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Review

# Proteomics-based allergen analysis in plants☆

*Rika Nakamura, Reiko Teshima**

*National Institute of Health Sciences (NIHS), 1-18-1, Kamiyoga, Setagaya-ku, Tokyo 158-8501, Japan*

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ABSTRACT

Plants may trigger hypersensitivity reactions when individuals with allergies consume foods derived from plant materials or inhale plant pollen. As each plant food or pollen contains multiple allergens, proteomics is a powerful tool to detect the allergens present. Allergen-targeted proteomics, termed allergenomics, has been used for comprehensive identification and/or quantification of plant allergens, because it is a simple and inexpensive tool for rapid detection of proteins that bind to IgE. There are increasing numbers of reports on the applications of allergenomics.

In this review, we outline some of the applications of proteomics, including: (i) identification of novel allergens, (ii) allergic diagnoses, (iii) quantification of allergens, and (iv) natural diversity of allergens, and finally discuss (v) the use of allergenomics for safety assessment of genetically modified (GM) plants.

**Biological significance statement**

Recently, the number of allergic patients is increasing. Therefore, a comprehensive analysis of allergens (allergenomics) in plants is highly important for not only risk assessment of food plants but also diagnosis of allergic symptoms. In this manuscript, we reviewed the recent progress of allergenomics for identification, quantification and profiling of allergens. This article is part of a Special Issue entitled: Translational Plant Proteomics.



## Contents



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* *Corresponding author at: Division of Novel Foods and Immunochemistry, National Institute of Health Sciences (NIHS), 1-18-1 Kamiyoga, Setagaya-ku, Tokyo 158-8501, Japan.* Tel.: +81 3 3700 1349; fax: +81 3 3707 6950.
E-mail address: rteshima@nihs.go.jp (R. Teshima).

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## 1. Introduction

Plants may trigger hypersensitive (allergic) reactions in some people after inhalation of plant pollens or consumption of foods derived from plant materials. Inhalation of pollens can cause pollinosis, resulting in symptoms such as rhinitis, sneezing, and itching. After eating certain plant foods, sensitive people may suffer diarrhea, emesis, and anaphylaxis, which is a severe systematic allergic reaction [1]. These allergenic reactions are type I allergies, which are mediated by IgE antibodies. The substances in plants that can trigger type I allergic reactions, i.e., allergens, are proteins. After absorbing or adhering to the human body, plant allergens bind to specific IgE antibodies in the blood and cause cross-linking of IgE receptors (Fc epsilon receptor I) on mast cells, which evokes degranulation of these cells that store chemical mediators, such as histamines, proteases, and cytokines, in their granules [2]. Chemical mediators that are released extracellularly may cause allergenic reactions in local tissues.

Each plant can contain several allergens, and the main allergen causing allergic reactions differs among individual patients. To detect the allergens in plants, western blotting, which is an immunochemical method for detecting the binding between a patient's IgE and separated plant proteins on a membrane, has been employed. In recent years, proteomic techniques that target allergens, i.e., allergenomics, have become powerful tools for comprehensive allergen analysis [3–6]. At first, proteomic analyses were used to detect novel allergens by identifying proteins after separation by 2-DE and MS (Fig. 1A). Proteomics has accelerated identification of multiple allergens in plants, compared to conventional methods involving protein isolation processes. In addition to conventional allergenomics methods for detecting allergens, new allergenomics techniques, which consider the properties of the allergens, have been developed [7–9].

Plant allergens have various roles; some such as are storage proteins, some are enzymatic, and others are structural proteins [10–13]. Plant allergens are classified into families according to their functions and structures, as shown in Table 1. The binding

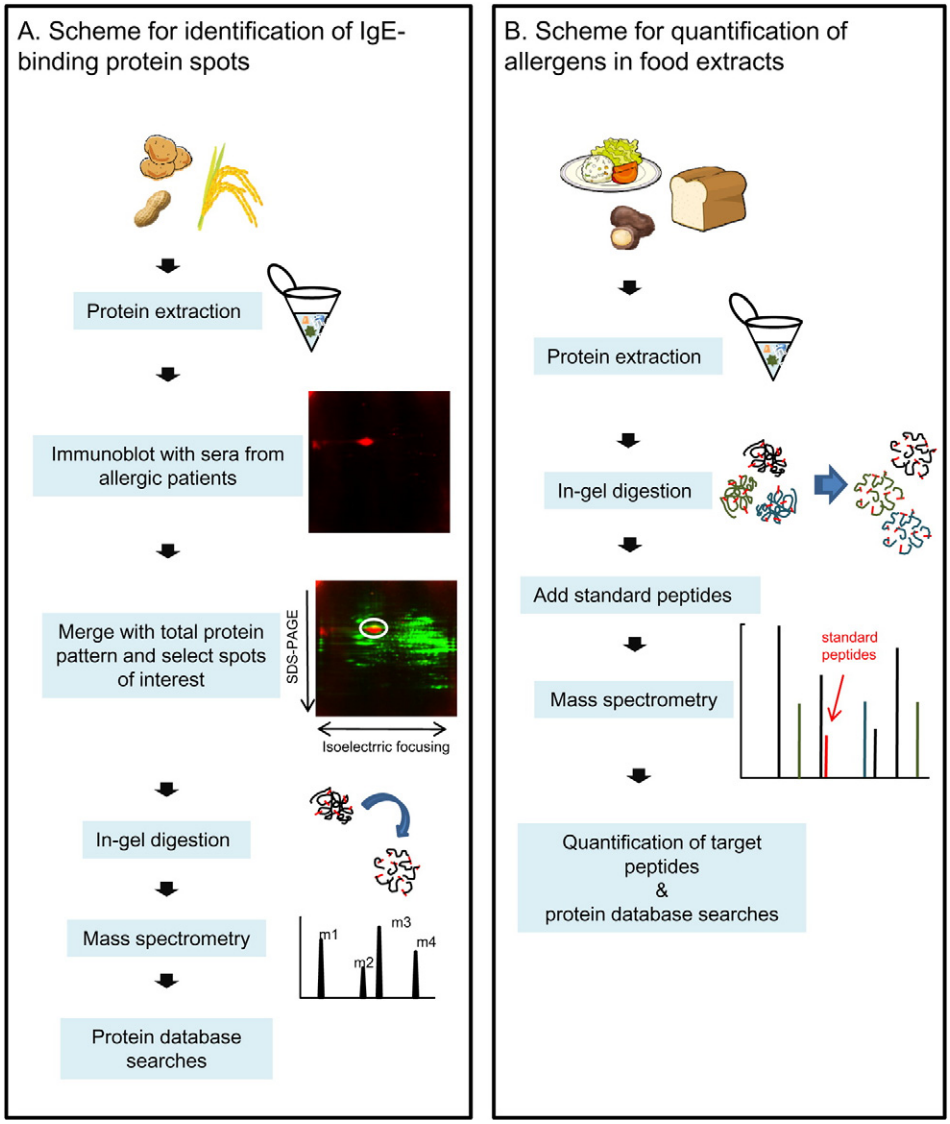


**Fig. 1 – A. Scheme for identification of IgE-binding protein spots. B. Scheme for quantification of allergens in food extracts.**

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