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(71) **Applicant** *(for all designated States except US)*: **CIRCASSIA LIMITED** [GB/GB]; The Oxford Science Park, Oxford OX4 4GA (GB).

(72) **Inventors; and**
(75) **Inventors/Applicants** *(for US only)*: **HAFNER, Rod** [GB/GB]; Circassia Limited, The Oxford Science Park, Oxford OX4 4GA (GB). **LAIDLER, Paul** [GB/GB]; Circassia Limited, The Oxford Science Park, Oxford OX4 4GA (GB). **LAYTON, Guy** [GB/GB]; Circassia Limited, The Oxford Science Park, Oxford OX4 4GA (GB). **LARCHE, Mark** [CA/CA]; Department of Medicine, HSC 4H20, McMaster University, 1200 Main Street West, Hamilton, Ontario L8N 3Z5 (CA).

(74) **Agent**: **WOODS, Geoffrey, Corlett**; J.A. Kemp & Co., 14 South Square, Gray's Inn, London WC1R 5JJ (GB).

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(54) **Title**: PEPTIDES FOR VACCINE

(57) **Abstract**: The present invention relates to compositions comprising peptides for preventing or treating allergy to house dust mites, and in particular to optimal combinations of peptides for preventing or treating said allergy.

WO 2010/089554 A1

GRASS PEPTIDES FOR VACCINE

Incorporating by Reference

The contents of the following priority applications are incorporated herein by reference: United Kingdom Patent Application No. 0901928.2 filed 5 February 2009, United Kingdom Patent Application No. 0901927.4 filed 5 February 2009, United Kingdom Patent Application No. 0912578.2 filed 20 July 2009, International Patent Application No. PCT/GB09/01995 filed 14 August 2009 and United Kingdom Patent Application No. 0917871.6 filed 12 October 2009,

Field of the Invention

The present invention relates to compositions for preventing or treating allergy to grass.

Background of the Invention

T-cell antigen recognition requires antigen presenting cells (APCs) to present antigen fragments (peptides) on their cell surface in association with molecules of the major histocompatibility complex (MHC). T cells use their antigen specific T-cell receptors (TCRs) to recognise the antigen fragments presented by the APC. Such recognition acts as a trigger to the immune system to generate a range of responses to eradicate the antigen which has been recognised.

Recognition of external antigens by the immune system of an organism, such as man, can in some cases result in diseases, known as atopic conditions. Examples of the latter are the allergic diseases including asthma, atopic dermatitis and allergic rhinitis. In this group of diseases, B lymphocytes generate antibodies of the IgE class (in humans) which bind externally derived antigens, which are referred to in this context as allergens since these molecules elicit an allergic response. Production of allergen-specific IgE is dependent upon T lymphocytes which are also activated by (are specific for) the allergen. Allergen-specific IgE antibodies bind to the surface of cells such as basophils and mast cells by virtue of the expression by these cells of surface receptors for IgE.

Crosslinking of surface bound IgE molecules by allergen results in degranulation of these effector cells causing release of inflammatory mediators such as histamine, 5-hydroxtryptamine and lipid mediators such as the sulphidoleukotrienes. In addition to IgE-dependent events, certain allergic diseases such as asthma are characterised by IgE-independent events.

Allergic IgE-mediated diseases are currently treated with agents which provide symptomatic relief or prevention. Examples of such agents are anti-histamines, β2 agonists, and glucocorticosteroids. In addition, some IgE-mediated diseases are treated by desensitisation procedures that involve the periodic injection of allergen components or extracts. Desensitisation treatments may induce an IgG response that competes with IgE for allergen, or they may induce specific suppressor T cells that block the synthesis of IgE directed against allergen. This form of treatment is not always effective and poses the risk of provoking serious side effects, particularly general anaphylactic shock. This can be fatal unless recognised immediately and treated with adrenaline. A therapeutic treatment that would decrease or eliminate the unwanted allergic-immune response to a particular allergen, without altering the immune reactivity to other foreign antigens or triggering an allergic response itself would be of great benefit to allergic individuals.

Grass allergens are universally recognised as a major cause of allergic diseases in humans and animals, including asthma, allergic rhinitis and allergic dermatitis. Proteins present in grass pollen are particularly important. For example, approximately 90% of hayfever sufferers are allergic to grass pollen. Hayfever is the common term for a form of seasonal allergy characterised by sneezing, runny nose and itching eyes. The term “hayfever” arose because this form of allergic disease is most prevalent during “haying season”, which corresponds to the flowering season of many grasses, when grass plants release the highest quantities of pollen. It is particularly prevalent in summer, typically from the end of May to the end of August (in the Northern Hemisphere).

It has been calculated that for adults in the United States, hayfever is the 5th leading chronic disease and a major cause of work absenteeism, resulting in nearly 4 million missed or lost workdays each year, resulting in a total cost of more than $700 million in total lost productivity. Allergies are also the most frequently reported chronic condition in children, limiting activities for more than 40% of them. Each year, allergies account for more than 17 million outpatient office visits in the United States; seasonal allergies such as hayfever account for more than half of these allergy visits.

A therapeutic or preventative treatment would therefore be of great benefit to humans that suffer or are at risk of suffering from grass allergy.

Summary of the Invention

Grass pollen allergens are typically classified into groups, with most species expressing at least one pollen allergen in each group. Examples of groups include:

- the Group 1 grass pollen allergens, which include, for example, the proteins Lol p 1 from Rye grass (*Lolium perenne*) and Phl p 1 from Timothy grass (*Phleum pratense*); and
- the Group 5 grass pollen allergens, which include, for example, the proteins Lol p 5a and Lol p 5b from Rye, Phl p 5 from Timothy, and Cyn d 5 from Bermuda grass (*Cynodon dactylon*).

The present inventors have discovered that certain peptide fragments derived from the major allergens in the pollens of grass species are particularly useful in desensitising individuals to these allergens. The polypeptide combinations of the invention have been selected for their ability to bind to many MHC Class II molecules, and cause T cell proliferation with minimal histamine release. The compositions, products, vectors and formulations of the invention may therefore be provided to individuals for preventing or treating allergy to grass by tolerisation.

The peptides of the invention were selected as MHC class II-binding T cell epitopes through use of *in silico* analysis to predict peptide-MHC interactions and MHC class II binding assays. Additional epitopes were identified by homology. Peptides and peptide combinations of the invention were further selected on the basis of *in vitro* T cell response assays.

The peptide combinations of the invention, however, provide a broad coverage of efficacy over the human population by targeting multiple different MHC molecules. A vaccine formulated with peptides of the invention would therefore have broad utility.

The inventors' work has produced peptide combinations with the following characteristics:

- the combination binds to many different MHC Class II molecules
- the combination gives significant stimulation of cytokine release in grass

allergic individuals

- the peptides of the combinations do not give significant histamine release.

The peptide combinations are selected from an extensive analysis of grass epitope sequences to identify core peptides having particularly good MHC binding properties and cytokine response profiles in grass allergic individuals. The combinations may comprise a core of three such peptides, one of each being selected from the most prevalent grasses, Timothy, Perennial Rye and Bermuda. The combinations may comprise a core of four such peptides, each of these peptides being selected from peptides shown to be particularly effective in combination with each other.

Providing a core group of peptides in this manner, including a core group of polypeptides representing the three most prevalent grasses, preferably a core group of four or more different individual polypeptides in the same composition provides a variety of MHC-binding epitopes, and so builds in redundancy to allow for the polymorphic nature of the MHC. Providing a core group of the invention, preferably four or more different individual polypeptides having particularly good MHC binding properties and cytokine response profiles also provides multiple T cell epitopes, allowing recruitment of a broad range of T cell specificities for induction of tolerance. Thus, a composition of the invention has beneficial additive effects over use of single polypeptides. The Inventors have also shown that compositions of the invention were able to provide extremely high coverage of a polymorphic study population as measured by cytokine responses.

Accordingly, the present invention provides a composition suitable for use in preventing or treating allergy to grass pollen by tolerisation comprising:

(a) at least one of the polypeptides Tim07B (KIPAGELQIIDKIDA), Tim 10B (KYTVFETALKKAITAMSE), Tim 04A (WGAIWRIDTPDKL), Tim 07G (FKVAATAANAAPANDK) or a variant of any thereof;

(b) at least one of the polypeptides Ber01 (SGKAFGAMAKKGQED), Ber02 (FIPMKSSWGA), Ber02C (KSSWGAIWRIDPKKPLK) and Ber 02B KDSDEFIPMKSSWGAIWR or a variant of any thereof; and

(c) at least one of the polypeptides Bio04A (LKKAVTAMSEAEK), Rye09B (PEVKYAVFEAALTKAIT), Bio02A (KYDAYVATLTEALR), Bio03A (KFIPTLVAAVKQAYAAKQ), Rye 08A (ETYKFIPSLEAAVKQAY), Rye 05C (NAGFKAAVAAAANAPPK), or a variant of any thereof,

wherein said variant is:

I) a longer polypeptide of up to 30 amino acids in length which comprises the sequence of the corresponding polypeptide specified in (a), (b) or (c), or

II) a polypeptide of 9 to 30 amino acids in length which comprises a sequence that has at least 65% homology to the sequence of the corresponding polypeptide specified in (a), (b) or (c), which sequence is capable of tolerising to said corresponding polypeptide; or

III) a polypeptide of length 9 to 30 amino acids which comprises a sequence of at least 9 contiguous amino acids of the sequence of the corresponding polypeptide specified in (a), (b) or (c), or a sequence that has at least 65% homology to said at least 9 contiguous amino acids, which sequence of at least 9 contiguous amino acids or homologous sequence is capable of tolerising to said corresponding polypeptide.

The invention further provides a composition suitable for use in preventing or treating allergy to grass pollen by tolerisation comprising at least four different polypeptides selected from :

(a) Tim07B (KIPAGELQIIDKIDA) or a variant thereof;
(b) Ber01 (SGKAFGAMAKKGQED) or a variant thereof;
(c) Bio04A (LKKAVTAMSEAEK) or a variant thereof;
(d) Rye09B (PEVKYAVFEAALTKAIT) or a variant thereof;
(e) Ber02 (FIPMKSSWGA) or a variant thereof;
(f) Ber02C (KSSWGAIWRIDPKKPLK) or a variant thereof;
(g) Bio03A (KFIPTLVAAVKQAYAAKQ) or a variant thereof; and
(h) Bio02A (KYDAYVATLTEALR) or a variant thereof;

wherein said variant is:

I) a longer polypeptide of up to 30 amino acids in length which comprises the sequence of the corresponding polypeptide specified in (a) to (h), or

II) a polypeptide 9 to 30 amino acids in length which comprises a sequence that has at least 65% homology to the sequence of the corresponding polypeptide specified in (a) to (h), which sequence is capable of tolerising to said corresponding polypeptide; or

III) a polypeptide of length 9 to 30 amino acids which comprises a sequence of at least 9 contiguous amino acids of the sequence of the corresponding polypeptide specified in (a) to (h), or a sequence that has at least 65% homology to said at least 9 contiguous amino acids, which sequence of at least 9 contiguous amino acids or homologous sequence is capable of tolerising to said corresponding polypeptide.

The compositions of the invention are typically capable of tolerising at least 50% or at least 60% of a panel of grass pollen allergic individuals in the population and/or comprises at least one further polypeptide up to a total of fourteen polypeptides, wherein the further polypeptides:(a) comprise a sequence having at least 65% sequence identity to at least 9 or more contiguous amino acids in any of SEQ ID NO: 1 to 73 described below; and (b) are 9 to 30 amino acids in length.

Description of the sequences mentioned herein

SEQ ID NOS: 1 to 73 provide the polypeptide sequences of the invention as set out in Tables 2 to 4. SEQ ID NOS: 1 to 27 correspond to peptides derived from Group 1 grass allergens. SEQ ID NOS: 28 to 73 correspond to peptides derived from Group 5 allergens.

Detailed description of the invention

The invention concerns peptides which can be used in tolerisation. Such peptides may be derived from any grass allergen described herein or be variants thereof as described below. A difficulty associated with approaches to desensitisation based on peptide immunisation lies in how to select an appropriate size and region of the allergen as the basis for the peptide to be used for immunisation. The size of the peptide of choice is crucial. If the peptide is too small, the vaccine would not be effective in inducing an immunological response. If the peptides are too large, or if the whole antigen is introduced into an individual, there is the risk of inducing adverse reactions, such as anaphylaxis, which may be fatal.

The polypeptides of the invention have been selected to retain T cell specificity whilst being small enough in size to not possess significant tertiary structure that would enable them to retain the conformation of an IgE-binding epitope of the whole molecule. The polypeptides of the invention therefore do not induce significant crosslinking of adjacent specific IgE molecules on cells such as mast cells and basophils and consequently do not cause significant histamine release.

An advantage of the invention is the ability of the peptides to broadly target Major Histocompatibility Complex (MHC) molecules. T cell receptors (TCRs) are highly variable in their specificity. Variability is generated, as with antibody molecules, through gene recombination events within the cell. TCRs recognise antigen in the form of short peptides bound to molecules encoded by the genes of the Major Histocompatibility Complex (MHC). These gene products are the same molecules that give rise to "tissue types" used in transplantation and are also referred to as Human Leukocyte Antigen molecules (HLAs) which terms may be used interchangeably. Individual MHC molecules possess peptide binding grooves which, due to their shape and charge are only capable of binding a limited group of peptides. The peptides bound by one MHC molecule may not necessarily be bound by other MHC molecules.

When a protein molecule such as an antigen or allergen is taken up by antigen presenting cells such as B lymphocytes, dendritic cells, monocytes and macrophages, the molecule is enzymatically degraded within the cell. The process of degradation gives rise to peptide fragments of the molecule which, if they are of the appropriate size, charge and shape, may then bind within the peptide binding groove of certain MHC molecules and be subsequently displayed upon the surface of antigen presenting cells. If the peptide/MHC complexes are present upon the antigen presenting cell surface in sufficient numbers they may then activate T cells which bear the appropriate peptide/MHC-specific T cell receptors.

Due to the polymorphic nature of the MHC, individuals in an outbred population such as man will express different combinations of MHC molecules on their cell surfaces. Since different MHC molecules can bind different peptides from the same molecule based on the size, charge and shape of the peptide, different individuals will display a different repertoire of peptides bound to their MHC molecules. Identification of universal MHC-binding peptide epitopes in an outbred population such as man is more difficult than in inbred animals (such as certain strains of laboratory mice). On the basis of differential MHC expression between individuals and the inherent differences in peptide binding and presentation which this brings, it is unlikely that a single peptide can be identified which will be of use for desensitisation therapy in man.

As discussed below, the invention addresses this problem by providing compositions based on more than one peptide i.e. peptide combinations. These combinations are based on core groups of peptides identified experimentally as showing surprisingly strong responses in grass allergic patients when tested individually, and particularly when provided in combination. These core subsets of peptides have advantageous properties when included in grass peptide vaccines.

The core groups may comprise at least one peptide derived from Timothy grass, at least one peptide derived from Perennial Rye and at least one peptide derived from Bermuda grass, each peptide showing particularly good individual response characteristics. The inclusion of such peptides in combination allows for coverage of the three most prevalent grasses, and additionally extends to coverage of other grasses by homology, as discussed further below.

Additionally a core group may comprise at least four peptides selected from peptides having the most highly ranked individual response characteristics from the group tested, and further shown to provide optimal response characteristics for a grass vaccine when provided together combination.

Such peptide combinations preferably comprise at least one peptide derived from a Group I grass allergen or a variant thereof and at least one peptide derived from a Group V grass allergen or a variant thereof. The classification of grass allergens as Group I and Group V grass allergens is well known to the skilled person, and is further discussed herein. A preferred Group I grass allergen is the Bermuda Grass allergen, Cyn d 1. A preferred Group V grass allergen is the Rye Grass allergen, Lol p 5. In some embodiments, the invention relates to a composition comprising at least one peptide derived from Cyn d1 or a variant thereof and at least one peptide derived from Lol p 5 or a variant thereof. Compositions based on combinations of Cyn d 1 and Lol p 5 peptides or variants thereof are further discussed below.

Preferred peptides of the invention may comprise, consist of, or consist essentially of the sequences shown in any of SEQ ID NOS: 1 to 73. Variants of these specific peptides may also be used. The variants may comprise, consist of, or consist essentially of sequences which are fragments of either any of SEQ ID NOS: 1 to 73 or homologues of any of SEQ ID NOS: 1 to 73.

The invention thus provides a composition suitable for use in preventing or treating allergy to grass pollen by tolerisation comprising:

(a) at least one of the polypeptides Tim07B (KIPAGELQIIDKIDA), , Tim 10B (KYTVFETALKKAITAMSE), Tim 04A (WGAIWRIDTPDKL), Tim 07G (FKVAATAANAAPANDK), or a variant of any thereof;

(b) at least one of the polypeptides Ber01 (SGKAFGAMAKKGQED), Ber02 (FIPMKSSWGA), Ber02C (KSSWGAIWRIDPKKPLK), and Ber 02B KDSDEFIPMKSSWGAIWR, or a variant of any thereof; and

(c) at least one of the polypeptides Bio04A (LKKAVTAMSEAEK), Rye09B (PEVKYAVFEAALTKAIT), Bio02A (KYDAYVATLTEALR), Bio03A (KFIPTLVAAVKQAYAAKQ), Rye 08A (ETYKFIPSLEAAVKQAY), Rye 05C (NAGFKAAVAAAANAPPK), or a variant of any thereof,

wherein said variant is:

I) a longer polypeptide of up to 30 amino acids in length which comprises the sequence of the corresponding polypeptide specified in (a), (b) or (c), or

II) a polypeptide of 9 to 30 amino acids in length which comprises a sequence that has at least 65% homology to the sequence of the corresponding polypeptide specified in (a), (b) or (c), which sequence is capable of tolerising to said corresponding polypeptide; or

III) a polypeptide of length 9 to 30 amino acids which comprises a sequence of at least 9 contiguous amino acids of the sequence of the corresponding polypeptide specified in (a), (b) or (c), or a sequence that has at least 65% homology to said at least 9 contiguous amino acids, which sequence of at least 9 contiguous amino acids or homologous sequence is capable of tolerising to said corresponding polypeptide.

Other preferred variants of a) to c) are:

i) polypeptides having a length of 9 to 30 amino acids and comprising a region consisting of:

- any of the corresponding sequences of a) to c), or
- a sequence which has at least 65% homology to any of the corresponding sequences of a) to c) which sequence is capable of tolerising an individual to any of the sequences of a) to c), or

ii) polypeptides having a length of 9 to 30 amino acids and comprising a region consisting of a sequence that represents either:

- a fragment of any of the sequences of a) to c), or
- a homologue of a fragment of any of the sequences of a) to c),

which sequence is capable of tolerising an individual to any of the sequences of a) to c) and has a length of at least 9 amino acids, and wherein said homologue has at least 65% homology to any 9 contiguous amino acids in any of the sequences of a) to c); wherein optionally none of the four polypeptides are variants of the same original sequence defined by any one of a) to c).

The composition thus comprises a minimum of three polypeptides, a first polypeptide being a polypeptide of a) or a variant thereof, a second polypeptide being a polypeptide of b) or a variant thereof, and a third polypeptide being a polypeptide of c) or a variant thereof. Thus, for instance the composition may comprise a variant of Tim07B, Ber01 and a variant of Rye09B. Preferably, the above composition comprises in addition to the core three polypeptides a fourth polypeptide of a), b), or c) or a variant of any thereof. The composition may comprise four, five, six, seven, eight or more polypeptides of a), b), c) or variants thereof.

In some aspects, the composition may comprise two, three, four or more polypeptides of a) or variants thereof. In additional aspects, the composition may comprise two, three, four or more polypeptides of b) or variants thereof. In further aspects the composition may comprise two, three, four, five, six or more polypeptides of c) or variants thereof. These selections are subject to the composition comprising at least one polypeptide of a) or a variant thereof, at least one polypeptide of b) or a variant thereof. A preferred combination of three polypeptides selected from groups a), b) and c) is the polypeptide Tim07B or a variant thereof, the polypeptide Ber01 or a variant thereof, and the polypeptide Bio04A or a variant thereof.

The composition may comprise at least two polypeptides selected from group a) or variants thereof, at least two polypeptides selected from group b) or variants thereof and at least two polypeptides selected from group c) or variants thereof.

A preferred composition may comprise the polypeptide Tim07B or a variant thereof and at least two, three or four polypeptides selected from group b) or variants thereof. This preferred composition may comprise two or three polypeptides selected from group c) or variants thereof, preferably including Bio04A or a variant thereof. Another preferred composition may comprise the polypeptide Tim07B or a variant thereof and at least two, three or four polypeptides selected from group c) or variants thereof. This preferred composition may comprise two or three polypeptides selected from group b) or variants thereof, preferably including Ber01 or a variant thereof.

All the above compositions based on a) to c) may comprise further polypeptides selected from any of SEQ ID NOs 1 to 74 or variants thereof not previously selected according to a) to c).

The invention also provides a composition suitable for use in preventing or treating allergy to grass pollen by tolerisation comprising at least four different polypeptides selected from :

(a) Tim07B (KIPAGELQIIDKIDA) or a variant thereof;
(b) Ber01 (SGKAFGAMAKKGQED) or a variant thereof;
(c) Bio04A (LKKAVTAMSEAEK) or a variant thereof;
(d) Rye09B (PEVKYAVFEAALTKAIT) or a variant thereof;
(e) Ber02 (FIPMKSSWGA) or a variant thereof;
(f) Ber02C (KSSWGAIWRIDPKKPLK) or a variant thereof;
(g) Bio03A (KFIPTLVAAVKQAYAAKQ) or a variant thereof; and
(h) Bio02A (KYDAYVATLTEALR) or a variant thereof;

wherein said variant is:

I) a longer polypeptide of up to 30 amino acids in length which comprises the sequence of the corresponding polypeptide specified in (a) to (h), or

II) a polypeptide 9 to 30 amino acids in length which comprises a sequence that has at least 65% homology to the sequence of the corresponding polypeptide specified in (a) to (h), which sequence is capable of tolerising to said corresponding polypeptide; or

III) a polypeptide of length 9 to 30 amino acids which comprises a sequence of at least 9 contiguous amino acids of the sequence of the corresponding polypeptide specified in (a) to (h), or a sequence that has at least 65% homology to said at least 9 contiguous amino acids, which sequence of at least 9 contiguous amino acids or homologous sequence is capable of tolerising to said corresponding polypeptide.

Other preferred variants of a) to h) are:

i) polypeptides having a length of 9 to 30 amino acids and comprising a region consisting of:

- any of the corresponding sequences of a) to h), or
- a sequence which has at least 65% homology to any of the corresponding sequences of a) to h) which sequence is capable of tolerising an individual to any of the sequences of a) to h), or

ii) polypeptides having a length of 9 to 30 amino acids and comprising a region consisting of a sequence that represents either:

- a fragment of any of the sequences of a) to h), or
- a homologue of a fragment of any of the sequences of a) to h),

which sequence is capable of tolerising an individual to any of the sequences of a) to h) and has a length of at least 9 amino acids, and wherein said homologue has at least 65% homology to any 9 contiguous amino acids in any of the sequences of a) to h); wherein optionally none of the four polypeptides are variants of the same original sequence defined by any one of a) to h).

The composition thus comprises a minimum of four polypeptides, each of said four polypeptides being selected from polypeptides of a) to h) or variants thereof. The above composition may comprise additional polypeptides of a) to h) or a variant of any thereof, such as five, six, seven, eight or more polypeptides of a) to h) or variants thereof.

In some aspects, the composition may comprise a polypeptide of a) or a variant thereof, at least one polypeptide selected from b), e) or f) or a variant of any thereof, and at least one polypeptide selected from c), d), g) or h) or a variant thereof.

Alternatively, the composition may preferably comprise a polypeptide of a) or a variant thereof and at least two or three polypeptides selected from b), e) or f) or a variant of any thereof. This composition may preferably include the polypeptide Ber01 or a variant thereof. In another embodiment, the composition may comprise a polypeptide of a) or a variant thereof and at least two, three or four polypeptides selected from c), d), g) or h) or a variant of any thereof. This composition may preferably include the polypeptide Bio04A or a variant thereof.

All such compositions may preferably comprise the polypeptide Tim07B or a variant thereof, the polypeptide Ber01 or a variant thereof, and the polypeptide Bio04A or a variant thereof.

The above compositions selected from a) to h) preferably comprise at least four different polypeptides of a) to h) or comprise at least four variants each corresponding to different original or baseline sequences of a) to h). Thus, the compositions are typically selected on the basis of four different epitope sequences of origin. Preferably, the composition comprises at least one epitope sequence of Bermuda origin, at least one epitope sequence of Rye Grass origin and at least one epitope sequence of Timothy origin. The relevant epitope sequences may be selected from any of SEQ ID NOs 1 to 74 or variants thereof.

All of the above compositions based on a) to h) may thus comprise further polypeptides selected from any of SEQ ID NOs 1 to 74 or variants thereof not previously selected according to a) to h). All selections are subject to the composition comprising at least four polypeptides selected from a) to h) or variants thereof.

Optionally, any composition of specific polypeptides described herein may comprise further polypeptides up to a total of fourteen unique polypeptides. The further polypeptides will typically relate to (i.e. are typically homologues and/or fragments of) the other sequences, i.e. SEQ ID NOS: 1 to 73, that are not amongst the polypeptides already selected. The further peptides are typically functional variants of one of the peptides of SEQ ID NOS: 1 to 73. The further polypeptides may be identical to any of SEQ ID NOS: 1 to 73. The composition may therefore comprise up to fourteen different polypeptides as provided in any of SEQ ID NOS: 1 to 73, subject to at least one polypeptide being selected from each of (a) and (b) as defined above. However, the optional further polypeptides do not need to be 100%

identical to any of SEQ ID NOS: 1 to 73. They are preferably at least 65% identical to at least 9 (for example at least 10, 11, 12 or 13) or more contiguous amino acids in any of SEQ ID NOS: 1 to 73, not already selected amongst the at least one polypeptide selected from each of (a) and (b). These contiguous amino acids may comprise a MHC class II epitope, for example which binds to any of the MHC molecules mentioned herein.

The invention also provides products and formulations comprising the polypeptides of the invention and compositions, products and vectors comprising polynucleotides capable of expressing the polypeptides of the invention for use in preventing or treating grass allergy by tolerisation. Such tolerisation will typically be to an epitope (for example a MHC class II-binding T cell epitope) present in any of SEQ ID NOS: 1 to 74.

Grass species

The grass species Rye (*Lolium perenne*), Timothy (*Phleum pratense*) and Bermuda (*Cynodon dactylon*) are responsible for a high proportion of grass allergy worldwide, particularly allergies associated with grass pollen, such as hayfever. Other important grass species include Velvet grass (*Holcus lanatus)*, Orchard grass (*Dactylis glomerata*), Canary grass (*Phalaris canariensis*) and Meadow grass / Kentucky bluegrass (*Poa pratensis*).

Rye is one of the most common grasses in the world, and is widely used as a source of animal fodder. It is native to Europe, but has been introduced on all continents worldwide and is common in all temperate zones. It can flower throughout the summer, but typically between May and July in the northern hemisphere. Rye is well adapted to mild, humid temperate climates, and grows best on rather heavy, rich, moist soils. It also grows well on well-manured lighter soils with sufficient moisture. It dislikes shade and requires a well-drained soil. Rye typically grows in locations with a soil pH in the range of about 6 to about 7, though it can tolerate a range from about 4.5 to about 8.5, preferably with an annual precipitation in the range of about 21 to about 180cm.

Timothy is another of the most common grasses in the world and is a primary source of animal fodder. It is native and widespread in most of Europe, North Africa and northern Asia. It has been introduced and is widespread in North and South America, South Africa and Australia. Timothy grass typically grows in locations with an annual precipitation in the range of about 35 to about 180cm, an annual temperature range of about 4 to about 22°C, and a soil pH of about 4.5 to about 8. It is best adapted to a cool, humid, temperate climate, growing best on heavy, deep and moist or even wet soils. The optimum temperature for growth is 18° - 21°C varying with day/night temperatures of 15°/10°C and 21°/15°C. The Timothy flowering season is typically confined to the early summer and Timothy pollen is a major cause of grass allergy during this season. In studies, up to 21% of patients with allergic rhinitis or other symptoms have been found to be responsive to Timothy pollen.

Bermuda grass typically grows in locations with an annual precipitation of about 9 to about 429cm, an annual temperature range of about 5 to about 28°C, and a soil pH in the range of about 4 to about 8.5, preferably about 6 to about 7. The Bermuda flowering season is typically in late summer (August to October in the northern hemisphere). Bermuda plants produce high quantities of pollen and are therefore a major cause of hayfever. Bermuda plants have also been reported to cause contact dermatitis. Bermuda is widely grown throughout the world, predominantly in warm climates, and is typically found between the latitudes of about 30° north and about 30° south.

Peptide fragments of Group 1 and Group 5 grass pollen allergens

The major allergens of grass include the Group 1 grass pollen allergens and Group 5 grass pollen allergens. Proteins from different species are assigned to groups based on amino acid sequence homology. For example, Group 1 major grass pollen allergens include the Timothy protein Phl p 1 and the Rye protein Lol p 1, and the Group 5 major grass pollen allergens include the Timothy protein Phl p 5 and the Rye protein Lol p 5.

The present inventors have identified the regions in certain grass pollen allergen proteins which comprise MHC Class II-binding T cell epitopes. The present inventors have also shown that regions corresponding to MHC Class II-binding T cell epitopes within the major grass pollen allergens are highly conserved between representatives in a given group, see for example, Example 2. Based on this information, peptides derived from the relevant regions of a protein in a given Group are suitable for preventing or treating grass allergy by tolerisation to the grass allergens in that Group. For example, the relevant regions from, for example, Phl p 1 of Timothy or Lol p 1 of Rye are suitable for use in preventing or treating grass allergy by tolerisation to the Group 1 grass allergens.

The peptides of the invention are derived from the Group 1 (SEQ ID NOS: 1 to 27) and Group 5 (SEQ ID NOS: 28 to 73) grass allergens. The terms "peptide" and "polypeptide" are used interchangeably herein. The above proteins are also referred to herein as "the allergens".

Tables 2 to 4 set out the sequences of the peptides of the invention, indicating the parent protein from which each peptide derives.

Where a composition of the invention comprises four or more polypeptides selected from polypeptides of a) to h) or variants thereof, the composition typically comprises at least one polypeptide or variant thereof (for example a functional variant) selected from each of a) SEQ ID NOS: 1 to 27; and b) SEQ ID NOs: 28 to 73. The composition may comprise at least two, at least three, at least four, at least five, at least six, or at least seven polypeptides or variants thereof (for example functional variants) selected from each of a) SEQ ID NOS: 1 to 27; and b) SEQ ID NOs: 28 to 73. In some embodiments, the composition may comprise at least one polypeptide or variant thereof (for example a functional variant) selected from each of a) SEQ ID NOS: 1 to 10; and b) SEQ ID NOS: 28 to 52. The composition may comprise at least two, at least three, at least four, at least five, at least six, or at least seven polypeptides or variants thereof (for example functional variants) selected from each of a) SEQ ID NOS: 1 to 10; and b) SEQ ID NOS: 28 to 52.

As outlined above, preferred compositions based on the polypeptides of a) to h) or variants thereof therefore include those which comprise at least one peptide derived from Cyn d 1 or a variant thereof and at least one peptide derived from Lol p5 or a variant thereof. Particularly preferred compositions are those which comprise at least one peptide derived from Cyn d 1 or a variant thereof, at least one peptide derived from Lol p5 or a variant thereof and at least one peptide derived from Phl p 5. In some embodiments, the compositions of a) to h) may comprise two, three, four or more peptides derived from Cyn d 1 or variants thereof and/or two, three, four or more peptides derived from Lol p 5 or variants thereof. In some embodiments, the compositions may consist or consist essentially of peptides derived from Cyn d 1 and Lol p 5 or variants thereof. In other embodiments, the composition optionally does not comprise a peptide derived from Lol p1 or a variant thereof.

As discussed below, compositions based on Cyn d 1 and Lol p 5 peptides are of particular utility in the treatment of grass allergy.

Particularly preferred compositions of the invention include those which comprise, consist or consist essentially of:

a) at least one of the polypeptides of SEQ ID NOs: 1, 2 and 5, or variants thereof as defined herein;

b) at least one of the polypeptides of SEQ ID NO:s 28, 29, 31 and 46, or variants thereof as defined herein; and optionally

c) the polypeptide of SEQ ID NO: 69 or a variant thereof as defined in herein.

These compositions provide a particularly preferred Cyn d 1 peptide, a particularly preferred Lol p5 peptide, and optionally a particularly preferred Phl p5 peptide. More preferably, the compositions comprise at least two or all three polypeptides as defined in a) and at least two or at least three polypeptides as defined in b). Still preferably the composition includes a polypeptide as defined in c). It is particularly preferred that the composition comprises i) SEQ ID NO: 1, ii) one of SEQ ID NO: 2 and SEQ ID NO: 5; and iii) SEQ ID NO: 46.

Specific preferred compositions include Combinations 1 to 10 as set out in Table 7. In such compositions, one or more of the individual polypeptides of SEQ ID NO:s 1, 2, 5, 28, 29, 31, 46 and 69 can optionally be substituted for a variant thereof. In some embodiments two, three, four, five or more of the polypeptides of SEQ ID NO:s 1, 2, 5, 28, 29, 31, 46 and 69 present in Combinations 1 to 10 can be substituted for variants thereof. The number of polypeptides substituted for variants thereof typically depends on the total number of polypeptides included in the composition. For example, in combinations based on four polypeptides (i.e. Combinations 6, 8, 10), it is preferred that only one or two polypeptides are substituted for variants thereof. Alternatively, any composition comprising four or more polypeptides selected from any of SEQ ID NOS: 1, 69, 31, 46, 2, 5, 29, 28, 43, 53, 35, 27, 4, and 70 or variants thereof is also preferred.

A even more preferred composition comprises, consists or consists essentially of the polypeptides of SEQ ID NO:s 1, 2, 5, 28, 31, 91 and 93 or variants thereof. Other preferred compositions comprise SEQ ID NO:s 1, 2, 5, 28, 31, 91 and 93 or in place of one, two or three, four or more of these polypeptides, variants thereof. In some embodiments, the above seven peptide compositions do not comprise any further polypeptides or do not comprise any further polypeptides derived from grass allergens. In preferred embodiments, the compositions comprise SEQ ID NO:s 1, 2, 5, 28, 31, 91 and 93 or variants thereof and do not contain any further proteins with more than 20% homology to a protein of any species of grass mentioned herein. The above compositions may comprise further non-peptide constituents such as carriers or adjuvants.

The invention also provides a product comprising,

(a) the polypeptide Tim07B (KIPAGELQIIDKIDA), Tim10B (KYTVFETALKKAITAMSE), Tim 04A (WGAIWRIDTPDKL), Tim 07G (FKVAATAANAAPANDK) or a variant of any thereof as described herein;

(b) at least one of the polypeptides Ber01 (SGKAFGAMAKKGQED) Ber02 (FIPMKSSWGA), Ber02C (KSSWGAIWRIDPKKPLK) and Ber02B KDSDEFIPMKSSWGAIWR or a variant of any thereof as described herein; and

(c) at least one of the polypeptides Bio04A (LKKAVTAMSEAEK), Rye09B (PEVKYAVFEAALTKAIT), and Bio02A (KYDAYVATLTEALR), Bio03A (KFIPTLVAAVKQAYAAKQ), Rye 08A (ETYKFIPSLEAAVKQAY), Rye 05C (NAGFKAAVAAAANAPPK) or a variant of any thereof as described herein, wherein each different polypeptide is for simultaneous, separate or sequential use in preventing or treating allergy to grass pollen by tolerisation.

The four or more polypeptides in the product of the invention may be selected according to the same criteria outlined above in relation to the composition for use in the prevention or treatment of grass allergy by tolerisation of the invention.

Variants

The composition or products of the invention may therefore comprise variants of any of SEQ ID NOS: 1 to 73. The variant typically comprises 1, 2, 3 or more of the MHC class II epitopes present in the corresponding peptide of SEQ ID

NOS: 1 to 73.

Functional variants are mentioned herein. Such a variant may be able to tolerise an individual to a class II MHC epitope present in the corresponding peptide of SEQ ID NOS: 1 to 59, and thus it will typically comprise sequence that binds to the same MHC class II molecule and/or is recognised by a T cell which recognises the corresponding epitope in the polypeptide of SEQ ID NOS: 1 to 73. The sequence is thus capable of tolerising against the corresponding sequence in the native polypeptide. The variant polypeptide may thus tolerise against the corresponding native polypeptide.

Variants of SEQ ID NOS: 1 to 73 may be fragments derived by truncation, e.g. by removal of one or more amino acids from the N and/or C-terminal ends of a polypeptide. Fragments may also be generated by one or more internal deletions, provided that the core 9 amino acids that makes up the T cell epitope is not substantially disrupted.

For example, a variant of SEQ ID NO: 1 may comprise a fragment of SEQ ID NO: 1, i.e. a shorter sequence. This may include a deletion of one, two, three or four amino acids from the N-terminal end of SEQ ID NO: 1 or from the C-terminal end of SEQ ID NO: 1. Such deletions may be made from both ends of SEQ ID NO: 1. A variant of SEQ ID NO: 1 may include additional amino acids (for example from the sequence of the parent protein from which the peptide derives) extending beyond the end(s) of SEQ ID NO: 1. A variant may include a combination of the deletions and additions discussed above. For example, amino acids may be deleted from one end of SEQ ID NO: 1, but additional amino acids from the full length parent protein sequence may be added at the other end of SEQ ID NO: 1. The same discussion of variants above also applies to SEQ ID NOS: 2 to 73.

A variant peptide may include one or more amino acid substitutions from the amino acid sequence of any of SEQ ID NOS: 1 to 73 or a fragment thereof. A variant peptide may comprise sequence having at least 65% sequence identity to at least 9 or more contiguous amino acids in any of SEQ ID NOS: 1 to 73. More preferably a suitable variant may comprise at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 98% amino acid identity to at least 9 contiguous amino acids of any of SEQ ID NOS: 1 to 73. This level of amino acid identity may be seen at any section of the peptide, although it is preferably the core region. The level of amino acid identity is over at least 9 contiguous amino acids but it may be at least 10, 11, 12, 13, 14, 15 or at least 16 or 17 amino acids, depending on the size of the peptides of comparison. Accordingly, any of the above-specified levels of identity may be across the entire length of sequence.

Examples of preferred variants selected on the basis of sequence identity to particularly preferred peptides of the invention are:

Variants of Ber01 (SEQ ID NO: 1): SGKAFGAMAKKGEED (SEQ ID NO:74), Holcus lanatus, Hol l 1; Poa pratensis Poa p 1; SGHAFGSMAKKGEED (SEQ ID NO: 75), Dactylis glomerata, Dac g 1; Lolium perenne Lol p 1; SGIAFGSMAKKGDED (SEQ ID NO: 76), Phleum pratense, Phl p 1, SGTAFGAMAKKGEEE (SEQ ID NO: 77), Zea mays, Zea m 1.

Variants of Bio02A (SEQ ID NO: 28): KYDAYVATLTESLR (SEQ ID NO: 78), Hordeum vulgare, Hor v 5; KYDAYVATLSEALR (SEQ ID NO: 79), Phleum pratense, Phl p 5; Poa pratensis, Poa p 9; KYDAFVAALTEALR (SEQ ID NO: 80), Dactylis glomerata, Dac g 5; KYDAFVTTLTEALR (SEQ ID NO: 81), Holcus lanatus, Hol l 5.

Variants of Bio03A (SEQ ID NO: 29): KFIPTLEAAVKQAYAA (SEQ ID NO: 82), Dactylis glomerata, Dac g 5; Phalarus aquatica, Pha a 5; KFIPALEAAVKQAYAA (SEQ ID NO: 83), Phleum pratense, Phl p 5.

Variants of Tim07B (SEQ ID NO: 69): KIPAGELQIVDKIDA (SEQ ID NO: 84), Dactylis glomerata, Dac g 5; Phalarus aquatica, Pha a 5; KIPTGELQIVDKIDA (SEQ ID NO: 85), Lolium perenne, Lol p 5; KIPAGEQQIIDKIDA (SEQ ID NO: 86), Poa pratensis, Poa p 5. Tim07B is also conserved in Holcus lanatus, Hol l5b.

Variants of Bio04A (SEQ ID NO: 31): LKKAITAMSEAQK (SEQ ID NO: 87), Phleum pratense, Phl p5; Holcus lanatus, Hol l 5b; LKKAITAMSQAQK (SEQ ID NO: 88), Poa pratensis, Poa p 5.

Variants of Ber02C (SEQ ID NO: 5): KESWGAIWRIDTPDK (SEQ ID NO: 89), Phalaris aquatica, Pha a 1; Phleum pratense, Phl p 1.

Variants of Rye09B (SEQ ID NO: 46): PQVKYAVFEAALTKAIT (SEQ ID NO: 90), Phleum pratense, Phl p 5.

Thus, SEQ ID NO:s 74 to 90 are preferred variants which may be used as substitutes for the above native peptides in a composition of the invention. Other referred variants for native peptides of the invention are derived from maize allergens. Maize allergens have close homology to grass pollen allergens and so sequences derived from maize may contain cross-reactive epitopes of use in tolerisation against grass pollen allergy.

In connection with amino acid sequences, "sequence identity" refers to sequences which have the stated value when assessed using ClustalW (Thompson et al., 1994, supra) with the following parameters:
Pairwise alignment parameters -Method: accurate, Matrix: PAM, Gap open penalty: 10.00, Gap extension penalty: 0.10; Multiple alignment parameters -Matrix: PAM, Gap open penalty: 10.00, % identity for delay: 30, Penalize end gaps: on, Gap separation distance: 0, Negative matrix: no, Gap extension penalty: 0.20, Residue-specific gap penalties: on, Hydrophilic gap penalties: on, Hydrophilic residues: GPSNDQEKR. Sequence identity at a particular residue is intended to include identical residues which have simply been derivatized.

A variant peptide may comprise 1, 2, 3, 4, 5 or more, or up to 10 amino acid substitutions from any of SEQ ID NOS: 1 to 73. Substitution variants preferably involve the replacement of one or more amino acids with the same number of amino acids and making conservative amino acid substitutions. For example, an amino acid may be substituted with an alternative amino acid having similar properties, for example, another basic amino acid, another acidic amino acid, another neutral amino acid, another charged amino acid, another hydrophilic amino acid, another hydrophobic amino acid, another polar amino acid, another aromatic amino acid or another aliphatic amino acid. Some properties of the 20 main amino acids which can be used to select suitable substituents are as follows:

Ala	aliphatic, hydrophobic, neutral	Met	hydrophobic, neutral
Cys	polar, hydrophobic, neutral	Asn	polar, hydrophilic, neutral
Asp	polar, hydrophilic, charged (-)	Pro	hydrophobic, neutral
Glu	polar, hydrophilic, charged (-)	Gln	polar, hydrophilic, neutral

Phe	aromatic, hydrophobic, neutral	Arg	polar, hydrophilic, charged (+)
Gly	aliphatic, neutral	Ser	polar, hydrophilic, neutral
His	aromatic, polar, hydrophilic, charged (+)	Thr	polar, hydrophilic, neutral
Ile	aliphatic, hydrophobic, neutral	Val	aliphatic, hydrophobic, neutral
Lys	polar, hydrophilic, charged(+)	Trp	aromatic, hydrophobic, neutral
Leu	aliphatic, hydrophobic, neutral	Tyr	aromatic, polar, hydrophobic

Further variants include those in which instead of the naturally occurring amino acid the amino acid which appears in the sequence is a structural analog thereof. Amino acids used in the sequences may also be modified, e.g. labelled, providing the function of the peptide is not significantly adversely affected.
Where the peptide has a sequence that varies from the sequence of any of SEQ ID NOS: 1 to 73 or a fragment thereof, the substitutions may occur across the full length of the sequence, within the sequence of any of SEQ ID NOS: 1 to 73 or outside the sequence of any of SEQ ID NOS: 1 to 73. For example, the variations described herein, such as additions, deletions, substitutions and modifications, may occur within the sequence of any of SEQ ID NOS: 1 to 73. A variant peptide may comprise or consist essentially of the amino acid sequence of any of SEQ ID NOS: 1 to 73 in which one, two, three, four or more amino acid substitutions have been made. A variant peptide may comprise a fragment of the parent protein that is larger than any of SEQ ID NOS: 1 to 73. In this embodiment, the variations described herein, such as substitutions and modifications, may occur within and/or outside the sequence of any of SEQ ID NOS: 1 to 73.

The variant peptides of the invention are 9 to 30 amino acids in length inclusive. Preferably, they may be from 9 to 20 or more preferably 13 to 17 amino acids in length. The peptides may be the same length as the peptide sequences in any one of SEQ ID NOS: 1 to 73.

The peptides may be chemically derived from the polypeptide allergen, for example by proteolytic cleavage or can be derived in an intellectual sense from the polypeptide allergen, for example by making use of the amino acid sequence of the polypeptide allergen and synthesising peptides based on the sequence. Peptides may be synthesised using methods well known in the art.

The term "peptide" includes not only molecules in which amino acid residues are joined by peptide (-CO-NH-) linkages but also molecules in which the peptide bond is reversed. Such retro-inverso peptidomimetics may be made using methods known in the art, for example such as those described in Meziere *et al* (1997) J. Immunol.159, 3230-3237. This approach involves making pseudopeptides containing changes involving the backbone, and not the orientation of side chains. Meziere *et al* (1997) show that, at least for MHC class II and T helper cell responses, these pseudopeptides are useful. Retro-inverse peptides, which contain NH-CO bonds instead of CO-NH peptide bonds, are much more resistant to proteolysis.

Similarly, the peptide bond may be dispensed with altogether provided that an appropriate linker moiety which retains the spacing between the carbon atoms of the amino acid residues is used; it is particularly preferred if the linker moiety has substantially the same charge distribution and substantially the same planarity as a peptide bond. It will also be appreciated that the peptide may conveniently be blocked at its N-or C-terminus so as to help reduce susceptibility to exoproteolytic digestion. For example, the N-terminal amino group of the peptides may be protected by reacting with a carboxylic acid and the C-terminal carboxyl group of the peptide may be protected by reacting with an amine. Other examples of modifications include glycosylation and phosphorylation. Another potential modification is that hydrogens on the side chain amines of R or K may be replaced with methylene groups ($-NH_2 \rightarrow -NH(Me)$ or $-N(Me)_2$).

Analogues of peptides according to the invention may also include peptide variants that increase or decrease the peptide's half-life *in vivo*. Examples of analogues capable of increasing the half-life of peptides used according to the invention include peptoid analogues of the peptides, D-amino acid derivatives of the peptides, and peptide-peptoid hybrids. A further embodiment of the variant polypeptides used according to the invention comprises D-amino acid forms of the polypeptide. The preparation of polypeptides using D-amino acids rather than L-amino acids greatly decreases any unwanted breakdown of such an agent by normal metabolic processes, decreasing the amounts of agent which needs to be administered, along with the frequency of its administration.

The peptides provided by the present invention may be derived from splice variants of the parent proteins encoded by mRNA generated by alternative splicing of the primary transcripts encoding the parent protein chains. The peptides may also be derived from amino acid mutants, glycosylation variants and other covalent derivatives of the parent proteins which retain at least an MHC-binding property of the allergens. Exemplary derivatives include molecules wherein the peptides of the invention are covalently modified by substitution, chemical, enzymatic, or other appropriate means with a moiety other than a naturally occurring amino acid. Further included are naturally occurring variants of the parent proteins found in different mites. Such a variant may be encoded by an allelic variant or represent an alternative splicing variant.

Variants as described above may be prepared during synthesis of the peptide or by post- production modification, or when the peptide is in recombinant form using the known techniques of site- directed mutagenesis, random mutagenesis, or enzymatic cleavage and/or ligation of nucleic acids.

In accordance with the invention, the further one or more peptides that the composition may comprise are preferably functional variants of any of SEQ ID NOS: 1 to 73. That is, the peptides are preferably capable of inducing an immune response. In particular, they may be capable of inducing a late phase response in an individual with grass allergy. This may be tested by the ability of the peptide to induce T cell proliferation in a sample of T cells. Methods of testing the induction of T cell proliferation are well known in the art and one such method is exemplified in Example 4. Preferably the one or more further peptides are capable of causing T cell proliferation in at least 20 % of samples of T cells, wherein each sample is obtained from different grass allergic individuals in the population. The compositions of the invention are preferably capable of inducing T cell proliferation in 30 % or more samples of T cells obtained from of a panel of grass allergic individuals. More preferably, the compositions are capable of inducing T cell proliferation in 35% or more, 40 % or more, 45 %, 50 %, 55 %, 60 %, 65 %, 70 %, 75 %, 80 %, 85 %, or 90 % or more of samples obtained from sensitized individuals in a panel.

The compositions may also be capable of inducing a significant release of one or more cytokines, preferably including one or more of Interferon gamma, Interleukin-10 and Interleukin-13 in samples of T cells obtained from sensitized individuals in a panel. A "significant" release may be determined by criteria similar to that described below in Example 5. Thus, the compositions may be capable of inducing a release of one or more cytokines in 35% or more, 40 % or more, 45 %, 50 %, 55 %, 60 %, 65 %, 70 %, 75 %, 80 %, 85 %, or 90 % or more of samples obtained from sensitized individuals in a panel. The number of individuals in a panel of grass allergic individuals may be any number greater than one, for example at least 2, 3, 5, 10, 15, 20, 30, 50, 80, or at least 100 individuals.

It is preferred if the peptides cause T cell proliferation, but do not lead to the release of histamine from basophils or mast cell preparations from a sensitised individual. There may be some histamine release, but preferably the composition does not cause significant amounts of histamine to be released. Significant histamine release may be considered to be the release of 20% or more of the total available leukocyte histamine when a sample of leukocytes from an individual is stimulated with a composition *in vitro*. A normal individual typically has an approximate leukocyte histamine content of 150ng/10^7 cells.

Suitable variants capable of binding to TCRs may be derived empirically or selected according to known criteria. Within a single peptide there are certain residues which contribute to binding within the MHC antigen binding groove and other residues which interact with hypervariable regions of the T cell receptor (Allen et al (1987) Nature 327: 713-5).

Within the residues contributing to T cell receptor interaction, a hierarchy has been demonstrated which pertains to dependency of T cell activation upon substitution of a given peptide residue. Using peptides which have had one or more T cell receptor contact residues substituted with a different amino acid, several groups have demonstrated profound effects upon the process of T cell activation. Evavold & Allen (1991) Nature 252: 1308-10) demonstrated the dissociation of T cell proliferation and cytokine production. In this *in vitro* model, a T cell clone specific for residues 64-76 of haemoglobin (in the context of I-E^k), was challenged with a peptide analogue in which a conservative substitution of aspartic acid for glutamic acid had been made. This substitution did not significantly interfere with the capacity of the analogue to bind to I-E^k.

Following *in vitro* challenge of a T cell clone with this analogue, no proliferation was detected although IL-4 secretion was maintained, as was the capacity of the clone to help B cell responses. In a subsequent study the same group demonstrated the separation of T cell-mediated cytolysis from cytokine production. In this instance, the former remained unaltered while the latter was impaired. The efficacy of altered peptide ligands *in vivo* was initially demonstrated in a murine model of EAE (experimental allergic encephalomyelitis) by McDevitt and colleagues (Smilek *et al* (1991) Proc Natl Acad Sci USA 88 : 9633-9637). In this model EAE is induced by immunisation with the encephalitogenic peptide Ac1-11 of MBP (myelin basic protein). Substitution at position four (lysine) with an alanine residue generated a peptide which bound well to its restricting element ($A\alpha^uA\beta^u$), but which was non-immunogenic in the susceptible PL/JxSJLF1 strain and which, furthermore prevented the onset of EAE when administered either before or after immunisation with the encephalitogenic peptide. Thus, residues can be identified in peptides which affect the ability of the peptides to induce various functions of T-cells.

Advantageously, peptides may be designed to favour T-cell proliferation and induction of desensitisation. Metzler and Wraith have demonstrated improved tolerogenic capacity of peptides in which substitutions increasing peptide-MHC affinity have been made (Metzler & Wraith(1993) Int Immunol ~ : 1159-65). That an altered peptide ligand can cause long-term and profound anergy in cloned T cells was demonstrated by Sloan-Lancaster *et al* (1993) Nature 363: 156-9.

The compositions of the invention may be capable of inducing a late phase response in an individual that is sensitised to the allergens. The term "late phase response" includes the meaning as set forth in Allergy and Allergic Diseases (1997) A. B. Kay (Ed.), Blackwell Science, pp 1113-1130. The late phase response may be any late phase response (LPR). Preferably, the peptides may be capable of inducing a late asthmatic response (LAR) or a late rhinitic response, or a late phase skin response or a late phase ocular response. Whether or not a particular peptide can give rise to a LPR can be determined using methods well known in the art; a particularly preferred method is that described in Cromwell O, Durham SR, Shaw RJ, Mackay J and Kay AB. Provocation tests and measurements of mediators from mast cells and basophils in asthma and allergic rhinitis. In: Handbook of Experimental Immunology (4) Chapter 127, Editor: Weir DM, Blackwell Scientific Publications, 1986.

Thus, preferably, the individual peptides of the invention are able to induce a LPR in an individual who has been sensitised to the allergens. Whether or not an individual has been sensitised to the allergens may be determined by well known procedures such as skin prick testing with solutions of allergen extracts, induction of cutaneous LPRs, clinical history, allergen challenge and radioallergosorbent test (RAST) for measurement of allergen specific IgE. Whether or not a particular individual is expected to benefit from treatment may be determined by the physician based, for example, on such tests.

Desensitising or tolerising an individual to the allergens means inhibition or dampening of allergic tissue reactions induced by the allergens in appropriately sensitised individuals. It has been shown that T cells can be selectively activated, and then rendered unresponsive. Moreover the anergising or elimination of these T-cells leads to desensitisation of the patient for a particular allergen. The desensitisation manifests itself as a reduction in response to an allergen or allergen-derived peptide, or preferably an elimination of such a response, on second and further administrations of the allergen or allergen-derived peptide. The second administration may be made after a suitable period of time has elapsed to allow desensitisation to occur; this is preferably any period between one day and several weeks. An interval of around two weeks is preferred.

Although the compositions of the invention may be able to induce a LPR in a grass allergic individual, it should be appreciated that when a composition is used to treat a patient it is preferable that a sufficiently low concentration of the composition is used such that no observable LPR will occur but the response will be sufficient to partially desensitise the T cells such that the next (preferably higher) dose may be given, and so on. In this way the dose is built up to give full desensitisation but often without ever inducing a LPR in the patient. Although, the composition or peptide is able to do so at a higher concentration than is administered.

The compositions of the invention may be capable of inducing a late phase response in 50 % or more of a panel of grass allergic individuals from the population.

More preferably, the compositions are capable of inducing a LPR in 55% or more, 60 % or more, 65 % or more, 70% or more, 75% or more, 80% or more, 85% or more, or 90 % or more of sensitized individuals in a panel. Whether or not the compositions are able to induce a LPR in a certain percentage of a panel of subjects can be determined by methods which are well known in the art.

It will be understood that the peptides of the invention comprise a T cell epitope that consists of a core 9 amino acids which are the minimal essential sequence required for MHC class II binding. However, the peptides may also comprise additional residues flanking the core 9 amino acids. The peptides may therefore comprise a region containing a T cell epitope, in which some residues may be modified without affecting the function of the epitope. Accordingly, functional variants of the peptides as defined above include peptides which are altered to improve their solubility relative to the native sequence of the peptides. Improved solubility is advantageous for the tolerisation of subjects to allergens from which the peptides of the invention derive, since administration of poorly soluble agents to subjects causes undesirable, non-tolerising inflammatory responses. The solubility of the peptides may be improved by altering the residues which flank the region containing a T cell epitope. A peptide of the invention may be engineered to be more soluble such that it comprises:

i) N terminal to the residues of the peptide which flank a T cell epitope: one to six contiguous amino acids corresponding to the two to six contiguous amino acids immediately N terminal to said residues in the sequence of the protein from which the peptide derives; and/or

ii) C terminal to the residues of the peptide which flank a T cell epitope: one to six contiguous amino acids corresponding to the one to six contiguous amino acids immediately C terminal to the said residues in the sequence of the protein from which the peptide derives; or

iii) both N and C terminal to the residues of the peptide which flank a T cell epitope, at least one amino acid selected from arginine, lysine, histidine, glutamate and aspartate.

Optionally, the peptides may additionally be engineered to be more soluble such that:

i) any cysteine residues in the native sequence of the peptide are replaced with serine or 2-aminobutyric acid; and /or

ii) any hydrophobic residues in the upto three amino acids at the N or C terminus of the native sequence of the peptide, which are not comprised in a T cell epitope, are deleted; and/or

iii) any two consecutive amino acids comprising the sequence Asp-Gly in the upto four amino acids at the N or C terminus of the native sequence of the peptide, which are not comprised in a T cell epitope, are deleted; and/or

iv) one or more positively charged residues are added at the N- and/or C-terminus.

Examples of peptides engineered to improve solubility are Rye 09B and Tim07B as described in Example 8. The variants with improved solubility are shown in Table 8. Thus, peptides Rye 09B1 (SEQ ID NO: 91), KPEVKYAVFEAALTKAIT; Rye 09B2 (SEQ ID NO: 92), KKPEVKYAVFEAALTKAIT, Tim 07B1, (SEQ ID NO: 93), KKIPAGELQIIDKIDA, Tim 07B2 (SEQ ID NO: 94), KKIPAGELQIIDKIDAK are preferred examples of variants with improved solubility. SEQ ID NO:s 91 to 94 may therefore preferentially be used as substitutes for the above native peptides in a composition of the invention.

Nucleic acids and vectors

The individual peptides that make up the compositions and products of the invention may be administered directly, or may be administered indirectly by expression from an encoding sequence. For example, a polynucleotide may be provided that encodes a peptide combination of the invention, such as any combination of peptides described above. A peptide combination of the invention may thus be produced from or delivered in the form of a polynucleotide which encodes, and is capable of expressing, it. Any reference herein to the use, delivery or administration of a peptide combination of the invention is intended to include the indirect use, delivery or administration of such a peptide combination via expression from a polynucleotide that encodes it.

Accordingly, the invention provides a composition for use in preventing or treating

allergy to grass by tolerisation comprising at least one polynucleotide sequence which when expressed causes the production of a composition suitable for use in preventing or treating allergy to grass by tolerisation as described above.

The invention also provides a product comprising four or more different polynucleotides encoding polypeptides of a) to h) or variants thereof as described above; and wherein each different encoded polypeptide is for simultaneous, separate of sequential use in the prevention or treatment of allergy to grass in a human.

The terms "nucleic acid molecule" and "polynucleotide" are used interchangeably herein and refer to a polymeric form of nucleotides of any length, either deoxyribonucleotides or ribonucleotides, or analogs thereof. Non-limiting examples of polynucleotides include a gene, a gene fragment, messenger RNA (mRNA), cDNA, recombinant polynucleotides, plasmids, vectors, isolated DNA of any sequence, isolated RNA of any sequence, nucleic acid probes, and primers. A polynucleotide of the invention may be provided in isolated or purified form.

A nucleic acid sequence which "encodes" a selected polypeptide is a nucleic acid molecule which is transcribed (in the case of DNA) and translated (in the case of mRNA) into a polypeptide *in vivo* when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a start codon at the 5' (amino) terminus and a translation stop codon at the 3' (carboxy) terminus. For the purposes of the invention, such nucleic acid sequences can include, but are not limited to, cDNA from viral, prokaryotic or eukaryotic mRNA, genomic sequences from viral or prokaryotic DNA or RNA, and even synthetic DNA sequences. A transcription termination sequence may be located 3' to the coding sequence.

Polynucleotides of the invention can be synthesised according to methods well known in the art, as described by way of example in Sambrook et al (1989, Molecular Cloning - a laboratory manual; Cold Spring Harbor Press).

The polynucleotide molecules of the present invention may be provided in the form of an expression cassette which includes control sequences operably linked to the inserted sequence, thus allowing for expression of the peptide of the invention *in* *vivo* in a targeted subject. These expression cassettes, in turn, are typically provided within vectors (e.g., plasmids or recombinant viral vectors) which are suitable for use as reagents for nucleic acid immunization. Such an expression cassette may be administered directly to a host subject. Alternatively, a vector comprising a polynucleotide of the invention may be administered to a host subject. Preferably the polynucleotide is prepared and/or administered using a genetic vector. A suitable vector may be any vector which is capable of carrying a sufficient amount of genetic information, and allowing expression of a peptide of the invention.

The present invention thus includes expression vectors that comprise such polynucleotide sequences. Thus, the present invention provides a vector for use in preventing or treating allergy to grass by tolerisation comprising four or more polynucleotide sequences which encode different polypeptides of the invention and optionally one or more further polynucleotide sequences which encode different polypeptides as defined herein. The vector may comprise 4, 5, 6 or 7 polynucleotide sequences which encode different polypeptides of the invention. The vector preferably comprises a first polynucleotide sequence that encodes a polypeptide selected from SEQ ID NO:s 1 to 27 or a variant thereof as described above, and a second polynucleotide sequence that encodes a polypeptide selected from SEQ ID NO:s 28 to 73 or a variant thereof as described above. This (first) vector may be used in combination with one or more other vectors providing coding sequences for different polypeptides of the invention not encoded by the first vector.

Furthermore, it will be appreciated that the compositions and products of the invention may comprise a mixture of polypeptides and polynucleotides. Accordingly, the invention provides a composition or product as defined herein, wherein in place of any one of the polypeptide is a polynucleotide capable of expressing said polypeptide.

Expression vectors are routinely constructed in the art of molecular biology and may for example involve the use of plasmid DNA and appropriate initiators, promoters, enhancers and other elements, such as for example polyadenylation signals which may be necessary, and which are positioned in the correct orientation, in order to allow for expression of a peptide of the invention. Other suitable vectors would be apparent to persons skilled in the art. By way of further example in this regard we refer to Sambrook *et al.*

Thus, a polypeptide of the invention may be provided by delivering such a vector to a cell and allowing transcription from the vector to occur. Preferably, a polynucleotide of the invention or for use in the invention in a vector is operably linked to a control sequence which is capable of providing for the expression of the coding sequence by the host cell, i.e. the vector is an expression vector.

"Operably linked" refers to an arrangement of elements wherein the components so described are configured so as to perform their usual function. Thus, a given regulatory sequence, such as a promoter, operably linked to a nucleic acid sequence is capable of effecting the expression of that sequence when the proper enzymes are present. The promoter need not be contiguous with the sequence, so long as it functions to direct the expression thereof. Thus, for example, intervening untranslated yet transcribed sequences can be present between the promoter sequence and the nucleic acid sequence and the promoter sequence can still be considered "operably linked" to the coding sequence.

A number of expression systems have been described in the art, each of which typically consists of a vector containing a gene or nucleotide sequence of interest operably linked to expression control sequences. These control sequences include transcriptional promoter sequences and transcriptional start and termination sequences. The vectors of the invention may be for example, plasmid, virus or phage vectors provided with an origin of replication, optionally a promoter for the expression of the said polynucleotide and optionally a regulator of the promoter. A "plasmid" is a vector in the form of an extrachromosomal genetic element. The vectors may contain one or more selectable marker genes, for example an ampicillin resistence gene in the case of a bacterial plasmid or a resistance gene for a fungal vector. Vectors may be used *in vitro*, for example for the production of DNA or RNA or used to transfect or transform a host cell, for example, a mammalian host cell. The vectors may also be adapted to be used *in vivo*, for example to allow *in vivo* expression of the polypeptide.

A "promoter" is a nucleotide sequence which initiates and regulates transcription of a polypeptide-encoding polynucleotide. Promoters can include inducible promoters (where expression of a polynucleotide sequence operably linked to the promoter is induced by an analyte, cofactor, regulatory protein, etc.), repressible promoters (where expression of a polynucleotide sequence operably linked to the promoter is repressed by an analyte, cofactor, regulatory protein, etc.), and constitutive promoters. It is intended that the term “promoter” or “control element” includes full-length promoter regions and functional (e.g., controls transcription or translation) segments of these regions.

A polynucleotide, expression cassette or vector according to the present invention may additionally comprise a signal peptide sequence. The signal peptide sequence is generally inserted in operable linkage with the promoter such that the signal peptide is expressed and facilitates secretion of a polypeptide encoded by coding sequence also in operable linkage with the promoter.

Typically a signal peptide sequence encodes a peptide of 10 to 30 amino acids for example 15 to 20 amino acids. Often the amino acids are predominantly hydrophobic. In a typical situation, a signal peptide targets a growing polypeptide chain bearing the signal peptide to the endoplasmic reticulum of the expressing cell. The signal peptide is cleaved off in the endoplasmic reticulum, allowing for secretion of the polypeptide via the Golgi apparatus. Thus, a peptide of the invention may be provided to an individual by expression from cells within the individual, and secretion from those cells.

Alternatively, polynucleotides of the invention may be expressed in a suitable manner to allow presentation of a peptide of the invention by an MHC class II molecule at the surface of an antigen presenting cell. For example, a polynucleotide, expression cassette or vector of the invention may be targeted to antigen presenting cells, or the expression of encoded peptide may be preferentially stimulated or induced in such cells.

In some embodiments, the polynucleotide, expression cassette or vector will encode an adjuvant, or an adjuvant will otherwise be provided. As used herein, the term "adjuvant" refers to any material or composition capable of specifically or non-specifically altering, enhancing, directing, redirecting, potentiating or initiating an antigen-specific immune response.

Polynucleotides of interest may be used *in vitro, ex vivo* or *in vivo* in the production of a peptide of the invention. Such polynucleotides may be administered or used in the prevention or treatment of allergy by tolerisation.

Methods for gene delivery are known in the art. See, e.g., U.S. Patent Nos. 5,399,346, 5,580,859 and 5,589,466. The nucleic acid molecule can be introduced directly into the recipient subject, such as by standard intramuscular or intradermal injection; transdermal particle delivery; inhalation; topically, or by oral, intranasal or mucosal modes of administration. The molecule alternatively can be introduced *ex vivo* into cells that have been removed from a subject. For example, a polynucleotide, expression cassette or vector of the invention may be introduced into APCs of an individual *ex vivo*. Cells containing the nucleic acid molecule of interest are re-introduced into the subject such that an immune response can be mounted against the peptide encoded by the nucleic acid molecule. The nucleic acid molecules used in such immunization are generally referred to herein as "nucleic acid vaccines."

The polypeptides, polynucleotides, vectors or cells of the invention may be present in a substantially isolated form. They may be mixed with carriers or diluents which will not interfere with their intended use and still be regarded as substantially isolated. They may also be in a substantially purified form, in which case they will generally comprise at least 90%, e.g. at least 95%, 98% or 99%, of the proteins, polynucleotides, cells or dry mass of the preparation.

Antigen presenting cells (APCs)

The invention encompasses the use *in vitro* of a method of producing a population of APCs that present the peptides of the invention on their surface, that may be subsequently used in therapy. Such a method may be carried out *ex vivo* on a sample of cells that have been obtained from a patient. The APCs produced in this way therefore form a pharmaceutical agent that can be used in the treatment or prevention of grass allergy by tolerisation. The cells should be accepted by the immune system of the individual because they derive from that individual. Delivery of cells that have been produced in this way to the individual from whom they were originally obtained, thus forms a therapeutic embodiment of the invention.

Formulations and compositions

The peptides, polynucleotides, vectors and cells of the invention may be provided to an individual either singly or in combination. Each molecule or cell of the invention may be provided to an individual in an isolated, substantially isolated, purified or substantially purified form. For example, a peptide of the invention may be provided to an individual substantially free from the other peptides. Alternatively, four or more peptides in the composition may be coupled chemically together, using standard peptide coupling reagents, to provide a single peptide containing the preferred epitopes. Such peptides would be screened for basophil histamine release to confirm lack of histamine release as per the individual peptides. In a further embodiment, four or more peptides in the composition may be provided as part of a single polypeptide chain i.e by recombinant means from an encoding polynucleotide. The four or more peptides may be fused contiguously, or may alternatively be separated by appropriate linkers.

Whilst it may be possible for the peptides, polynucleotides or compositions according to the invention to be presented in raw form, it is preferable to present them as a pharmaceutical formulation. Thus, according to a further aspect of the invention, the present invention provides a pharmaceutical formulation for use in preventing or treating allergy to grass by tolerisation comprising a composition, vector or product according to the invention together with one or more pharmaceutically acceptable carriers or diluents and optionally one or more other therapeutic ingredients. The carrier (s) must be 'acceptable' in the sense of being compatible with the other ingredients of the formulation and not deleterious to the recipient thereof. Typically, carriers for injection, and the final formulation, are sterile and pyrogen free. Preferably, the carrier or diluent is thioglycerol.

Formulation of a composition comprising the peptide, polynucleotides or cells of the invention can be carried out using standard pharmaceutical formulation chemistries and methodologies all of which are readily available to the reasonably skilled artisan.

For example, compositions containing one or more molecules or cells of the invention can be combined with one or more pharmaceutically acceptable excipients or vehicles. Auxiliary substances, such as wetting or emulsifying agents, pH buffering substances and the like, may be present in the excipient or vehicle. These excipients, vehicles and auxiliary substances are generally pharmaceutical agents that do not induce an immune response in the individual receiving the composition, and which may be administered without undue toxicity. Pharmaceutically acceptable excipients include, but are not limited to, liquids such as water, saline, polyethyleneglycol, hyaluronic acid, glycerol, thioglycerol and ethanol. Pharmaceutically acceptable salts can also be included therein, for example, mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients, vehicles and auxiliary substances is available in Remington's Pharmaceutical Sciences (Mack Pub. Co., N.J. 1991).

Such compositions may be prepared, packaged, or sold in a form suitable for bolus administration or for continuous administration. Injectable compositions may be prepared, packaged, or sold in unit dosage form, such as in ampoules or in multi-dose containers containing a preservative. Compositions include, but are not limited to, suspensions, solutions, emulsions in oily or aqueous vehicles, pastes, and implantable sustained-release or biodegradable formulations. Such compositions may further comprise one or more additional ingredients including, but not limited to, suspending, stabilizing, or dispersing agents. In one embodiment of a composition for parenteral administration, the active ingredient is provided in dry (for e.g., a powder or granules) form for reconstitution with a suitable vehicle (e. g., sterile pyrogen-free water) prior to parenteral administration of the reconstituted composition. The pharmaceutical compositions may be prepared, packaged, or sold in the form of a sterile injectable aqueous or oily suspension or solution. This suspension or solution may be formulated according to the known art, and may comprise, in addition to the active ingredient, additional ingredients such as the dispersing agents, wetting agents, or suspending agents described herein. Such sterile injectable formulations may be prepared using a non-toxic parenterally-acceptable diluent or solvent, such as water or 1,3-butane diol, for example. Other acceptable diluents and solvents include, but are not limited to, Ringer's solution, isotonic sodium chloride solution, and fixed oils such as synthetic mono-or di-glycerides. Other parentally-administrable compositions which are useful include those which comprise the active ingredient in microcrystalline form, in a liposomal preparation, or as a component of a biodegradable polymer systems. Compositions for sustained release or implantation may comprise pharmaceutically acceptable polymeric or hydrophobic materials such as an emulsion, an ion exchange resin, a sparingly soluble polymer, or a sparingly soluble salt.

Alternatively, the peptides or polynucleotides of the present invention may be encapsulated, adsorbed to, or associated with, particulate carriers. Suitable particulate carriers include those derived from polymethyl methacrylate polymers, as well as PLG microparticles derived from poly(lactides) and poly(lactide-co-glycolides). See, e.g., Jeffery et al. (1993) Pharm. Res. 10:362-368. Other particulate systems and polymers can also be used, for example, polymers such as polylysine, polyarginine, polyornithine, spermine, spermidine, as well as conjugates of these molecules.

The formulation of any of the peptides, polynucleotides or cells mentioned herein will depend upon factors such as the nature of the substance and the method of delivery. Any such substance may be administered in a variety of dosage forms. It may be administered orally (e.g. as tablets, troches, lozenges, aqueous or oily suspensions, dispersible powders or granules), topically, parenterally, subcutaneously, by inhalation, intravenously, intramuscularly, intrasternally, transdermally, intradermally, sublingually, instranasally, buccally or by infusion techniques. The substance may also be administered as suppositories. A physician will be able to determine the required route of administration for each particular individual.

The compositions or formulations of the invention will comprise a suitable concentration of each peptide/polynucleotide/cell to be effective without causing adverse reaction. Typically, the concentration of each peptide in the composition will be in the range of 0.03 to 200 nmol/ml. More preferably in the range of 0.3 to 200 nmol/ml, 3 to 180 nmol/ml, 10 to 150 nmol/ml, 5 to 200nmol/ml or 30 to 120 nmol/ml. The composition or formulations should have a purity of greater than 95% or 98% or a purity of at least 99%.

In one aspect of the invention an adjuvant may be used in combination with the polypeptide/polynucleotides/cells of the invention. The adjuvant is preferably administered in an amount which is sufficient to augment the effect of the polypeptide/polynucleotides/cells of the invention or vice versa. The adjuvant or other therapeutic agent may be an agent that potentiates the effects of the molecule of the invention. For example, the other agent may be an immunomodulatory molecule or an adjuvant which enhances the response to the peptide or cell of the invention.

In one embodiment, therefore, the peptides, polynucleotides, cells or compositions of the invention are used for therapy in combination with one or more other therapeutic agents. The agents may be administered separately, simultaneously or sequentially. They may be administered in the same or different compositions. Accordingly, in a method of the invention, the subject may also be treated with a further therapeutic agent.

A composition may therefore be formulated which comprises a molecule and/or cell of the invention and also one or more other therapeutic molecules. A composition of the invention may alternatively be used simultaneously, sequentially or separately with one or more other therapeutic compositions as part of a combined treatment.

Non-limiting examples of adjuvants include vitamin D, rapamycin and glucocorticoid steroids such as dexamethasone, fluticasone, budesonide, mometasone, beclomethasone, hydrocortisone, cortisone acetate, prednisone, prednisolone, methylprednisolone, betamethasone and triamcinolone. A preferred glucocorticoid is dexamethasone.

Therapeutic methods and individual to be treated

The present invention relates to peptides, polynucleotides, vectors and cells that are capable of desensitising or tolerising human individuals to the allergens described above and are therefore useful in the prevention or treatment of grass allergy. The invention provides compositions, products, vectors and formulations for use in preventing or treating allergy to grass by tolerisation. The compositions of the invention may be used to reduce allergic symptoms or improve the condition of an allergic individual. The invention also provides a method of tolerising or desensitizing a grass allergic individual comprising administering, either singly or in combination the polypeptides/polynucleotides/cells of the invention as described above.

The individual to be treated or provided with the composition or formulation of the invention is preferably human. It will be appreciated that the individual to be treated may be known to be sensitised to the allergens, at risk of being sensitised or suspected of being sensitised. The individual can be tested for sensitisation using techniques well known in the art and as described herein. Alternatively, the individual may have a family history of allergy to grass. It may not be necessary to test an individual for sensitisation to grass because the individual may display symptoms of allergy when exposed to grass. By exposure is meant proximity to, for example, a grass plant, or a substance or product derived from a grass plant, or a substance or product containing or comprising either of the above. The substance or product derived from a grass plant is typically grass pollen. By proximity is meant 10 metres or less, 5 metres or less, 2 metres or less, 1 metre or less, or 0 metres from the items described above. Symptoms of allergy can include itchy eyes, runny nose, breathing difficulties, red itchy skin or rash.

The individual to be treated may be of any age. However, preferably, the individual may be in the age group of 1 to 90, 5 to 60, 10 to 40, or more preferably 18 to 35.

Preferably, the individual to be treated is from a population that has MHC allele frequencies within the range of frequencies that are representative of the Caucasian population. Reference population allele frequencies for 11 common DRB1 allele families are shown in Table A (Data from HLA Facts Book, Parham and Barber).

Table A

DRB1	1	3	4	7	8	11	12	13	14	15	16
%	6.4	14.7	15.7	8.8	3.4	8.3	3.9	14.7	2.9	17.6	2.5

Reference population %	9.4	11.1	12.8	13.2	3.7	13.4	2.3	10.2	3.2	10.7	3.6

Reference frequencies were obtained by analysis of multiple studies reporting frequencies and the figures shown are mean values. Preferably therefore, the individual to be treated is from a population that has equivalent MHC allele frequencies as the reference population for the alleles referred to Table A (such as for at least 1, 2, 3, 4, 5 or all of the alleles), for example within the ranges of those figures plus or minus 1, 2, 3, 5, 10, 15 or 20%.

Preferably the individual is from a population where the allele frequencies of the following DRB1 alleles is:

4 – at least 9%

7 – at least 10%

11 – at least 8%.

The individual may have had allergy to grass for at least 2 weeks, 1 month, 6 months, 1 year or 5 years. The individual may suffer from a rash, nasal congestion, nasal discharge and/or coughing caused by the allergy. The individual may or may not have been administered with other compositions/compounds which treat grass allergy. The individual may live in a geographical region which has:

- a temperate climate, and/or:
- a typical soil pH in the range of about 3.5, 4 or 4.5 to about 5.5, 6, 7 or 8; and/or
- a mean annual precipitation no less than about 9, 10, 11, 12, 13, 14, 15, 16, 17 18, 19 or 20cm per year and no greater than about 180cm, 250cm, 300cm, 400cm or 500cm per year; and/or
- an annual minimum temperature of no less than about -5°C, -4°C, -3°C, -2°C, -1°C, 0°C, 1°C, 2°C, 3°C, 4°C or 5°C and/or
- an annual maximum temperature of no greater than about 35°C, about 30°C, about 29°C, about 28°C, about 27°C, about 26°C about 25°C, about 24°C, about 23°C or about 22°C; and/or
- lies between the latitudes of about 30° north and about 30° south.

The individual typically suffers from allergy to grass in a particular season. The season typically corresponds to the flowering season of grass, which is typically summer, preferably early summer (for example from May to June in the Northern hemisphere) or late summer (for example August to October in the Northern hemisphere). The grass allergic individual is typically allergic to grass pollen.

Combination immunotherapy

Since many individuals are allergic, or may require desensitizing to several polypeptide antigens, the current invention also provides means of desensitizing individuals that are allergic to multiple antigens. “Tolerance” induced in an individual to a first polypeptide antigen or allergen can create in the individual a “tolerogenic environment” wherein inappropriate immune responses to other antigens can be downregulated in order to provide tolerance to other antigens.

This finding means that individuals allergic to multiple allergens can be treated in a greatly reduced time period, and that individuals seriously allergic to some allergens (e.g., peanuts) but more mildly allergic to other allergens (e.g., cat dander) can benefit from a therapy wherein tolerance to the milder allergen is established and then this tolerogenic environment is used to provide tolerance to the other, more extreme allergen. In addition, individuals suffering from an autoimmune disorder who are additionally sensitised (or otherwise immune) to an unrelated antigen or allergen can benefit from a treatment regime wherein tolerance to the unrelated antigen or allergen is first established and then this tolerogenic environment is used to provide tolerance to the autoantigen associated with the autoimmune disorder.

A method is therefore provided for desensitising a grass allergic individual to grass allergen as described above and one or more further different polypeptide antigens. The method entails, in a first step, administering to the individual a composition/product/formulation (primary composition) according to the invention as described herein and wherein the administration is carried out in a manner sufficient to generate a hyporesponsive state against grass allergen. Once a hyporesponsive state has been established toward grass allergen, or at least a shift toward desensitisation has occurred, the method entails administration of a secondary composition comprising a second, different polypeptide antigen to which the individual is to be sensitised. Administration of the secondary composition is carried out in such a way as to take advantage of the tolerogenic environment established by use of the primary composition, where it is now possible to establish tolerance to the second, different polypeptide antigen. The secondary composition is coadministered with either the first primary composition or a larger fragment of the grass allergen(s). By "coadministered" it is meant either the simultaneous or concurrent administration, e.g., when the two are present in the same composition or administered in separate compositions at nearly the same time but at different sites, as well as the delivery of polypeptide antigens in separate compositions at different times. For example, the secondary composition may be delivered prior to or subsequent to delivery of the first composition at the same or a different site. The timing between deliveries can range from about several seconds apart to about several minutes apart, several hours apart, or even several days apart. Furthermore, different delivery methods can be employed.

Classes of suitable allergens include, but are not limited to dust mite allergens, pollens, animal dander (especially cat dander), grasses, molds, dusts, antibiotics, stinging insect venoms, and a variety of environmental (including chemicals and metals), drug and food allergens. Common tree allergens include pollens from cottonwood, popular, ash, birch, maple, oak, elm, hickory, and pecan trees; common plant allergens include those from mugwort, ragweed, English plantain, sorrel-dock and pigweed; plant contact allergens include those from poison oak, poison ivy and nettles; common grass allergens include rye grass, Timothy, Johnson, Bermuda, fescue and bluegrass allergens; common allergens can also be obtained from molds or fungi such as Alternaria, Fusarium, Hormodendrum, Aspergillus, Micropolyspora, Mucor and thermophilic actinomycetes; epidermal allergens can be obtained from house or organic dusts (typically fungal in origin), or from animal sources such as feathers, and dog dander; common food allergens include milk and cheese (dairy), egg, wheat, nut (e.g., peanut), seafood (e.g., shellfish), pea, bean and gluten allergens; common environmental allergens include metals (nickel and gold), chemicals (formaldehyde, trinitrophenol and turpentine), Latex, rubber, fiber (cotton or wool), burlap, hair dye, cosmetic, detergent and perfume allergens; common drug allergens include local anesthetic and salicylate allergens; antibiotic allergens include penicillin, tetracycline and sulfonamide allergens; and common insect allergens include bee, wasp and ant venom, and cockroach calyx allergens. Particularly well characterized allergens include, but are not limited to, the major cat allergen Fel d 1, bee venom phospholipase A2 (PLA) (Akdis et al. (1996) J. Clin. Invest. 98:1676-1683), birch pollen allergen Bet v 1 (Bauer et al. (1997) Clin. Exp. Immunol. 107:536-541), and the multi-epitopic recombinant grass allergen rKBG8.3 (Cao et al. (1997) Immunology 90:46-51).

Particularly preferred T cell epitopes are derived from the allergens: cat dander protein Fel d 1; House dust mite proteins Der p 1, Der p 2 and Der p 7; Ragweed protein amb a 1.1, a 1.2, a 1.3 or a 1.4; Rye grass proteins Lol p 1 and Lol p 5; Timothy grass proteins Phl p 1 and Phl p 5; Bermuda grass protein Cyn d 1; Alternaria alternate proteins Alt a 1, Alt a 2 and Enolase (Alt a 6); Birch protein Bet v 1 and P14; German Cockroach proteins Bla g 1, Bla g 2, Bla g 3, Bla g 4, Bla g 5 and Bla g 6; Mugwort protein Art v 1; Russian thistle protein Sal k 1 and Sal k 2; peanut Ara h 1, Ara h 2, Ara h 3, Ara h 4, Ara h 5, Ara h 6, plant profilins or lipid transfer proteins or a human leukocyte antigen.

These and other suitable allergens are commercially available and/or can be readily prepared as extracts following known techniques.

Preferably, the second polypeptide allergen is a grass allergen or a grass allergen fragment, more particularly a grass allergen or grass allergen fragment selected from the list of grass allergen sequences indexed by database accession numbers (NCBI Entrez accession numbers) below. NCBI is the National Center for Biotechnology information and is a division of the US National Institutes of Health. The NCBI web site, from which access to the database may be sought, is www.ncbi.nlm.nih.gov/. Allergen sequences indexed by database accession numbers.

75232277 Dac g 1, 75139988 Dac g 1, 75232276 Dac g 1, 33149335 Dac g 1, 33149333 Dac g 1, 75163303 Dac g 5, 75163399 Dac g 5, 75163400 Dac g 5, 14423124 Dac g 5, 14423122 Dac g 5, 14423120 Dac g 5, 1171005 Hol l 1, 3860384 Hol l 1, 414703 Hol l 1, 1167836 Hol l 1, 1085628 Hol l 1, 2266625 Hol l 5, 2266623 Hol l 5, 75172041 Hol l 5, 75098038 Hol l 5, 75098037 Hol l 5, 11991229 Hol l 5, 2266623 Hol l 5, 2506771 Hor v 1, 282991 Hor v 1, 75219009 Hor v 5, 126385 Lol p 1, 168314 Lol p 1 , 6599300 Lol p 1, 75274600 Lol p 1, 168316 Lol p 1, 3210053 Lol p 1, 3210049 Lol p 1, 3210047 Lol p 1 , 3210050 Lol p 1, 3210044 Lol p 1, 3210043 Lol p 1, 3210041 Lol p 1, 3210039 Lol p 1, 3210037 Lol p 1, 3210036 Lol p 1, 3210035 Lol p 1, 3210034 Lol p 1, 3210033 Lol p 1, 3210032 Lol p 1, 3210030 Lol p 1, 100636 Lol p 1320616 Lol p 1, 320614 Lol p 1, 100638 Lol p 1, 100636 Lol p 1, 320614 Lol p 1, 100637 Lol p 1, 126386 Lol p 2a, 126387 Lol p 3, 2498581 Lol p 5 a, 4416516 Lol p 5 a, 485371 Lol p 5 a, 100639 Lol p 5 a, 3409495 Lol p 5 a, 3409494 Lol p 5 a, 3409493 Lol p 5 a , 3409489 Lol p 5 a, 3409488 Lol p 5 a, 3409487 Lol p 5 a, 3409486 Lol p 5 a, 3409484 Lol p 5 a, 3409483 Lol p 5 a, 3409481 Lol p 5 a, 3409479 Lol p 5 a, 3409478 Lol p 5 a. 3409477 Lol p 5 a, 3409476 Lol p 5 a, 3409475 Lol p 5 a, 3409474 Lol p 5 a, 3409473 Lol p 5 a, 3409472 Lol p 5 a, 3409471 Lol p 5 a, 3409470 Lol p 5 a, 3409469 Lol p 5 a, 3409468 Lol p 5 a, 3409467 Lol p 5 a, 3409466 Lol p 5 a, 3409456 Lol p 5 a, 3209999 Lol p 5 a, 3210002 Lol p 5 a. 3210003 Lol p 5 a, 3210004 Lol p 5 a, 3210005 Lol p 5 a, 3210006 Lol p 5 a, 3210007 Lol p 5 a, 3210008 Lol p 5 a, 3210009 Lol p 5 a, 3210010 Lol p 5 a, 3210011 Lol p 5 a, 3210012 Lol p 5 a, 3210013 Lol p 5 a, 3210014 Lol p 5 a, 3210015 Lol p 5 a, 3210017 Lol p 5 a, 3210018 Lol p 5 a, 3210019 Lol p 5 a, 3210020 Lol p 5 a, 3210021 Lol p 5 a, 3210022 Lol p 5 a, 3210023 Lol p 5 a, 3210024 Lol p 5 a, 3210025 Lol p 5 a, 3210026 Lol p 5 a, 542129 Lol p 5 a, 2498582 Lol p 5 b, 3409457 Lol p 5 b, 626028 Lol p 5 b, 542131 Lol p 5 b, 455288 Lol p 5 b, 6634467 Lol p 5c, 455288 Lol p isoform 9, 1582249 Lol p 11, Additional Lolium sequences : 135480; 417103; 687261; 687259; 1771355; 2388662; 631955; 542131; 542130; 542129; 100636; 626029; 542132; 320616; 320615; 320614; 100638; 100634; 82450; 626028; 100639; 283345; 542133; 1771353; 1763163; 1040877; 1040875; 250525; 551047; 515377; 510911; 939932; 439950; 2718; 168316; 168314; 485371; 2388664; 2832717; 2828273; 548867; 3409458 Pha a 1, 3210038 Pha a 1, 2498576 Pha a 1, 1246116 Pha a 1, 3210031 Pha a 1, 3210027 Pha a 1, 3210028 Pha a 1, 3210029 Pha a 1, 82450 Pha a 1, 409328 Pha a 1, 2498580 Pha a 5, 2498579 Pha a 5, 2498578 Pha a 5, 2498577 Pha a 5, 1246120 Pha p 5, 1246119 Pha p 5, 1246118

Pha p 5, 1246117 Pha p 5, 3409480 Pha p 5, 3409482 Pha p 5 , 3409490 Pha p 5, 1171008 Phl p 1, 28373838 Phl p 1, 28373839 Phl p 1, 473360 Phl p 1, 3901094 Phl p 1, 1582250 Phl p 1, 75221090 Phl p 1, 3210052 Phl p 1, 3210046 Phl p 1, 3210040 Phl p 1, 629812 Phl p 1, 481432 Phl p 1, 1684718 Phl p 5, 13430402 Phl p 5, 3135501 Phl p 5, 3135499 Phl p 5, 3135497 Phl p 5, 1684720 Phl p 5, 40644796 Phl p 5, 3309039 Phl p 5, 3309041 Phl p 5, 739542 Phl p 5, 3309047 Phl p 5, 3309045 Phl p 5, 3309043 Phl p 5, 3135503 Phl p 5, 626037 Phl p 5, 2851456 Phl p 5a, 2398757 Phl p 5a, 1092249 Phl p 5a, 29500897 Phl p 5a, 422005 Phl p 5a, 3409492 Phl p 5a, 2851457 Phl p 5b, 481397 Phl p 5b, 1096197 Phl p 5b, 2398759 Phl p 5b, 3409491 Phl p 5b; Additional Phleum sequences: 458878; 548863; 2529314; 2529308; 2415702; 2415700; 2415698; 542168; 542167; 626037; 542169; 541814; 542171; 253337; 253336; 453976; 439960; 75267691 Poa p 1, 4090265 Poa p 1, 280414 Poa p 1, 320620 Poa p 1, 250525 Poa p 5, 75172042 Poa p 5, 113562 Poa p 9, 113561 Poa p 9, 113560 Poa p 9, 729944 Zea m 1, 115502168 Zea m 1b, 11550238 Zea m 1d, 115502167 Zea m 1c, 122238295 Zea m 1, 75272187 Zea m 1, 115502389 Zea m 1, 162459584 Zea m 1, 89892723 Zea m 1, .293902 Zea m 1, 89892721 Zea m 1, 114794319 Zea m 1, 478272 Zea m 1.

Delivery methods

Once formulated the compositions of the invention can be delivered to a subject *in vivo* using a variety of known routes and techniques. For example, a composition can be provided as an injectable solution, suspension or emulsion and administered via parenteral, subcutaneous, epidermal, intradermal, intramuscular, intraarterial, intraperitoneal, intravenous injection using a conventional needle and syringe, or using a liquid jet injection system. Compositions can also be administered topically to skin or mucosal tissue, such as nasally, intratracheally, intestinal, rectally or vaginally, or provided as a finely divided spray suitable for respiratory or pulmonary administration. Other modes of administration include oral administration, suppositories, sublingual administration, and active or passive transdermal delivery techniques.

Where a peptide of the invention is to be administered, it is preferred to administer the peptide to a site in the body where it will have the ability to contact suitable antigen presenting cells, and where it, or they, will have the opportunity to contact T cells of the individual. Where an APC is to be administered, it is preferred to administer the APC to a site in the body where it will have the ability to contact, and activate, suitable T cells of the individual.

Delivery regimes

Administration of the peptides/polynucleotides/cells (such as the composition containing a plurality of peptides) may be by any suitable method as described above. Suitable amounts of the peptide may be determined empirically, but typically are in the range given below. A single administration of each peptide may be sufficient to have a beneficial effect for the patient, but it will be appreciated that it may be beneficial if the peptide is administered more than once, in which case typical administration regimes may be, for example, once or twice a week for 2-4 weeks every 6 months, or once a day for a week every four to six months. As will be appreciated, each peptide or polynucleotide, or combination of peptides and/or polynucleotides may be administered to a patient singly or in combination.

Dosages for administration will depend upon a number of factors including the nature of the composition, the route of administration and the schedule and timing of the administration regime. Suitable doses of a molecule of the invention may be in the order of up to 15μg, up to 20μg, up to 25μg, up to 30μg, up to 50μg, up to 100μg, up to 500 μg or more per administration. Suitable doses may be less than 15μg, but at least 1ng, or at least 2ng, or at least 5ng, or at least 50ng, or least 100ng, or at least 500ng, or at least 1μg, or at least 10μg. For some molecules of the invention, the dose used may be higher, for example, up to 1 mg, up to 2 mg, up to 3 mg, up to 4 mg, up to 5 mg or higher. Such doses may be provided in a liquid formulation, at a concentration suitable to allow an appropriate volume for administration by the selected route.

Kits

The invention also relates to a combination of components described herein suitable for use in a treatment of the invention which are packaged in the form of a kit in a container. Such kits may comprise a series of components to allow for a treatment of the invention. For example, a kit may comprise one or more different peptides, polynucleotides and/or cells of the invention, or one or more peptides, polynucleotides or cells of the invention and one or more additional therapeutic agents suitable for simultaneous administration, or for sequential or separate administration. The kit may optionally contain other suitable reagent(s) or instructions and the like.

The invention is illustrated by the following Examples:

Example 1

MHC Class II binding search

The aim of this study is to identify a distinct panel of peptides with strong affinities for the eight most common human MHC Class II HLA-DRB1* allotypes. In order to identify binding peptides in the major grass allergens Rye Lol p 1, Rye Lol p Va, p Vb, p 5a and p 5b, Bermuda Cyn d 1 and Timothy Phl p 5, an *in silico* approach known as "peptide threading" was employed using the commercially available EpiMatrix algorithm (EpiVax Inc.) This is a bioinformatic analysis of peptides from a sequence for the potential to be accommodated within the binding groove of MHC class II HLA-DR molecules. EpiMatrix is a matrix-based algorithm that ranks 9 amino acid long segments, overlapping by 8 amino acids, from any polypeptide sequence by estimated probability of binding to each of the selected MHC molecules. (De Groot et al., AIDS Research and Human Retroviruses 13:539-41 (1997)). The procedure for developing matrix motifs was published by Schafer et al, 16 Vaccine 1998 (1998). In this Example, binding potential for HLA DR1, DR3, DR4, DR7, DR8, DR11, DR13 and DR15 is assessed. Putative MHC ligands are selected by scoring each 9-mer frame in a protein sequence. This score is derived by comparing the sequence of the 9-mer to the matrix of amino acid sequences known to bind to each MHC allele. Retrospective studies have demonstrated that EpiMatrix accurately predicts published MHC ligands (Jesdale et al., in Vaccines '97 (Cold Spring Harbor Press, Cold Spring Harbor, N.Y., 1997)). Successful prediction of peptides which bind to multiple MHC molecules has also been confirmed.

Estimated probability of binding to a selected MHC molecule is calculated by EpiMatrix as follows. The peptides are scored by estimating the relative promotion or inhibition of binding for each amino acid, compared to known MHC binders for a given MHC allele. This information is summed across the peptide and a summary score (EMX score) is assigned to the entire peptide. After comparing the EMX score to the scores of known MHC ligands, EpiMatrix arrives at an "estimated binding probability" (abbreviated as EBP, but not strictly a probability). The EBP describes the proportion of peptides with EpiMatrix scores as high or higher that will bind to a given MHC molecule. EBPs range from 100% (highly likely to bind) to less than 1% (very unlikely to bind).

The polypeptide sequences analysed by EpiMatrix are shown in Table 1:

Table 1

Ber01 ori	SGKAFGAMAKKGQEDKLRKA
Ber02 ori	PKDSDEFIPMKSSWGAIWRIDPKKPLKGP
Ber03 ori	RLTSEGGAHLVQDDVIPANWKPDTVYTSK
Bio01 ori	QKLIEKINAGFKAAVAA
Bio02 ori	AYVATLTEALRVIAGTL
Bio03 ori	KFIPTLVAAVKQAYAAKQAT
Bio04 ori	TALKKAVTAMSEAEKEA
Bio05 ori	NDKFTVFESAFNKALNE
Rye01 ori	LDAKSTWYGKPTGAGPKDNG
Rye02 ori	GHAFGSMAKKGEEQNVRSAG
Rye03 ori	GSNPNYLAILVKYVDGDGDV
Rye04 ori	KESWGAVWRIDTPDKLTGPF
Rye05 ori	DVNAGFKAAVAAAANAPPAD
Rye06 ori	GATPEAKYDAFVTALTEALR
Rye07 ori	GELQIVDKIDAAFKIAATAANAAPTNDKF
Rye08 ori	GAYETYKFIPSLEAAVKQAY
Rye09 ori	PEVKYAVFEAALTKAITAMTQAQKAGKPA
Tim10 ori	PEVKYTVFETALKKAITAMSEAQ

Based on the results of the EpiMatrix analysis of these sequences, core peptides were identified which were predicted to have good MHC binding properties. The selected peptides are shown in Table 2. Peptides highlighted in grey and marked * are not selected peptides. These correspond to the original sequences analysed in EpiMatrix, from which the subsequent selected peptides derive. For example, Ber01 derives from Ber01 ori.

Table 2

Group 1 peptides

SEQ ID NO:	**Peptide name**	**Peptide Sequence**	**Allergen Group**	**Protein of origin**	
74	Ber01 ori	SGKAFGAMAKKGQEDKLRKA	1	Ber Cyn d1	*
1	Ber01	SGKAFGAMAKKGQED	1	Ber Cyn d1	
75	Ber02 ori	PKDSDEFIPMKSSWGAIWRIDPKKPLKGP	1	Ber Cyn d1	*
2	Ber02	FIPMKSSWGA	1	Ber Cyn d1	
3	Ber02A	WGAIWRIDPKKPL	1	Ber Cyn d1	
4	Ber02B	KDSDEFIPMKSSWGAIWR	1	Ber Cyn d1	
5	Ber02C	KSSWGAIWRIDPKKPLK	1	Ber Cyn d1	
6	Ber02D	MKSSWGAIWRIDPKKPLK	1	Ber Cyn d1	
7	Ber02E	MKSSWGAIWRIDPPKPLK	1	Ber Cyn d1	
76	Ber03 ori	RLTSEGGAHLVQDDVIPANWKPDTVYTSK	1	Ber Cyn d1	*
8	Ber03A	IPANWKPDTVYTSK	1	Ber Cyn d1	
9	Ber04	KATFYGSDPRGAAP	1	Ber Cyn d1	
10	Ber05	AYHFDLSGKAFG	1	Ber Cyn d1	
77	Rye01 ori	LDAKSTWYGKPTGAGPKDNG	1	Rye Lol p1	*
11	Rye01	LDAKSTWYGKPTGAG	1	Rye Lol p1	

12	Rye01A	KWLDAKSTWYGKPTGAG	1	Rye Lol p1	
78	Rye02 ori	GHAFGSMAKKGEEQNVRSAG	1	Rye Lol p1	*
13	Rye02	FGSMAKKGEEQNVRSAG	1	Rye Lol p1	
14	Rye02A	HAFGMAKKGEEQNVRSAG	1	Rye Lol p1	
79	Rye03 ori	GSNPNYLAILVKYVDGDGDV	1	Rye Lol p1	*
15	Rye03A	SNPNYLAILVKYVD	1	Rye Lol p1	
80	Rye04 ori	KESWGAVWRIDTPDKLTGPF	1	Rye Lol p1	*
16	Rye04	WGAVWRIDTPDKL	1	Rye Lol p1	
17	Rye04A	KESWGAVWRIDTPDKL	1	Rye Lol p1	
18	Rye04B	KESWGAVWRIDTPDKLGP	1	Rye Lol p1	
19	Rye12	APYHFDLSGHAFGS	1	Rye Lol p1	

Group 5 peptides

81	Bio02 ori	AYVATLTEALRVIAGTL	5	Rye Lol p 5b	*
28	Bio02A	KYDAYVATLTEALR	5	Rye Lol p 5b	
82	Bio03 ori	KFIPTLVAAVKQAYAAKQAT	5	Rye Lol p 5b	*
29	Bio03A	KFIPTLVAAVKQAYAAKQ	5	Rye Lol p 5b	
30	Bio03B	YKFIPTLVAAVKQAYAAKQ	5	Rye Lol p 5b	
83	Bio04 ori	TALKKAVTAMSEAEKEA	5	Rye Lol p 5b	*
31	Bio04A	LKKAVTAMSEAEK	5	Rye Lol p 5b	
32	Bio04B	PETALKKAVTAMSEAEK	5	Rye Lol p 5b	
84	Bio05 ori	NDKFTVFESAFNKALNE	5	Rye Lol p Va	*
33	Bio05B	KFTVFESAFNKALNE	5	Rye Lol p Va	

85	Rye05 ori	DVNAGFKAAVAAAANAPPAD	5	Rye Lol p Va	*
34	Rye05A	FKAAVAAAANAPPADKFK	5	Rye Lol p Va	
35	Rye05C	NAGFKAAVAAAANAPPK	5	Rye Lol p Va	
86	Rye06 ori	GATPEAKYDAFVTALTEALR	5	Rye Lol p Va	*
36	Rye06A	KYDAFVTALTEALR	5	Rye Lol p Va	
37	Rye06B	PEAKYDAFVTALTEALR	5	Rye Lol p Va	
87	Rye07 ori	GELQIVDKIDAAFKIAATAA NAAPTNDKF	5	Rye Lol p Va	*
38	Rye07A	GELQIVDKIDAAFK	5	Rye Lol p Va	
39	Rye07B	KIPTGELQIVDKIDA	5	Rye Lol p Va	
40	Rye07G	FKIAATAANAAPTNDK	5	Rye Lol p Va	
41	Rye07H	AFKIAATAANAAPTNDK	5	Rye Lol p Va	
88	Rye08 ori	GAYETYKFIPSLEAAVKQAY	5	Rye Lol p Va	*
42	Rye08	YKFIPSLEAAVKQAY	5	Rye Lol p Va	
43	Rye08A **	ETYKFIPSLEAAVKQAY	5	Rye Lol p Va	
44	Rye08B	DSYKFIPTLVAVK	5	Rye Lol p Va	
89	Rye09 ori	PEVKYAVFEAALTKAITAMT QAQKAGKPA	5	Rye Lol p Va	*
45	Rye09A	LTKAITAMTQAQKAGK	5	Rye Lol p Va	
46	Rye09B	PEVKYAVFEAALTKAIT	5	Rye Lol p Va	
47	Rye09D	KYAVFEAALTKAITAMT	5	Rye Lol p Va	
48	Rye11	DKFKIFEAAFSESSK	5	Rye Lol p Va	
49	Rye13	TPLRRTSSRSSRP	5	Rye Lol p Va	
50	Rye14	DVAYKAAEAHPRGQ	5	Rye Lol p Va	
51	Rye15	ALRVIAGTLEVHA	5	Rye Lol p Vb	
52	Rye16	FENTFNNAIKVSLG	5	Rye Lol p Vb	

90	Tim10 ori	PEVKYTVFETALKKAITAMSEAQ	5	Tim Phl p5	*
53	Tim10B	KYTVFETALKKAITAMSE	5	Tim Phl p 5	
54	Tim10C	LKKAITAMS	5	Tim Phl p 5	
55	Tim10D	PETALKKAITAMS	5	Tim Phl p 5	

Tim = Timothy grass; Rye = Rye grass; Cyn = Bermuda grass

Any peptides indicated above which have an N terminal glutamate (E) or glutamine (Q) residue, for example Rye 08A, may have this residue replaced with pyroglutamate to improve stability during manufacture, without affecting function of the peptide. The data from further testing of these peptides is typically obtained using peptides where such replacement has taken place.

A further EpiMatrix analysis was performed on the entire sequences of three known Timothy grass sequences: Timothy Grass Phl p 1 (NCBI Accession no. 1N10A), Timothy Grass Phl p Va (NCBI Accession no. Q40962), and Timothy Grass Phl p Vb (Accession no. Q40963). This analysis identified further core peptides (and their flanking sequences) which are predicted to have good MHC class-II binding. These sequences are shown below in Tables 3A-C. In each table:

"Residues in main sequence" gives the location of the peptide within the sequences that were analysed. The core peptide (underscored middle amino acids in bold) defines the actual binding sequence that was identified during the analysis. The stabilizing flanks (N-terminal and C-terminal, not bold) were included for use with the core sequence and are typically required to aid manufacture of the peptides. "Number of hits" refers to the number of high predicted binding affinities for all MHC types tested within the sequence. The "EpiMatrix Cluster Score" is derived from the number of hits normalized for the length of the cluster. Cluster Score is thus the excess or shortfall in predicted aggregate MHC binding properties relative to a random peptide standard. A score above 10 is considered to indicate broad MHC binding properties.

Table 3

A) 1N10A – Phl p 1

RESIDUES IN MAIN SEQUENCE (INCLUDING FLANKS)	SEQUENCE	Hydrophobicity	EpiMatrix HITS (EXCLUDING FLANKS)	EpiMatrix CLUSTER SCORE (EXCLUDING FLANKS)	SEQ ID NO:
120 - 142	GDE**QKLRSAGELELQFRRVK**CKY	-1.15	10	13.23	20
157 - 175	NPN**YLALLVKYVNGDG**DVV	0.19	8	14.11	21
191 - 209	KES**WGAIWRIDTPDKL**TGP	-0.85	8	13.79	22
229 - 241	PEG**WKADTSYES**K	-1.77	6	12.78	23

B) Q40962 – Phl p Va

RESIDUES IN MAIN SEQUENCE (INCLUDING FLANKS)	SEQUENCE	Hydrophobicity	EpiMatrix HITS (EXCLUDING FLANKS)	EpiMatrix CLUSTER SCORE (EXCLUDING FLANKS)	SEQ ID NO:
42 - 60	IEK**INAGFKAALAGAG**VQP	0.41	8	13.04	56
55 - 78	GAG**VQPADKYRTFVATFGPAS**NKA	-0.32	12	17.23	57
98 - 122	ALT**SKLDAAYKLAYKTAEGATP**EAK	-0.38	11	14.26	58
164 - 184	IEK**VDAAFKVAATAANAA**PAN	0.37	9	12.44	59
206 - 226	YES**YKFIPALEAAVKQAY**AAT	0.04	8	14.18	60
232 - 253	EVK**YTVFETALKKAITAMS**EAQ	-0.06	12	17.18	61

C) Q40963 – Phl p Vb

RESIDUES IN MAIN SEQUENCE (INCLUDING FLANKS)	SEQUENCE	Hydrophobicity	EpiMatrix HITS (EXCLUDING FLANKS)	EpiMatrix CLUSTER SCORE (EXCLUDING FLANKS)	SEQ ID NO:
49 - 69	DIN**VGFKAAVAAAASVPA**ADK	0.63	13	21.17	62
115 - 138	FDS**FVASLTEALRVIAGALEV**HAV	1.10	11	15.59	63
158 - 176	IDK**IDAAFKVAATAAA**TAP	0.66	8	13.93	64

206 - 232	IPS**LEAAVKQAYAATVAAAPQ VKY**AVF	0.69	11	12.1	65
229 - 247	YAV**FEAALTKAITAMS**EVQ	0.66	9	14.1	66

Example 2

Homology search

The sequences of each of the peptides identified above as MHC Class II-binding were used to probe the sequence of alternative proteins in the grass allergen group from which the parent sequence derived. For example, peptide Rye01 is from Lol p 1, therefore the sequence of Rye01 was used to probe for conserved sequences in Group 1 from other grass species, in particular Timothy. The results of this analysis are shown below for the residues of Rye Lol p 1 as indicated, compared with corresponding sequences from Timothy Phl p 1 and Bermuda Cyn d 1:

Rye 19-38: LDAKSTWYGKPTGAGPKDNG (RYE 01 ori)
Timothy LDAKSTWYGKPTGAGPKDNG

Rye 109-128: GHAFGSMAKKGEEQNVRSAG (Rye 02 ori)
Timothy GHAFGAMAKKGDEQKLRSAG
Cyn d 1 109-128: SGKAFGAMAKKGQEDKLRKA

Rye 154-173: GSNPNYLAILVKYVDGDGDV (Rye03 ori)
Timothy GSNPNYLALLVKYVNGDGDV

Rye 190-209: KESWGAVWRIDTPDKLTGPF (Rye04 ori)
Timothy GKDKWIELKESWGAIWRIDTPDKLTGPF
Cyn d 1 181-209 PKDSDEFIPMKSSWGAIWRIDPKKPLK

Cyn d 1 217-241 EGGAHLVQDDVIPANWKPDTVYTSK
Timothy EGGTKTEAEDVIPEGWKADTSYESK

Similarly, shown below are results for the residues of Rye Lol p 5 as indicated, compared with corresponding sequences from Timothy Phl p5 variants as indicated:

Rye 37-56:	DVNAGFKAAVAAAANAPPAD	(Rye 05 ori)
Phl p 5a	KINAGFKAALAGAGVQPAD	
Phl p Va	KINAGFKAALAGAGVQPAD	
Phl p 5	KINDGFKAALAAAAGVPPAD	
Phl p Vb	DINVGFKAAVAAAASVPAAD	
Phl p Vb	DINVGFKAAVAAAASVPAAD	

Rye 100-119:	GATPEAKYDAFVTALTEALR	(Rye 06 ori)
Phl p 5a	GATPEAKYDAYVATLSEALR	
Phl p Va	GATPEAKYDAYVATLSEALR	
Phl p 5	GATPEAKYDAYVATLSEALR	
Phl p Vb	GATPEAKFDSFVASLTEALR	
Phl p Vb	GATPEAKFDSFVASLTEALR	

Rye 145-164:	GELQIVDKIDAAFKIAATAA	(from Rye 07 ori)
Phl p 5a	GELQVIEKDAAFKVAATAA	
Phl p Va	GELQVIEKVDAAFKVAATAA	
Phl p 5	GELQFIEKVDSALKVAATAA	
Phl p Vb	GELQIIDKIDAAFKVAATAA	
Phl p Vb	GELQIIDKIDAAFKVAATAA	

Rye 154-173:	DAAFKIAATAANAAPTNDKF	(from Rye 07 ori)
Phl p 5a	DAAFKVAATAANAAPANDKF	
Phl p Va	DAAFKVAATAANAAPANDKF	
Phl p 5	DSALKVAATAANAAAANDKF	
Phl p Vb	DAAFKVAATAAATAPADDKF	
Phl p Vb	DAAFKVAATAAATAPADDKF	

Rye 190-209:	GAYETYKFIPSLEAAVKQAY	(Rye 08 ori)
Phl p 5a	GAYESYKFIPALEAAVKQAY	
Phl p Va	GAYESYKFIPALEAAVKQAY	
Phl p 5	GAYESYKFIPALEAAVKQAY	
Phl p Vb	GAYDTYKCIPSLEAAVKQAY	
Phl p Vb	GAYDTYKCIPSLEAAVKQAY	

Rye 217-236:	PEVKYAVFEAALTKAITAMT	(from Rye 09 ori)
Phl p 5a	PEVKYTVFETALKKAITAMS	
Phl p Va	PEVKYTVFETALKKAITAMS	
Phl p 5	PEVKYTVFETALKKAITAMS	
Phl p Vb	PEVKYTVFETALKKAITAMS	

Phl p Vb	AEVKYAVFEAALTKAITAMS

Rye 226-245: ori)	AALTKAITAMTQAQKAGKPA (from Rye 09
Phl p 5a	TALKKAITAMSEAQKAAKPA
Phl p Va	TALKKAITAMSEAQKAAKPA
Phl p 5	TALKKAITAMSEAQKAAKPA
Phl p Vb	AALTKAITAMSEVQKVSQPA
Phl p Vb	AALTKAITAMSEVQKVSQPA

Based on the sequences from Timothy grass proteins which were highly conserved with the Rye sequences selected in Example 1, additional peptides derived from these sequences were predicted as having good MHC binding properties. These additional peptides are shown in Table 4.

Table 4

Group 1 peptides

SEQ ID NO:	**Peptide name**	Peptide Sequence	**Group**	**Protein**
24	Tim02	FGAMAKKGDEQKLRSAG	1	Tim Phl p 1
25	Tim02A	HAFGAMAKKGDEQKLRSAG	1	Tim Phl p 1
26	Tim03A	SNPNYLALLVKYVNGD	1	Tim Phl p 1
27	Tim04A	WGAIWRIDTPDKL	1	Tim Phl p 1

Group 5 peptides

67	Tim05A	FKAAVAAAASVPAADKFK	5	Tim Phl p 5
68	Tim06A	KFDSFVASLTEALR	5	Tim Phl p 5
69	Tim07B	KIPAGELQIIDKIDA	5	Tim Phl p 5
70	Tim07G	FKVAATAANAAPANDK	5	Tim Phl p 5
71	Tim08	YKFIPALEAAVKQAY	5	Tim Phl p 5
72	Tim08A	PEESYKFIPALEAAVKQAY	5	Tim Phl p 5
73	Tim09A	LTKAITAMSEVQKVSQ	5	Tim Phl p 5

Example 3

In vitro binding analysis

The peptides identified as being potential MHC Class II-binding are pre-screened for solubility in an aqueous, acidic milieu and the peptides are tested in an in vitro MHC Class II binding assay.

Methods

The assay employed is a competitive MHC class II binding assay, wherein each peptide is analysed for its ability to displace a known control binder from each of the human MHC class II allotypes investigated. The allotypes and control peptides used in this study are typically those shown below:

Allotype	**Control Peptide**	**Sequence**
DRB1*0301	Myco. tuberculosis/leprae hsp 65 2-16	AKTIAYDEEARRGLE
DRB1*1101	Influenza haemagglutinin 307-319	PKYVKQNTLKLAT
DRB1*1501	Human myelin basic protein 85-99	ENPVVHFFKNIVTPR

Control peptides used in the in vitro binding assays

Each of the peptides from Tables 2 to 4 (excluding those marked *) are analysed in the competition assay and screened for relative binding compared to the control peptides. Due to the nature of the competitive assay the data for each peptide is determined as a ratio of its own IC50 to that of the control peptide. Thus, a peptide that has an IC50 value that is parity to the control peptide has an identical binding affinity, while peptides with a ratio less than one have a higher affinity and those with a ratio greater than one have a lower affinity.

Solubility in aqueous solution is an essential criterion for a peptide to be an effective therapeutic agent. Therefore, as a consequence of the solubility screen very hydrophobic peptides with a high frequency of large hydrophobic amino acid residues in multiple binding registers will be eliminated. This is a characteristic of promiscuous HLA-DRB1* binders. Peptides which bind to one or more of the MHC Class II allotypes are identified. It would be expected that such peptides would have the ability to bind similar allotypes that have not been tested through the homology of MHC structures.

Example 4

The following method is applied to the same peptides as in Example 3.

Cell proliferation assay

The cell proliferation assay is performed on PBMC's ($140x10^6$ cells required for all parameters to be tested). Proliferation is measured by the incorporation of the radiolabelled compound 3H-thymidine. In more detail, 100µl of the appropriate antigen or peptide concentration is distributed into the appropriate wells of 96 well plates. The plates are then placed into a humidified 5% CO2 incubator set at 37oC for a maximum of 4 hours. PBMC's isolated as described above are prepared to a concentration of $2x10^6$ cells/ml in complete medium at room temperature. 100µl of cell solution is then distributed into each of the wells of the 96 well plates containing antigen/peptide. The plates are then incubated for 6 to 8 days. The cultures are pulsed with tritiated thymidine solution by adding 10µl of tritiated thymidine stock solution (1.85MBq/ml in serum-free RPMI medium) to each well. The plates are then returned to the incubator for between 8 and 16 hours. Cultures are then harvested using a Canberra Packard FilterMate 196 cell harvester. Dried filter mats are counted using an appropriate beta scintillation counter.

Counts from wells containing peptide are compared statistically to wells containing media alone (12 wells per group). The non-parametric Mann-Whitney test is used. The same statistical test is used for all subjects. A statistically significant difference between media only wells and peptide-stimulated wells is considered a positive stimulation of PBMC's by the peptide.

Example 5

59 peptides identified by the EpiMatrix analysis of Example 1 that encompassed one or more epitopes predicted to bind to at least 5/8 MHC Class II alleles (HLA DR01, 03, 04, 07, 08, 11, 13, 15) were selected for further studies. In many cases the epitopes were predicted to bind all 8 of these alleles. Some sequences had two or more overlapping epitopes or non-overlapping but close epitopes binding to the same or different MHC Class II alleles. The selected peptides are shown in Tables 5A and 5B below.

44 peptides were tested for activity in the *in vitro* T cell cytokine release assay described using peripheral blood mononuclear cells (PBMCs) from 48 grass

allergic individuals. Peripheral blood mononuclear cells (PBMCs) were isolated from heparinised blood by Ficoll density gradient centrifugation. Results are shown in Table 5A. Another group of 15 peptides were tested in 28 grass allergic subjects. Results are shown in Table 5B. The subjects were from Hamilton and surrounding area in Ontario, Canada. The peptides were tested for stimulation of production of Interferon gamma (IFN-gamma), Interleukin-10 (IL-10) and Interleukin-13 (IL-13) in the supernatants of the PBMC cultures.

Cytokine release assay

Cytokine secretion profiles from PBMC's were analysed in response to the peptide stimulation. Supernatants from the cytokine release assay were tested for the presence of 3 cytokines, IFN-γ, IL-10 and IL-13, using ELISA assays. The presence of all 3 cytokines was assayed using a multiplex bead array(Luminex Corporation). The cytokine release assay typically required 40×10^6 PBMC's per subject. In more detail, 250µl of a 200µg/ml solution of the appropriate antigen or peptide concentration was distributed into the appropriate wells of 48 well plates. Plates were then incubated in a humidified 5% CO_2 incubator at 37°C for a maximum of 4 hours. 250µl of a 5×10^6 cell/ml PBMC suspension is then added to each well and the plates returned to the incubator for 5 days. Following stimulation, samples of culture supernatant were harvested for testing by multiplex bead assay according to standard protocols. Typically, the samples were harvested into 3 aliquots and frozen until the ELISA assays were performed..

A positive result for stimulation of cytokine secretion was taken where the reading was greater than four times the control well, where no peptide was added. Peptides giving a positive result for one or more cytokines in more than 18 out of the 48 subjects in the first group or 9 out of the 28 subjects in the second group were deemed to be particularly useful in the treatment of grass allergy. 20 of the 44 peptides tested in the first group of 48 subjects, and 8 of the 15 peptides tested in the second group of 28 subjects fulfilled the above criteria.

Table 5A shows the number of positives for the three cytokines out of the group of 48, and Table 5B shows the number of positives for the three cytokines out of the group of 28. Preferred peptides fulfilling the criteria defined above are highlighted in bold.

Table 5A

Peptide	IFN-γ +ve/48	IL-13 +ve/48	IL-10 +ve/48	>18/48 +ve for one or more cytokine?
Ber01	35	22	34	Yes
Ber02	26	21	15	Yes
Ber02A	17	15	7	No
Ber02B	22	17	3	Yes
Ber02C	29	18	9	Yes
Ber03A	8	7	23	Yes
Bio02A	15	12	31	Yes
Bio03A	26	19	9	Yes
Bio04A	28	16	37	Yes
Bio04B	22	16	27	Yes
Bio05B	8	8	34	Yes
Rye01	12	5	2	No
Rye01A	2	4	4	No
Rye02	4	5	1	No
Rye02A	12	6	1	No
Rye03A	3	5	0	No
Rye04	6	3	1	No
Rye04A	8	4	2	No
Rye05A	13	10	3	No
Rye05C	20	19	12	Yes
Rye06A	11	15	5	No
Rye06B	11	7	5	No
Rye07A	8	3	25	Yes
Rye07B	10	3	1	No
Rye07G	7	3	2	No
Rye07H	10	8	4	No
Rye08	9	6	2	No
Rye08A	18	9	32	Yes

Rye09A	6	5	11	No
Rye09B	28	24	16	Yes
Tim02	16	6	3	No
Tim02A	6	9	2	No
Tim03A	9	9	4	No
Tim04A	16	4	31	Yes
Tim05A	15	12	9	No
Tim06A	17	11	11	No
Tim07B	23	18	41	Yes
Tim07G	19	20	10	Yes
Tim08	16	17	14	No
Tim08A	21	10	8	Yes
Tim10B	16	24	22	Yes
Tim10C	6	4	3	No
Tim10D	28	8	3	Yes

Table 5B

Peptide	IFN-γ +ve/28	IL-13 +ve/28	IL-10 +ve/28	≥9/28 +ve for one or more cytokine?
Bio02D	21	8	21	Yes
Bio02E	13	2	24	Yes
Bio04	12	5	8	Yes
Bio05	11	5	1	Yes
Bio03B	13	8	4	Yes
Rye04B	3	6	0	No
Rye07A	1	4	1	No
Rye08B	2	3	1	No
Rye09D	6	4	13	Yes
Rye11	4	10	3	Yes
Rye12	10	8	5	Yes
Rye13	6	1	0	No

Rye14	5	3	0	No
Rye15	1	0	1	No
Rye16	4	3	4	No

Example 6

Ranking criteria for individual grass peptides

The 28 peptides which were selected as being particularly useful in the treatment of grass allergy on the basis of the criteria used in Example 5 were further evaluated in order to compare their characteristics. This involved calculation of the cumulative response observed to all 3 cytokines for each peptide i.e the total score (sum of the number of responders for the three cytokines). Pharmaceutical development aspects for each peptide were also considered on the basis of physical and chemical properties, in particular solubility, pI and hydrophobicity index (GRAVY). Epimatrix software was also used to predict binding strength to MHC class II HLA DR alleles, with values shown as high (1%) medium (5%) and low (10%) affinity for each specific MHC class II HLA DR allele shown.

The results of this analysis for 14 particularly preferred peptides are shown in Table 6. These particularly preferred peptides are allocated an internal ranking order of 1 to 14 which corresponds to the Inventors evaluation of their relative utility for the treatment of grass allergy. The 14 peptides were ranked according principally to the total score (sum of the number of responders for the three cytokines) with some weighting placed on the IFN-gamma response. Account was also taken of pharmaceutical development aspects and MHC coverage, as outlined above.

Table 6

Peptide	Total score	Pi	GRAVY	Epimatrix analysis of MHC binding affinity			Solubility mg/ml	RANK
				1%	5%	10%		
Ber01	91	8.22	-0.94	08, 11	01, 08, 15	03,04,08	>20	1

Ber02	62	8.75	-0.26		01, 04. 08, 11, 13	11,15	>20	5
Ber02B	42	6.12	-0.75		01, 04. 08, 11, 13	11,15	>20	13
Ber02C	56	10.46	-0.941	03,07,08	01, 11	04,13,15	>20	6
Bio02A	58	6.07	-0.157	01,04,07	08, 11, 13	03,15	>20	8
Bio03A	54	10.00	0.344	03	01, 03, 04, 08, 11, 13, 15		>20	7
Bio04A	81	8.50	-0.377	04	01, 03, 04, 08, 11, 13		>20	3
Rye05C	51	10.00	0.176	01,04	03, 08, 11, 13	04,15	10	11
Rye08A	58	6.24	-0.194	01,03,04, 11	13, 15	07	>20	9
Rye09B	68	6.56	0.447	01,07	01, 04, 11, 15	03, 08, 13	5	4
Tim04A	51	5.96	-0.408	03,04,07	01, 11	08, 15	2	12
Tim07B	82	4.56	0.107		03, 11, 15	01, 13	0.56	2
Tim07G	49	8.59	-0.062		01, 04, 08, 15	03, 07, 11	>20	14
Tim10B	62	8.43	-0.017	04	01, 03, 04, 08, 11, 13		1.65	10

The order of ranking for particularly preferred grass peptides is thus: 1, Ber01, (SEQ ID NO:1), Cyn d 1; 2, Tim07B (SEQ ID NO: 69), Phl p 5; 3, Bio04A (SEQ ID NO: 31), Lol p 5; 4, Rye09B (SEQ ID NO: 46), Lol p 5; 5, Ber02 (SEQ ID NO: 2), Cyn d 1; 6. Ber02C (SEQ ID NO: 5), Cyn d 1; 7, Bio03A (SEQ ID NO: 29), Lol p 5; 8, Bio02A (SEQ ID NO: 28), Lol p 5; 9, Rye08A, (SEQ ID NO: 43), Lol p 5; 10, Tim10B, (SEQ ID NO: 53), Phl p 5; 11, Rye05C (SEQ ID NO: 35), Lol p 5; 12, Tim04A (SEQ ID NO: 27), Phl p 1; 13, Ber02B (SEQ ID NO:4), Cyn d 1; 14, Tim07G (SEQ ID NO: 70), Phl p 5.

Surprisingly, the top ranked peptide, Ber01 and also 3 other peptides in the top 14 (Ber02, Ber02C and Ber02B) were derived from the Bermuda grass allergen Cyn d 1. Bermuda grass is a warm season perennial species adapted to tropical and subtropical climates. It grows best under extended periods of high temperatures, mild winters and moderate to high rainfall. Temperature is the main environmental factor that limits its adaptability to tropical and subtropical areas of the world. The northern limits of Bermuda grass extend into the transitional zone of the United States where low temperatures seldom drop below 10°F. For this reason it would not be expected that Bermuda grass allergens would be the major allergens recognised by subjects in Canada. Furthermore, Perennial ryegrass, although present, is not the most common grass in Canada and 6 of the top 14 peptides (Bio02A, Bio03A, Bio04A, Rye05C, Rye08A, Rye09B) were derived from Perennial rye allergens.

The following is a summary of grass types prevalent in Canada. Almost all forage grasses in Canada are improved cultivars of European species. Different grasses are adapted to grow in different areas of Canada, depending on soil and climate conditions. Timothy (Phleum pratense) is the most widely grown grass outside dry parts of the region, and is a dominant forage grass in eastern Canada. Crested wheatgrass (Agropyron cristatum) is a dominant forage grass in western Canada. Orchard grass (Dactylis glomerata) and Russian wild ryegrass (Elymus junceus) are dominant forage grasses in British Columbia. Bromegrass (Bromus inermis) is grown in eastern Canada and on the Prairies. Kentucky bluegrass (Poa pratensis) is commonly grown in many areas. In terms of prairie grasses, 3-awn grass (Aristida longiseta) is found in arid regions of British Columbia, and wild rice (Zizania aquatica) in eastern Canadian lakes. Certain genera (eg, Arctagrostis and Arctophila) are native to the Canadian Arctic. Turf grasses are developed from species that show desirable characteristics, eg, density of growth, fast growth after seeding, ability to remain green, etc. In Canada cold-hardiness and frequently drought resistance are also important. Popular Canadian lawn grass mixtures often include species of Poa (eg, Kentucky bluegrass, roughstalk bluegrass) and Festuca (especially creeping red fescue, chewing fescue), although other useful species have been developed.

Based on the prevalence of grass types in Canada, the observation that grass allergic individuals of Canadian origin are highly responsive to peptides from Bermuda grass and Perennial rye is unexpected. Such peptides therefore have the potential to have broad utility in treatment of grass allergic individuals worldwide. Also, the peptides which were found to induce high levels of response (ie a high total score) are commonly derived from allergen proteins conventionally described as "minor allergens", e.g Lol p 5 and Phl p 5. The major Timothy and Perennial Rye allergens recognized by IgE antibodies in grass allergic subjects are, respectively, Phl p 1 and Lol p 1. The induction of antibodies to these major allergens in allergic individuals is a T cell dependent process and so it would be expected that the peptides inducing high levels of T cell response would be mainly from Phl p 1 and Lol p 1.

The determination of the top 14 T cell stimulatory peptides from the group of 59 peptides tested in Example 5, and particularly identifying the top 8 peptides which can be used most optimally in combination involved a narrow and specific selection. A narrow subset of combinations were identified from a massive number of initially possible combinations of peptides. The total number of possible combinations for selecting 8 peptides from the top 14 ranked peptides is 3003. This number of combinations (3003) represents a very small proportion of the possible combinations of 8 peptides out of the original group of 73 peptides (13,442,126,049) . The possibility of identifying the top eight ranked peptides by chance is therefore miniscule.

Example 7

Combinations of grass peptides

Peptide combinations based on selections from the top 8 ranked peptides in Table 6 were investigated with a view to identifying optimal vaccines for the treatment of grass allergy. Cytokine assays were performed as in Example 5 for each mix. The results for ten optimal combinations are listed in Table 7. Combination 1 is the most optimal combination and comprises all 8 top ranked peptides. It should be noted that these specific combinations represent a miniscule proportion of the number of possible combinations of peptides originally screened in Examples 1 and 2.

Optimal grass vaccine mixes were selected on the basis of showing a significant release of IFN-γ, IL-10 and IL-13 in a large proportion of the study group of 48 allergic individuals. As such, providing preferred individual grass peptides in combination increases MHC coverage and and provides an optimised product of general utility as a grass vaccine. Optimal grass vaccine mixes were also selected on the basis of manufacturing considerations, including physical and chemical characteristics of each peptide in the combination.

Table 7

Peptide combination	IL-10 +ve/48	IL-13 +ve/48	IFN-γ10 +ve/48
1	47	41	48
2	47	41	48
3	47	39	48
4	46	39	48
5	44	39	47
6	41	39	46
7	47	40	48
8	46	40	48
9	44	40	48
10	40	40	48

Combinations:

1: Ber01; Ber02; Ber02C; Bio02A; Bio03A; Rye09B; Tim07B; Bio04A
2: Ber01; Ber02; Ber02C; Bio02A; Bio03A; Rye09B; Tim07B
3: Ber01; Ber02; Ber02C; Rye09B; Tim07B; Bio04A
4: Ber01; Ber02; Ber02C; Rye09B; Tim07B
5: Ber01; Ber02; Ber02C; Rye09B; Bio04A
6: Ber01; Ber02; Ber02C; Rye09B
7: Ber01; Ber02C; Bio03A; Rye09B; Tim07B; Bio04A
8: Ber01; Ber02C; Rye 09B; Tim07B
9: Ber01; Ber02C; Bio03A; Rye09B; Bio04A
10: Ber01; Ber02C; Bio03A; Rye09B

Combination 1 is the most optimal combination based on cytokine release characteristics and comprises all 8 top ranked peptides. This combination provides peptides derived from three grass allergens, Cyn d1 (Ber01; Ber02; Ber02C) , Lol p 5 (Bio03A; Rye09B, Bio04A) and Phl p 5 (Tim07B). The combination therefore accounts for regional variations in exposure to specific allergens, even though the data from the Canadian study group suggests this may not be an important factor.

It should be noted that each specific optimal combination represents a miniscule proportion of the number of possible combinations of peptides originally screened in the Examples. As outlined above, for example, the eight peptide mix of combination 1 represents one out of 13,442,126,049 potential combinations of the 73 peptides screened in Examples 1 and 2. The optimal combinations each provide a significant release of IFN-γ, IL-10 and IL-13 in ≥39/48 individuals.

It is noteworthy that high MHC coverage is maintained in Combinations 2 to 10 despite significant variation both in the number of peptides and in which specific peptides are included from the top 8 identified in Example 6. It can be seen that even selecting a mix of 4 peptides (Combination 10) still gives 100% coverage for IFN- γ response and 83% coverage for IL-10/IL-13 response. Combination 10 is based on 2 peptides from Bermuda grass and 2 peptides from Perennial Rye grass. The coverage obtained with such a mix is surprising, given both the lack of prevalence of these grasses in Canada, and the fact that peptides from Lol p 1, a major allergen recognised by IgE antibodies in grass allergic individuals are not included.

Example 8

Improving solubility

Two of the top 8 peptides, Rye09B and Tim07B, were identified as having solubility characteristics which could be improved (see Table 6). To improve solubility, various analogues were designed utilising one or more lysine residues at the N- or C-terminus of the peptide. The peptides were assessed in the Epimatrix software to ensure that the modifications had not affected the T cell epitope within the peptide and had not created a neoepitope. Two variant peptides were selected for Rye09B (Rye09B1 & Rye09B2) and Tim07B1 & Tim07B2). The sequences are shown in Table 8 together with the solubility values. The variants of Rye09B are twice as soluble as the native peptide. The variants of Tim07B are more than twenty times as soluble as the native peptide. In addition to improved solubility, both variants also retained their ability to induce T cell cytokine release when tested in a group of 10 subjects. These variants of Rye09B and Tim07B therefore are preferred alternatives to the native peptides, for example in any mix of grass peptides for therapeutic vaccine use.

Table 8

Peptide	Sequence	Solubility(mg/ml)	SEQ ID NO:
Rye09B1	KPEVKYAVFEAALTKAIT	10	91
Rye09B2	KKPEVKYAVFEAALTKAIT	10	92
Tim07B1	KKIPAGELQIIDKIDA	20	93
Tim07B2	KKIPAGELQIIDKIDAK	20	94

Example 9

Selection of a preferred grass vaccine

During trial manufacturing, one peptide from the top ranked peptides present in Combination 1 above (Bio03A) was found to be difficult to manufacture due to having a string of 5 contiguous hydrophobic amino acids. When assessing the impact of not including Bio03A in a grass vaccine, the overall coverage of the remaining seven top ranked peptides present in Combination 1 was analysed for the 48 subjects. In this seven peptide mix (Ber01, Ber02, Ber02C, Bio02A, Rye09B, Tim07B and Bio04A) Tim07B and Rye07B are optionally substituted for the variants Tim07B1 and Rye07B1 having improved solubility.

With the 8 peptides present, including Bio03A, 47/48 subjects (IL-10), 41/48 subjects (IL-13) and 48/48 subjects (IFN-gamma) subjects showed positive cytokine responses. In comparison, with seven peptides present, excluding Bio03A, 47/48 subjects (IL-10), 40/48 subjects (IL-13) and 48/48 subjects (IFN-gamma) showed positive cytokine responses. Therefore it was concluded that there would be little impact of not including Bio03A in a grass vaccine for manufacture.

The response properties of the above peptide combinations was compared with whole grass pollen extract containing Timothy, Perennial Rye, and Bermuda grass pollens (Greer Laboratories) and a further positive control, the mitogen SEB.

The whole grass pollen extract induced cytokine responses in 11/48 (IL-10), 42/48 (IL-13) and 43/48 (IFN-gamma) whilst the other positive control, the mitogen SEB, induced responses in 47/48 (IL-10), 48/48 (IL-13) and 48/48 (IFN-gamma). The seven peptide mix thus provides strong cytokine responses in similar percentages of the population as for whole grass allergen.

The selection of the peptides Ber01, Ber02, Ber02C, Bio02A, Rye09B, Tim07B and Bio04A for a preferred seven peptide grass vaccine was also based on homology considerations. When these seven peptide sequences are compared between different grasses, there is considerable homology in many cases increasing the probability that grass-allergic individuals will respond to the peptides. This means that the peptides have utility even in those subjects whose dominant allergic response is to a grass other than Bermuda, Timothy or Perennial rye. Homologous sequences from other grasses for the above seven peptides are shown as SEQ ID NOs 74 to 90 above. For example, the Ber01 peptide contains the 9 mer epitope FGAMAKKGQ which has close homologues in many other common grasses.

Furthermore, the seven vaccine peptides are derived from both group 1 and group 5 allergens from the three most prevalent grasses (Timothy, Perennial Rye and Bermuda grasses) and include epitopes with complete or significant homology to the other common grasses (Orchard, Velvet, Kentucky blue and Canary). The seven peptide sequences therefore maximise the breadth of coverage of grass pollen allergic individuals making the vaccine suitable for treating all grass pollen allergic individuals.

Example 10

Histamine release assay

The purpose of this assay was to identify whether the preferred seven peptide combination of Example 9 was capable of activating blood basophils (as a surrogate for tissue mast cells) resulting in histamine release that may result in allergic reactions during therapy. A combination of peptides that induces histamine release frequently may be considered unsuitable for use as a peptide vaccine.

Histamine release requires the crosslinking of adjacent specific IgE molecules on the surface of the basophil. The peptides being evaluated were small (10 to 18 amino acids in length) and should not, therefore, possess significant tertiary structure that would enable them to retain the conformation of an IgE-binding epitope of the whole molecule. Furthermore, peptide monomers in solution, even if they are bound by IgE, should not be able to crosslink adjacent IgE molecules.Histamine release from peripheral blood basophils isolated from peripheral whole blood obtained from grass allergic subjects was evaluated. Peripheral blood basophils were used as a surrogate for tissue mast cells which were not practical to assay. The assay required $3\text{x}10^6$ peripheral blood mononuclear cells (PBMC) per subject. PBMCs were incubated in vitro with the seven grass peptides from Example 9 in combination. Histamine release in response to whole Grass pollen allergen extract containing Timothy, Perennial Rye, and Bermuda grass pollens (Greer Laboratories) was included as a control. A positive control, representing total histamine release, generated by freeze/thawing the cells twice was also included in each assay.

Histamine concentrations were measured by ELISA and results expressed as a percentage of the positive control (% positive control). The assay was performed using the Immunotech Histamine Release Immunoassay kit according to the manufacturer's instructions. Following the *in vitro* challenge of PBMCs with peptides, peptide mixes, whole allergen or buffer in microtitre plate wells, supernatants were removed and the histamine in the samples converted to acyl histamine. Acylated samples were tested by a competitive acyl histamine ELISA.

Peptides were assayed for their ability to induce histamine release over a 5 log10 range (1 to 10,000 ng/mL). The concentration range assayed was selected based on theoretical *in vivo* doses of peptide that may be achieved during therapy. Based on delivery of peptides by intradermal injection, high local peptide concentrations of up to 10μg/mL per peptide could be present. Although unlikely, there is a risk that the full dose may be injected into the bloodstream. In this unlikely event, the maximum clinical dose of 20 μg (12 nmole) of each peptide entering a blood volume of 5 litres, would result in a theoretical maximum blood concentration of 4.0 ng/mL. This is at the lower end of the histamine release assay dose range and 2000 times lower than the top concentration used in the assay.

A whole grass allergen preparation containing Timothy, Perennial Rye and Bermuda grass pollens (Greer Laboratories) was used as a control for histamine release over a 5 log10 range from 10 to 100,000 ng/mL. A negative control for spontaneous histamine release was generated by incubating cells in buffer only.

Single measurements were performed for each dilution. After completion of the ELISA, individual histamine levels were determined by interpolation from the standard curve generated in the ELISA assay. Results from samples were adjusted to allow for dilution. Where two or more consecutive dilutions of a peptide/allergen preparation elicited >15% of the total histamine release seen in the freeze thawed positive control (>15% of positive control), or where a single value of >15% of positive control was achieved at the highest concentration tested (10 µg/mL for peptides), this was considered a "positive histamine release".

A total of 45 histamine release assays were completed during the study. Of these, 3 assays were rejected, due to unacceptably high levels (>15%) of histamine release in the medium plus buffer negative control wells or no response at all in the positive control wells. Therefore a total of 42 subjects were included in the analysis. The study findings are summarised in Table 9.

Protein Concentration (µg/mL)	Subjects with positive histamine release (>=15%)	Mean histamine release (% pos control) n=42	Range (% pos control)
Seven peptide combination * (10)	0/42	0	0-4
Whole grass (100)	32/42	41	2-152
Whole grass (0.01)	21/42	24	0-84

* Seven peptide combination: Ber01, Ber02, Ber02C, Bio02A, Rye09B1, Tim07B1 and Bio04A.

The whole grass allergen preparation induced 15% or higher histamine release in 32/42 (76%) of subjects at 100 ug/mL. Even at the lowest concentration of 10 ng/mL, the whole allergen induced high levels of histamine release in 21/42 individuals (50%).

In contrast, the seven peptide combination failed to elicit significant histamine release in any of the 42 subjects tested, even at the highest concentration for which data is shown, where each peptide was present at 10 µg/mL. This is a concentration 1000 fold higher than the concentration of whole allergen still giving very high levels of histamine release in over half of the subjects (10 ng/mL). The seven peptide combination therefore has negligible potential for causing IgE mediated reactions even in highly sensitive individuals.

Given the large excess of peptide dose tested in this assay compared to likely concentrations of the peptides following clinical dosing of a grass vaccine, it is not anticipated that administration of the seven peptide combination would cause significant histamine release either by IgE-mediated or direct peptide-mediated basophil or mast cell activation and degranulation. The histamine release data indicate that the seven peptide combination does not induce the activation of basophils and therefore has a very low potential for inducing IgE-mediated acute allergic reactions in grass allergic individuals, either systemically or locally in the skin.

CLAIMS

1. A composition suitable for use in preventing or treating allergy to grass pollen by tolerisation comprising:

(a) at least one of the polypeptides Tim07B (KIPAGELQIIDKIDA), Tim 10B (KYTVFETALKKAITAMSE), Tim 04A (WGAIWRIDTPDKL), Tim 07G (FKVAATAANAAPANDK) or a variant of any thereof;

(b) at least one of the polypeptides Ber01 (SGKAFGAMAKKGQED), Ber02 (FIPMKSSWGA), Ber02C (KSSWGAIWRIDPKKPLK) and Ber 02B KDSDEFIPMKSSWGAIWR or a variant of any thereof; and

(c) at least one of the polypeptides Bio04A (LKKAVTAMSEAEK), Rye09B (PEVKYAVFEAALTKAIT), Bio02A (KYDAYVATLTEALR), Bio03A (KFIPTLVAAVKQAYAAKQ), Rye 08A (ETYKFIPSLEAAVKQAY), Rye 05C (NAGFKAAVAAAANAPPK), or a variant of any thereof,

wherein said variant is:

I) a longer polypeptide of up to 30 amino acids in length which comprises the sequence of the corresponding polypeptide specified in (a), (b) or (c), or

II) a polypeptide of 9 to 30 amino acids in length which comprises a sequence that has at least 65% homology to the sequence of the corresponding polypeptide specified in (a), (b) or (c), and that is capable of tolerising to said corresponding polypeptide; or

III) a polypeptide of length 9 to 30 amino acids which comprises a sequence of at least 9 contiguous amino acids of the sequence of the corresponding polypeptide specified in (a), (b) or (c), or a sequence that has at least 65% homology to said at least 9 contiguous amino acids, which sequence of at least 9 contiguous amino acids or homologous sequence is capable of tolerising to said corresponding polypeptide.

2. A composition according to claim 1 comprising:
a) the polypeptide Tim07B (KIPAGELQIIDKIDA) or a variant thereof,
b) the polypeptide Ber01 (SGKAFGAMAKKGQED) or a variant thereof, and
c) the polypeptide Bio04A (LKKAVTAMSEAEK) or a variant thereof.

3. A composition suitable for use in preventing or treating allergy to grass pollen by tolerisation comprising at least four different polypeptides selected from:
(a) Tim07B (KIPAGELQIIDKIDA) or a variant thereof;
(b) Ber01 (SGKAFGAMAKKGQED) or a variant thereof;
(c) Bio04A (LKKAVTAMSEAEK) or a variant thereof;
(d) Rye09B (PEVKYAVFEAALTKAIT) or a variant thereof;
(e) Ber02 (FIPMKSSWGA) or a variant thereof;
(f) Ber02C (KSSWGAIWRIDPKKPLK) or a variant thereof;
(g) Bio03A (KFIPTLVAAVKQAYAAKQ) or a variant thereof; and
(h) Bio02A (KYDAYVATLTEALR) or a variant thereof;
wherein said variant is:
I) a longer polypeptide of up to 30 amino acids in length which comprises the sequence of the corresponding polypeptide specified in (a) to (h), or
II) a polypeptide 9 to 30 amino acids in length which comprises a sequence that has at least 65% homology to the sequence of the corresponding polypeptide specified in (a) to (h), and that is capable of tolerising to said corresponding polypeptide; or
III) a polypeptide of length 9 to 30 amino acids which comprises a sequence of at least 9 contiguous amino acids of the sequence of the corresponding polypeptide specified in (a) to (h), or a sequence that has at least 65% homology to said at least 9 contiguous amino acids, which sequence of at least 9 contiguous amino acids or homologous sequence is capable of tolerising to said corresponding polypeptide.

4. A composition according to claim 3 comprising

(a) the polypeptide Tim07B (KIPAGELQIIDKIDA) or a variant thereof;

(b) at least one of the polypeptides of Ber01 (SGKAFGAMAKKGQED), Ber02 (FIPMKSSWGA), and Ber02C (KSSWGAIWRIDPKKPLK) or a variant of any thereof; and

(c) at least one of the polypeptides of Bio04A (LKKAVTAMSEAEK), ye09B (PEVKYAVFEAALTKAIT), Bio02A (KYDAYVATLTEALR), and Bio03A (KFIPTLVAAVKQAYAAKQ) or a variant of any thereof; and

(a) at least one additional polypeptide of b) or c) not selected above.

5. A composition according to claim 4, comprising the polypeptide Tim07B (KIPAGELQIIDKIDA) or a variant thereof, the polypeptide Ber01 (SGKAFGAMAKKGQED) or a variant thereof, the polypeptide Bio04A (LKKAVTAMSEAEK) or a variant thereof, and at least one additional polypeptide of b) or c) not selected above.

6. The composition according to any one of the preceding claims further comprising one or more polypeptides of any of SEQ ID NOs 1 to 73 as shown in Tables 2 to 4 or variants thereof, not previously selected above.

7. The composition according to any one of the preceding claims, wherein the composition:

- is capable of tolerising at least 50% or at least 60% of a panel of grass pollen allergic individuals in the population, and/or
- comprises at least one further polypeptide up to a total of fourteen different polypeptides, wherein the further polypeptides:

(a) comprise a sequence having at least 65% sequence identity to at least 9 or more contiguous amino acids in any of SEQ ID NOs: 1 to 73 not selected above; and

(b) are 9 to 30 amino acids in length.

8. The composition according to any one of the preceding claims, comprising at least one said polypeptide which is 9 to 20 or 13 to 17 amino acids in length.

9. A composition according to any one of the preceding claims which comprises the polypeptides of any one of Combinations 1 to 10 as set forth in Table 7, wherein optionally one or more of said polypeptides can be substituted for a variant thereof as defined in 1 (I) or (II).

10. A composition according to any one of the preceding claims which comprises the polypeptides:

(a) Tim07B1 (KKIPAGELQIIDKIDA);
(b) Ber01 (SGKAFGAMAKKGQED);
(c) Bio04A (LKKAVTAMSEAEK);
(d) Rye09B1 (KPEVKYAVFEAALTKAIT);
(e) Ber02 (FIPMKSSWGA);
(f) Ber02C (KSSWGAIWRIDPKKPLK); and
(g) Bio02A (KYDAYVATLTEALR)

11. The composition according to any one of the preceding claims, wherein one or more of the polypeptides have one or more modifications selected from the following:

(i) N terminal acetylation;
(ii) C terminal amidation;
(iii) one or more hydrogens on the side chain amines of Arginine and/or Lysine replaced with a methylene group;
(iv) glycosylation; and
(v) phosphorylation.

12. The composition according to any one of the preceding claims wherein at least one of the peptides has been engineered to be soluble such that it comprises:

(i) N terminal to the residues of the peptide which flank a T cell epitope: one to six contiguous amino acids corresponding to the two to six contiguous amino acids immediately N terminal to said residues in the sequence of the protein from which the peptide derives; and/or

(ii) C terminal to the residues of the peptide which flank a T cell epitope: one to six contiguous amino acids corresponding to the one to six contiguous amino acids immediately C terminal to the said residues in the sequence of the protein from which the peptide derives; or

(iii) both N and C terminal to the residues of the peptide which flank a T cell epitope, at least one amino acid selected from arginine, lysine, histidine, glutamate and aspartate,

wherein the polypeptide has a solubility of at least 3.5mg/ml and the T cell epitope has a solubility of less than 3.5mg/ml.

13. The composition according to any one of the preceding claims wherein at least one of the peptides has been engineered to be soluble such that additionally:

(i) any cysteine residues in the native sequence of the peptide are replaced with serine or 2-aminobutyric acid; and /or

(ii) hydrophobic residues in the up to three amino acids at the N or C terminus of the native sequence of the peptide, which are not comprised in a T cell epitope, are deleted; and/or

(iii) any two consecutive amino acids comprising the sequence Asp-Gly in the up to four amino acids at the N or C terminus of the native sequence of the peptide, which are not comprised in a T cell epitope, are deleted; and/or

(iv) one or more positively charged residues are added at the N- and/or C-terminus.

14. The composition according to any one of the preceding claims wherein each polypeptide has a concentration in the range of 0.03 to 200 nmol/ml, 0.3 to 200 nmol/ml, 50 to 200 nmol/ml or 30 to 120 nmol/ml.

15. A composition for use in preventing or treating allergy to grass pollen by tolerisation comprising at least one polynucleotide sequence which when expressed causes the production of a composition as defined in any one of claims 1 to 13.

16. A vector for use in preventing or treating allergy to grass pollen by tolerisation comprising four or more polynucleotide sequences which each encode a different polypeptide as defined in any one of claims 1 to 13.

17. A product comprising:

(a) the polypeptide Tim07B (KIPAGELQIIDKIDA), Tim 10B (KYTVFETALKKAITAMSE), Tim 04A (WGAIWRIDTPDKL), Tim 07G (FKVAATAANAAPANDK) or a variant of any thereof as defined in claim 1 (I) or (II);

(b) at least one of the polypeptides Ber01 (SGKAFGAMAKKGQED) Ber02 (FIPMKSSWGA), Ber02C (KSSWGAIWRIDPKKPLK) and Ber02B KDSDEFIPMKSSWGAIWR or a variant of any thereof as defined in claim 1 (I) or (II); and

(c) at least one of the polypeptides Bio04A (LKKAVTAMSEAEK), Rye09B (PEVKYAVFEAALTKAIT), and Bio02A (KYDAYVATLTEALR), Bio03A (KFIPTLVAAVKQAYAAKQ), Rye 08A (ETYKFIPSLEAAVKQAY), Rye 05C (NAGFKAAVAAAANAPPK) or a variant of any thereof as defined in claim 1 (I) or (II),

wherein each different polypeptide is for simultaneous, separate or sequential use in preventing or treating allergy to grass pollen by tolerisation.

18. A pharmaceutical formulation for use in preventing or treating allergy to grass pollen by tolerisation comprising a composition according to any one of claims 1 to 15; a vector according to claim 16; or a product according to claim 17; and a pharmaceutically acceptable carrier or diluent.

19. The composition, vector or product according to claim 18, formulated for oral administration, topical administration, nasal administration, subcutaneous administration, sublingual administration, intradermal administration, buccal administration, epidermal or patch administration or for administration by inhalation or by injection.

20. The composition as defined in any one of claims 1 to 15 or product as defined in claim 17, additionally comprising a further polypeptide allergen for use in tolerising an individual to the further polypeptide allergen.

21. An in vitro method of determining whether T cells recognize a composition as defined in any one of claims 1 to 14 comprising contacting said T cells with said polypeptide and detecting whether said T cells are stimulated by said polypeptide.

22. A method according to claim 21 which is carried out to determine whether an individual has, or is at risk of having, an allergy to grass pollen.

INTERNATIONAL SEARCH REPORT

International application No
PCT/GB2010/000198

A. CLASSIFICATION OF SUBJECT MATTER
INV. C07K14/415 C07K7/06 C07K7/08 A61K38/04 A61K38/16
A61K39/36
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C07K A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, BIOSIS, CHEM ABS Data, WPI Data, EMBASE, Sequence Search

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y,P	WO 2009/022154 A2 (CIRCASSIA LTD [GB]; HAFNER RODERICK PETER [GB]; LARCHE MARK [CA]) 19 February 2009 (2009-02-19) example 2 page 27, line 29 - page 29 page 31 - page 33 page 48 page 54, paragraph 2 - last paragraph page 73, page 76 -----	1,3,4, 6-9, 11-22
Y,P	WO 2009/022157 A2 (CIRCASSIA LTD [GB]; HAFNER RODERICK PETER [GB]; LAIDLER PAUL [GB]) 19 February 2009 (2009-02-19) sequences 16,19,25,29,31,33,35 ----- -/--	1,3,4, 6-9, 11-22

☒ Further documents are listed in the continuation of Box C. ☒ See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search 31 May 2010	Date of mailing of the international search report 09/06/2010
Name and mailing address of the ISA/ European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Authorized officer Espen, Josée

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO 03/024998 A1 (UNIV MONASH [AU]; O'HEHIR ROBYN [AU]; ROLLAND JENNIFER [AU]) 27 March 2003 (2003-03-27) page 3, last paragraph; claim 9; figure 2; sequences 14,22,23 page 39, last paragraph	1,3,4, 6-9, 11-22
Y	WO 2007/140505 A2 (BIOMAY AG [AT]; VALENTA RUDOLF [AT]; FOCKE-TEJKL MARGARETE [AT]; LINHA) 13 December 2007 (2007-12-13) examples 14-18; table 3; sequences 11,13,14	1,3,4, 6-9, 11-22
Y	WO 96/03106 A2 (UNIV MANITOBA [CA]; MOHAPATRA SHYAM S [CA]) 8 February 1996 (1996-02-08) page 29; claim 7; sequences 19,24	1,3,4, 6-9, 11-22
Y	WO 2006/008018 A1 (MERCK PATENT GMBH [DE]; FIEBIG HELMUT [DE]; WALD MARTIN [DE]; NANDY AN) 26 January 2006 (2006-01-26) page 8, paragraph 2; claim 2; figure 1	1,3,4, 6-9, 11-22
Y	JUTEL ET AL: "Allergen-specific immunotherapy with recombinant grass pollen allergens" JOURNAL OF ALLERGY AND CLINICAL IMMUNOLOGY, MOSBY, INC, US LNKD- DOI:10.1016/J.JACI.2005.06.004, vol. 116, no. 3, 1 September 2005 (2005-09-01), pages 608-613, XP005068191 ISSN: 0091-6749 abstract	1,3,4, 6-9, 11-22
A	SWOBODA INES ET AL: "Mutants of the major ryegrass pollen allergen, Lol p 5, with reduced IgE-binding capacity: candidates for grass pollen-specific immunotherapy." EUROPEAN JOURNAL OF IMMUNOLOGY JAN 2002 LNKD- PUBMED:11782018, vol. 32, no. 1, January 2002 (2002-01), pages 270-280, XP002581444 ISSN: 0014-2980 abstract	1

INTERNATIONAL SEARCH REPORT

International application No.
PCT/GB2010/000198

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/GB2010/000198

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