

# Biology of Tree Pollen Allergens

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More than 25% of the population suffer from type I allergy. Pollens from trees of the Fagales, Oleaceae, and Cupressaceae belong to the most potent and frequent allergen sources. During the past 15 years, the nature of the most important allergens has been identified by molecular biological techniques, and recombinant allergens equivalent to the natural allergens have been produced. These advances provide insight into the biological functions of important allergens and allow the development of novel forms of diagnosis and therapy. In this review, we focus on Fagales allergens to illustrate the impact of recombinant allergens on diagnosis and therapy. We discuss structural similarities as a molecular basis for cross-reactivities and develop diagnostic concepts by using species-specific marker allergens as well as highly cross-reactive allergens. The identification of the allergen recognition profiles of patients with recombinant allergens allows a more precise selection of patients for available forms of allergy treatment. Moreover, we describe novel recombinant allergen-based forms of specific immunotherapy.

## Introduction

Pollen production is a general feature of numerous plants, but only wind-pollinated plants represent potent allergen sources [1]. This fact can be explained by the importance of respiratory allergen contact for allergic sensitization in early childhood [2,3]. The expression level of pollen allergens can be influenced by environmental factors, maturation of pollen, climate, and characteristics of certain plant species [4-8], and thus may affect overall allergenicity. The tree pollen allergens characterized to date represent low-molecular weight intracellular proteins and, sometimes, glycoproteins that are rapidly released after contact with aqueous solutions [9,10], and may be bound to respirable particles (eg, diesel exhaust particles). The latter fact has been related to the induction of strong Th2 immune responses to allergens due to possible adjuvant and/or immunomodulatory effects [11-13].

It is useful to classify important allergenic trees according to certain botanical orders that show a typical geo-

graphic distribution and are characterized by defined flowering periods [14]. The Fagales, including the families of the Betulaceae, Corylaceae, and Fagaceae, occur in North and Middle Europe, North-West Africa, East Asia, and from North America to the Andes, and predominantly flower in spring. The Oleaceae family reaches further south and is found in the Mediterranean area, where olive belongs to the most potent elicitor of type I allergy [14,15].

The Gymnosperms, especially the Cupressaceae/Taxodiaceae family, which grow in the Mediterranean areas, Australia, New Zealand, North America, South America, and certain parts of Asia, are responsible for allergic sensitization in these regions [16].

## Allergenic Trees: From a Botanical Classification to a Classification According to Allergenic Molecules

Cross-reactivity of IgE antibodies between different allergen sources has been established as the basis for the co-occurrence of allergic symptoms to a variety of allergen sources. The elucidation of cross-reactivities started with the introduction of the radioallergosorbent (RAST) technology into the field of allergy [17]. Several RAST inhibition studies have identified cross-reactive allergens in different allergen sources [18,19]. As far as plant, and especially tree-pollen, allergy is concerned, cross-reactivity follows strongly botanical relationships between allergen sources [20]. For example, it has been demonstrated that pollens of trees belonging to the order Fagales (eg, Fagaceae, Corylaceae, and Betulaceae) contain cross-reactive allergens [21,22]. This observation has led to clinical immunotherapy studies demonstrating that Fagales pollen allergy can be treated equally well with a mixture of pollen extracts from different members of the Fagales or birch-pollen extract alone [23-25]. Similar observations have been made for members of the Oleaceae family, in which extensive cross-reactivities have been described among olive, ash, privet, and lilac [26].

Likewise, there are cross-reactivities among pollens of the Cupressaceae/Taxodiaceae [27]. With the introduction of molecular biological methods, the individual allergens in most of the above-mentioned allergen sources have been characterized down to the molecular and structural level [28,29]. Using defined recombinant allergens, it has become possible to reveal the molecular basis for cross-reactivities and to identify precisely the cross-reactive allergens' IgE as well as T-cell epitopes [28,29]. In Table 1, we provide a list of allergens that have been identified in pol-

Table 1. Tree-pollen allergens

Fagales Betulaceae	Angiosperms				Gymnosperms	
	Hamamelidales		Hamamelidales		Hamamelidales	
	Hamamelidales Corylaceae	Fagaceae	Hamamelidales Platanaceae	Asteridae Scrophulariales Oleaceae	Coniferales Cupressaceae/Taxodiaceae	
Betula (birch)	Corylus (hazel)	Quercus (white oak)	Platanus (plane tree)	Olea (olive tree)	Cryptomeria (Japanese cedar)	
Alnus (alder)	Carpinus (hornbeam)	Castanea (chestnut)		Fraxinus (ash)	Juniperus (cedar, juniper)	
Bet v 1	Cor a 1	Que a 1	Pla a 1	Ligustrum vulgare (privet)	Cupressus (cypress)	
Bet v 2	Cor a 2		Pla a 2	Syringa vulgaris (lilac)		
Bet v 3	Cor a 8	Cas s 1		Ole e 1	Cry j 1	
Bet v 4	Cor a 10	Cas s 5		Ole e 2	Cry j 2	
Bet v 6		Cas s 8		Ole e 3		
Bet v 7	Car b 1			Ole e 4	Cha o 1	
Bet v 8				Ole e 5	Cha o 2	
Aln g 1				Ole e 6		
Aln g 4				Ole e 7	Cup a 1	
				Ole e 8	Cup a 3	
				Ole e 9	Cup s 1	
				Ole e 10	Jun a 2	
				Fra e 1	Jun a 3	
				Lig v 1	Jun o 4	
				Syr v 1	Jun v 1	
				Syr v 3	Cry j 1	
					Cry j 2	

<http://www.allergenonline.com>  
 International Union of Immunological Societies Allergen Nomenclature Sub-Committee <http://www.allergen.org/list.htm>  
 SDAP—Structural Database of Allergenic Proteins.

lens of trees of the Fagales, Hamamelidales, Scrophulariales, and Coniferales. The allergen sources are grouped according to botanical classifications, and allergens have been termed according to the international allergen nomenclature. Several allergen databases (*eg*, <http://www.allergenonline.com>, International Union of Immunological Societies Allergen Nomenclature Sub-Committee; <http://www.allergen.org/list.htm>; SDAP-Structural Database of Allergenic Proteins) are available, and further information about the spectrum of tree-pollen allergens can be obtained in recently published review articles [15,30,31].

### Molecular Classification of Tree Pollen Allergy: Allergy to Fagales Pollen as a Concrete Example

Trees of the Fagales order include the families of the Betulaceae, Fagaceae, and Corylaceae, which, according to RAST inhibition and immunochemical studies, contain cross-reactive allergens. Birch represents the most potent and frequent allergen source of the Fagales. Hence, the allergen spectrum of birch is well characterized [31].

Bet v 1, the major allergen of birch is a 17 kDa protein. The cDNA coding for Bet v 1 was one of the first allergen-encoding cDNAs isolated [32]. It revealed significant sequence homology to a group of proteins that are activated in plants under stressful conditions. Accordingly, these proteins were called pathogenesis-related plant proteins [32,33]. Until now, the biological function of Bet v 1 has not been revealed with certainty, although several assumptions have been made based on *in vitro* experiments and structural studies [34–36]. Evidence that members of the Bet v 1 family may protect plants from insects comes from a recent study that demonstrated insecticide activity of a Bet v 1-homologous protein from periwinkle, PR10 [37]. Recombinant Bet v 1 has been expressed in *Escherichia coli* as a biologically active allergen that binds the IgE of most birch-pollen allergic patients [38–40].

Based on homologies at a nuclear acid level, cDNAs coding for major allergens of related pollens such as alder (Aln g 1), hazel (Cor a 1), hornbeam (Car b 1), and apple (Mal d 1) could be isolated by reverse transcription and polymerase chain reaction (PCR) methods [41–44]. In accordance with earlier studies, examining immunologic cross-reactivities between the major allergens of Fagales pollen, fruits, vegetables, and spices, several Bet v 1-related allergens have been identified (*eg*, in carrot, celery, cherry, and pear) [45–49] (Fig. 1). Cross-reactivity experiments using pollen of several trees of the Fagales (alder, hazel, hornbeam), fruits, vegetables, and spices revealed that most epitopes are represented by Bet v 1, the major birch-pollen allergen [40,50]. The latter studies indicate that Bet v 1 is the initial sensitizing allergen for most patients suffering from Fagales-pollen allergy and birch-pollen-related plant-food allergy (oral allergy syndrome [OAS]) [40,50] (Fig. 1). Several other population studies confirmed that

Bet v 1 may be considered as a marker allergen for genuine sensitization to Fagales-pollen and birch-pollen-related food allergy [40,50,51].

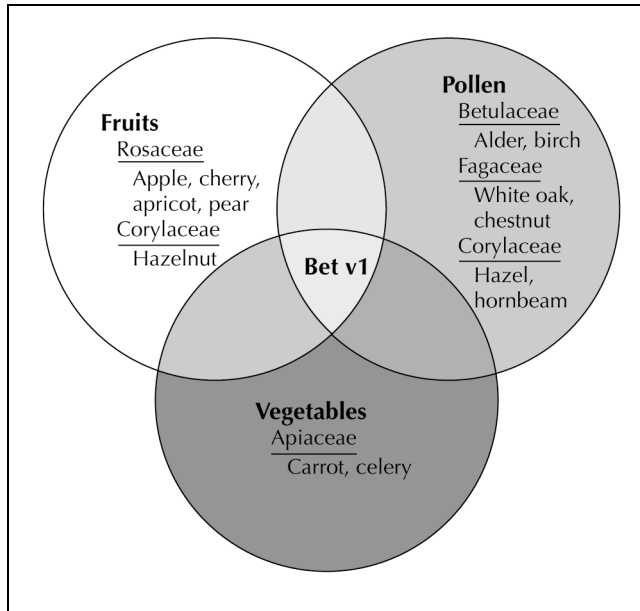
Bet v 2, the second well-described birch pollen allergen, belongs to the family of profilins, a group of ubiquitous actin-binding eukaryotic proteins with a molecular weight of 14 kDa [52,53]. Profilins can be found as cross-reactive allergens not only in pollen from unrelated plants (trees, grasses, weeds) but also in other plant tissues (fruits, vegetables, nuts, spices, and latex), and even in humans.

Besides Bet v 1 and Bet v 2, there is a third group of allergens with a wide distribution in pollen of different unrelated plants. Bet v 3 and Bet v 4 were identified as EF-hand calcium-binding proteins primarily expressed in mature pollen [54–56]. They show extensive cross-reactive activity to other pollens from grasses, weeds, and trees and, thus, can serve as marker allergens for plant polysensitization [57]. Bet v 3 is a 23.7 kDa protein containing three typical calcium-binding motifs [54]. Bet v 4, a protein of 9.3 kDa, contains only two calcium-binding domains [55,56] and, thus, constitutes another family of calcium-binding allergens that share epitopes with cross-reactive allergens from grass pollen (bermuda grass: Cyn d 7; timothy grass: Phl p 7), weeds (rape: Bra r 1 and Bra r 2), and tree pollens (alder: Aln g 4; olive: Ole e 3) [57].

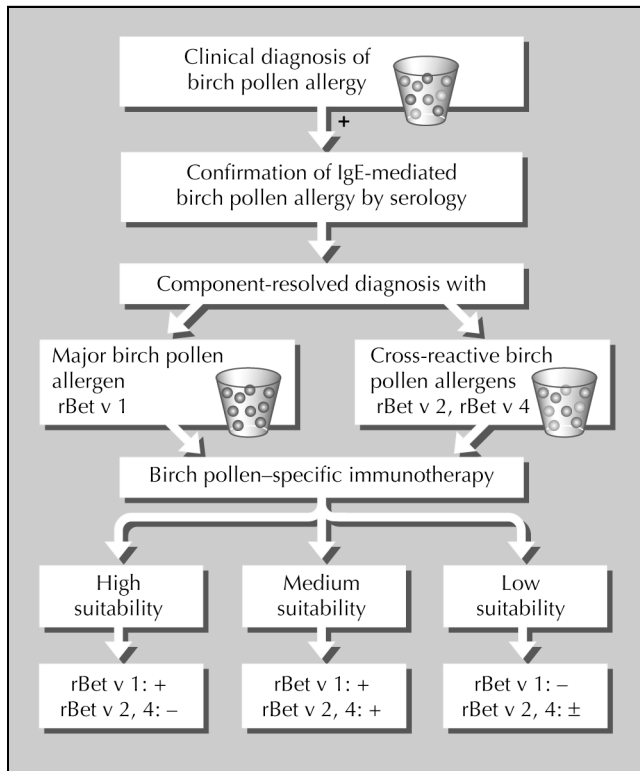
Several other birch-pollen allergens have been characterized. One of those, Bet v 6, was identified as an isoflavone reductase [58]; Bet v 7 is a cyclophilin [59]; and Bet v 8 is a plant pectin esterase [60]. The clinical relevance of Bet v 6–8 has not yet been investigated in detail. In summary, it can be stated that Bet v 1 is the major allergen of birch. It contains not only most of the epitopes present in birch pollen, but, owing to cross-reactivity, also those of pollens from trees of the Fagales order and related plant foods. Accordingly, Bet v 1 has been suggested as a diagnostic marker allergen to identify patients with a genuine birch-pollen sensitization [61]. However, highly cross-reactive allergens, such as Bet v 2 and Bet v 4, may be considered as marker allergens that are cross-reactive with numerous unrelated plants/plant products [61].

### Recombinant Birch Pollen Allergens for Novel Forms of Allergy Diagnosis

In 1991 the first study using recombinant birch pollen allergens for serological diagnosis of birch pollen allergy was published [38]. Since then, the common allergens from most allergen sources have been identified by molecular cloning techniques and produced as recombinant allergens, which can now be used for component-resolved diagnosis (CRD) of allergy [62–64]. The advantage of CRD versus allergen-extract-based diagnosis is that CRD allows the identification of the disease-eliciting allergens for each patient and, thus, establish a detailed IgE reactivity profile. By contrast, extract-based diagnosis only tells us that a patient reacts to unspecified components in the given



**Figure 1.** Redefinition of cross-reactivities among various allergen sources based on cross-reactivity to the major birch-pollen allergen, Bet v 1. Family names are underlined, and common names are listed.



**Figure 2.** A suggested decision tree for the selection of patients for birch-pollen-specific immunotherapy.

extract and, thus, only provides a determination of the allergen source.

The advantage of using recombinant allergens for diagnosis can be illustrated with a concrete example. Birch pollen allergy is frequently treated with allergen-specific

immunotherapy. The clinician has to make a careful decision as to which patient may be suitable for this treatment, because immunotherapy represents a sometimes risky, costly, and time-consuming treatment. From population studies, we know that clinically relevant sensitization to birch pollen can be found in patients who were not originally sensitized to birch. For example, it has been reported that allergic patients from Central Africa showed positive skin reactivity and serology to birch pollen although they were not exposed to birch [65•]. It turned out that these patients were sensitized to cross-reactive allergens from other plants. Such patients can be identified in populations all over the world, to a varying degree [51]. They are rather rare in countries with high exposure to birch pollen but are more frequently observed in countries with mixed vegetation (e.g., Middle and southern parts of Europe) [51]. Population studies performed with recombinant allergens can distinguish patients who are genuinely sensitized to birch pollen by their IgE reactivity to the major birch pollen allergen Bet v 1. In contrast, patients who exhibit positive skin tests to birch pollen extracts, but who have not been exposed to birch, have IgE to cross-reactive allergens, such as Bet v 2. Thus, the use of rBet v 1 for diagnostic testing to identify patients with genuine birch pollen sensitization and to confirm the diagnosis of birch pollen allergy before initiating immunotherapy with birch pollen extract is recommended. Figure 2 illustrates the possible diagnostic procedure for the confirmation of genuine birch pollen allergy. It is recommended to treat only those patients with birch pollen immunotherapy who react to the major allergen of birch, Bet v 1. There are two reasons for this suggestion. First, genuine sensitization to birch without reactivity to the major allergen is very unlikely. Second, most birch pollen extracts used for immunotherapy contain large amounts of Bet v 1 but are not standardized for other birch pollen allergens.

### Recombinant Birch Pollen Allergens for the Monitoring of Therapy and for Immunotherapy

The introduction of the recombinant allergens in the diagnosis of type I allergy not only facilitates the decision whether a patient is suitable for immunotherapy but allows the measurement of IgE and IgG responses in response to allergen-specific immunotherapy [66,67•,68•]. Studies using recombinant allergens for the monitoring of antibody profiles and levels during the course of immunotherapy have reemphasized the importance of blocking antibodies for successful immunotherapy [66,67•]. On the other hand, it has turned out that immunotherapy with crude allergen extracts may induce de novo IgE sensitizations to new allergens or extract components [66,68•,69]. The latter studies emphasize a need for patient-tailored forms of treatment, which, in fact, can only be achieved with defined recombinant allergens.

Due to the fact that recombinant allergens can be produced that contain most of epitopes present in complex

allergen sources, there is hope that recombinant allergens will replace traditional allergen extracts for immunotherapy [70•,71•]. Furthermore, it is possible to apply recombinant DNA technology and synthetic peptide chemistry to produce new generations of allergy vaccines with reduced allergenic activity [70•,71•]. Such candidate vaccines have already been tested for safety in patients and for efficacy in animal models. Currently, several immunotherapy trials are being conducted with recombinant allergen based vaccines. It may, therefore, be anticipated that the practice of immunotherapy will dramatically change in the near future [72].

## Conclusions

Advances made in the field of molecular allergen characterization have provided the basis for the transition from a botanical to a molecular classification of tree pollens. An overview over the most important tree pollen allergens is given, and the importance and usefulness of recombinant allergens for allergy diagnosis and treatment is exemplified for birch pollen and related allergies. The introduction of species-specific marker allergens and cross-reactive allergens allows the precise identification of a patient's sensitization profile as well as the monitoring of extract-based immunotherapy. Moreover, new allergy vaccines based on recombinant allergens have already entered clinical trials and will likely replace conventional, extract-based forms of allergen-specific treatment.

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