schmidtii, B. chichibuensis, B. populifolia* etc.). Bet-v1 protein family is well characterized and it includes many isoforms, which are tyical IgE epitopes.

Similar analysis of the next sequence (**LRAVESYLLAHS**), which is characterized with highest MHC class-II binding affinity, showed that this is a part from the structure of the pollen allergens with high IgE-binding properties Bet-v1, Car-b1 and Cor-a1 isolated from *Betula pendula, Carpinus betulus* and *Corylus avellana*, respectively, as well as from the structure of the beta-lactamase-like protein (85 % identity) in *Oscillatoria sp*. PCC 9029 (Cyanobacteria).

Next seven sequences with MHC class-II binding motifs (V**FEAALTKAI**TA, **YLALLVKYV**DGD, P**YHFDLSGHA**FG, IDAA**F-KIAATAA, YKLAYKTAE**GAT, QKM**IEKINVGFK, SYKFIPALEA**AV) are associated with pollen allergens isolated mainly from cereal plants (Poaceae) and they are presented in the structure of many well defined IgE-binding epitopes (Lol-p5a, Fes-p1, Fes-p5, Phl-p1, Phl-p5, Sec-c5, Zea-m1, Ory-s1, Cyn-d1, Dac-g1, Hol-l5b). In addition, most of these sequences had 70–100 % similarity with proteins in different bacteria and molds. For example, the pollen epitopes V**FEAALTKAI**TA, **YKLAYKTAE**GAT and QKM**IEKINVGFK** have high percent of identity with sequences of other proteins found in pathogens as *Mycobacterium*, *Toxoplasma*, *Leishmania*, *Lachnospiraceae* (Figure 1), *Burkholderia*, *Aspergillus*, *Mycoplasma* (Figure 2) or *Fusobacterium*, *Paracoccidioides*, *Helicobacter*, *Entamoeba*, *Bacteroides* (Figure 3), which cause different diseases in humans. Data suggest that previous infections with some of these pathogens could be responsible for the initial priming of the T-cells and production of antibodies cross-reacting later on with similar protein sequences typical for the pollen allergens.

The last two sequences (KVTVA**FNQFGPN** and RAE**VSYVHVNGA**) are part from pollen allergens (Cry, Cup, Jun) isolated from representatives of Cupressaceae (*Cupressus sempervirens, Juniperus oxycedrus, Cryptomeria japonica, Taxodium distichum, Hesperocyparis arizonica*). These sequences are also part from proteins of pathogenic organisms as *Burkholderia, Mycobacterium* and *Leishmania*.

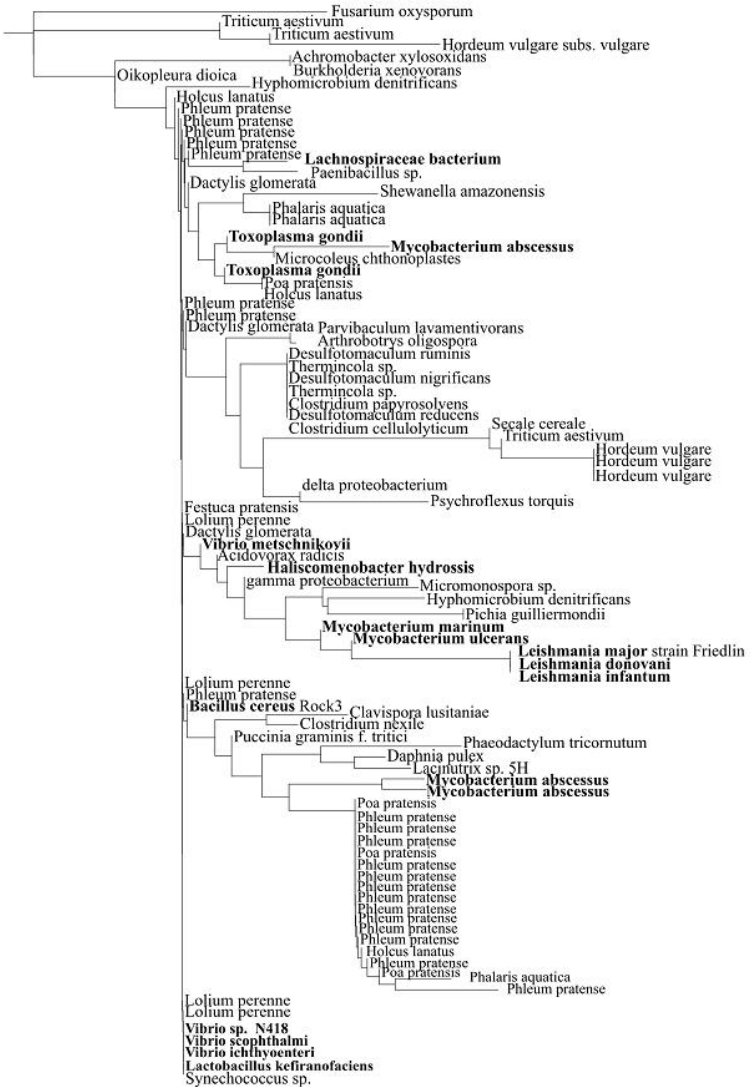

Figure 1. *Neighbor-joining tree generated from sequence alignment of the epitope V**FEAALTKAI**TA and other proteins with significant sequence similarities. Branch lenghts are proportional to sequence divergence.*

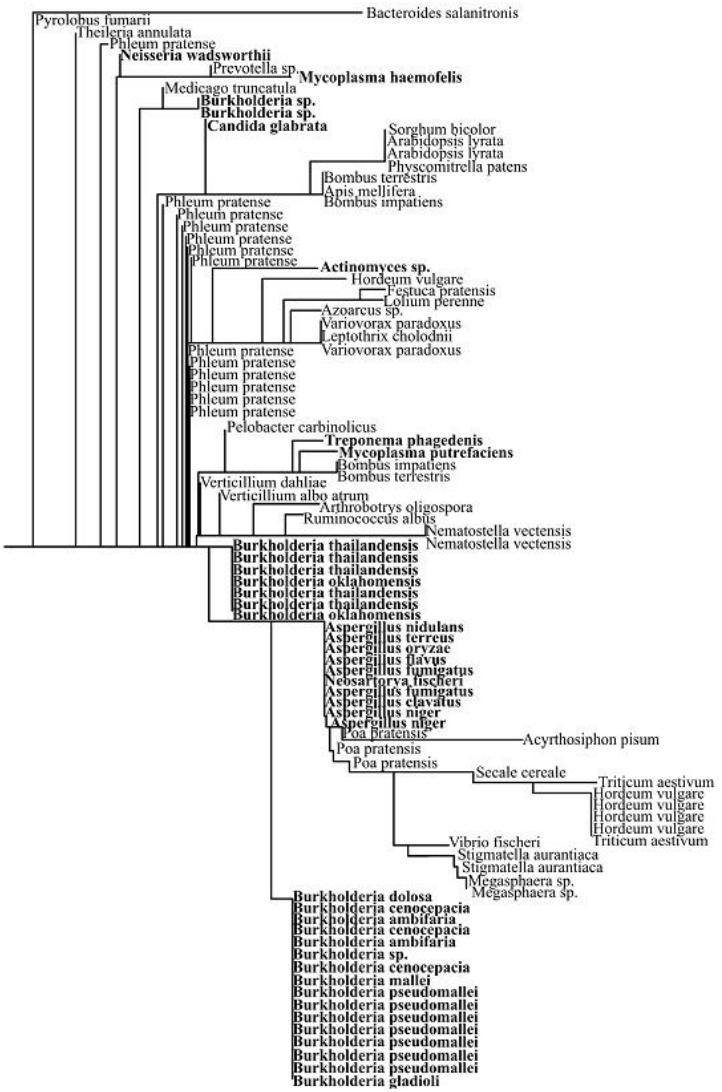

Figure 2. *Neighbor-joining tree generated from sequence alignment of the epitope **YKLAYKTAE**GAT and other proteins with significant sequence similarities. Branch lenghts are proportional to sequence divergence.*

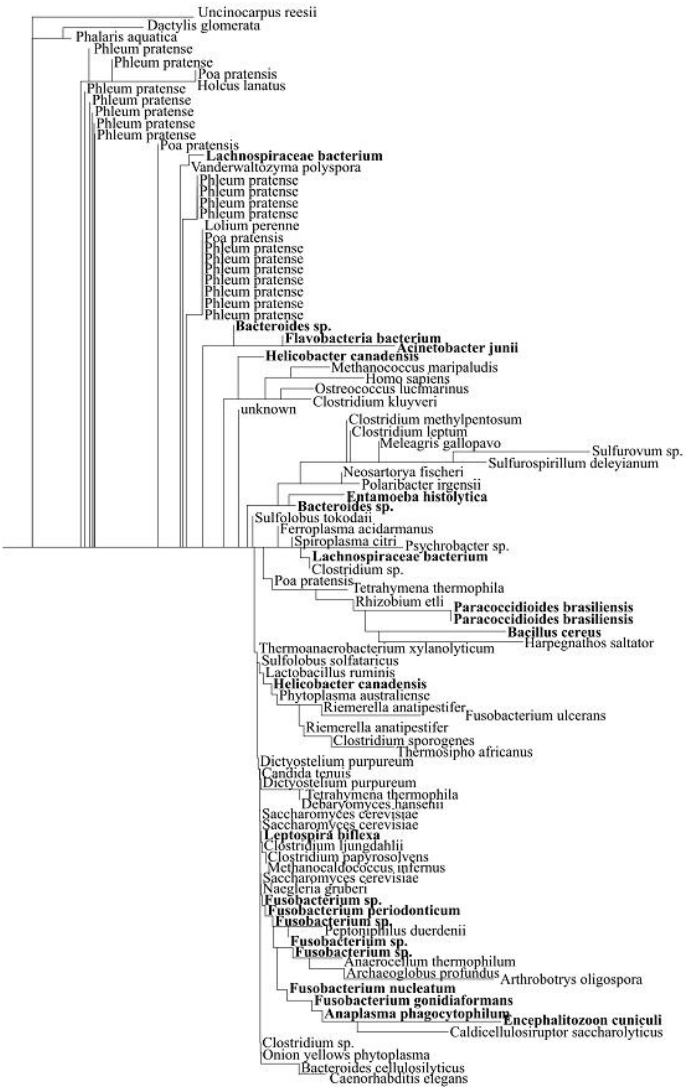

Figure 3. *Neighbor-joining tree generated from sequence alignment of the epitope QKM**IEKINVGFK** and other proteins with significant sequence similarities. Branch lenghts are proportional to sequence divergence.*

The immunotherapy of pollen allergy involves administration of allergen extracts to increase the patient's tolerance to those allergens that cause allergic symptoms. Several mechanisms have been proposed to explain the beneficial effects of the immunotherapy: reduction in specific IgE levels, induction of IgG (blocking) antibodies, reduced recruitment of effector cells, altered T cell cytokine balance (shift from T_H2 to T_H1), T cell anergy, induction of regulatory T cells (Frew, 2010). The best strategy for immunotherapy is to avoid allergen extracts or peptides containing B-cell epitopes and to use immunodominant T-cell that lead to induction of T cell anergy.

Thus, the development of immunomodulatory therapies might allow more general approaches to be developed, which would be particularly advantageous for those patients who are sensitized to multiple allergens. Among the most promising innovations is the development of modified pollen extracts that appear to reduce the allergic reactions. By knowing how this process works, we will be able to find better ways to prevent sensitization to allergens or to prevent allergic symptoms.

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ПОЛЕНОВИ АЛЕРГЕНИ И БИОИНФОРМАТИЧЕН АНАЛИЗ НА ИМУННИТЕ ЕПИТОПИ СВЪРЗАНИ С ПОЛЕНОВИ АЛЕРГИИ

Джемал Мотен, Пламен Стоянов, Иванка Тенева, Балик Джамбазов*

ПУ „Паисий Хилендарски“, Биологически факултет, ул. „Цар Асен“ № 24, 4000 Пловдив

****Автор за кореспонденция. E-mail: balik@uni-plovdiv.bg***

РЕЗЮМЕ

Поленовата алергия е една от най-често срещаните алергии в световен мащаб и се свързва с кpос-реактивността на IgE. Този тип алергия може да причини развитие на свръхчувствителност и към растителни храни предизвиквайки първична сенсибилизация на чувствителни индивиди, което от своя страна да доведе до крос-реактивност и вторична алергия към храни от растителен произход. Целта на настоящето изследване е да се сравнят известните до момента Т- и В-клетъчни поленови епитопи и да се анализира тяхната крос-реактивност. Чрез използването на биоинформатични методи са идентифицирани най-често срещаните амино-киселинни секвенции на поленовите епитопи. Селектирани са 16 често повтарящи се амино-киселинни секвенции в изследваните Т-и В-клетъчни епитопи, като 11 от тях съдържат MHC клас II свързващи участъци. Някои от амино-киселинните секвенции имат висок процент на идентичност с амино-киселинни секвенции на други протеини, изолирани от патогенни организми, което предполага, че предишни инфекции с подобни патогени, биха могли да инициират първоначалното сенсибилизиране на Т-клетките и производство на антитела с крос-реактивност към поленови алергени.

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