Editorial

Bioinformatics of Protein Allergenicity

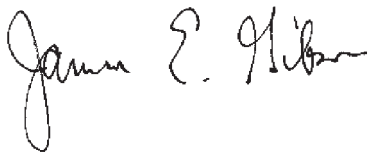
While the incidence of food allergy tends to be overestimated (i.e. food intolerances vs. true immune-mediated allergies) by the general population, clinically diagnosed food allergy affects approximately 2–4% of the adult population, and up to approximately 8% of children. Severe allergic reactions (anaphylaxis) to foods are relatively rare, occurring in approximately 3.2 individuals per 100,000 people per year. Anaphylaxis to food typically occurs in those who are genetically predisposed to allergy, have been previously sensitized to the allergen and who unintentionally consume the allergen. A small number of specific proteins contained in relatively few foods are responsible for most severe reactions and these are mediated by allergen specific IgE. At this time, there is no cure for food allergy and the disease must be managed through avoidance of the allergenic food. Consequently, an important public health consideration for novel proteins, including those associated with genetically modified crops, is the need to protect food-allergic subjects from unwanted exposure to allergens that cause their disease. In practice, this means that the risk assessment must assure that no known or likely allergen, especially food allergens (but including all known allergens) will be transferred or "hidden" in foods or fractions derived from genetically modified crops.

"It is widely recognized that bioinformatics alone cannot be used to predict whether a protein will be allergenic"

Novel protein allergenicity assessments that are conducted in the context of an overall risk and safety evaluation, utilize many sources of information in a weight-of-the-evidence testing approach. A comparison of the amino acid sequence of the novel (introduced) protein to the amino acid sequences of known allergens is one of several criteria used to evaluate the safety of a novel protein. The purpose of this evaluation is to determine if the amino acid sequence of the introduced protein is similar to the amino acid sequence of any known allergen. A similarity in sequence between the novel protein and a known allergen suggests that the protein could elicit a clinical reaction in a sensitized individual. It is widely recognized that bioinformatics alone cannot be used to predict whether a protein will be allergenic. If a novel protein demonstrates some similarity to a known allergen, additional testing, such as IgE binding studies using sera from appropriately diagnosed allergic subjects, should be considered to confirm the match.

In an effort to evaluate the current methodologies being used for identifying similarities to known allergens, the ILSI Health and Environmental Sciences Institute (HESI) hosted an expert workshop on February 22–24, 2005 in Mallorca, Spain. The primary goals for the workshop were to (i) review the state-of-the-science for conducting a sequence identity/bioinformatics evaluation in the context of a comprehensive allergenicity assessment for novel proteins; (ii) obtain consensus on the value and role of bioinformatics in evaluating novel proteins; and (iii) discuss the utility and methods of allergen specific IgE screening in the diagnosis of food allergy. This workshop was part of the committee's broader activities that are focused on advancing the scientific understanding of the relevant parameters for characterizing the allergenic potential of novel proteins and biotechnology derived products. Discussions during the workshop addressed a number of topics that are important for amino acid sequence identity evaluations, including structural biology of proteins, IgE cross-linking, IgE binding epitopes, serum IgE testing, and a review of allergen databases. The compendium of manuscripts that follows provides a detailed summary of each of the topics that were addressed as part of the workshop, and represent the consensus view of the workshop participants for each discussion topic.

HESI is a global branch of the International Life Sciences Institute, a public, non-profit making scientific foundation with branches throughout the world. HESI provides an international forum to advance the understanding and application of scientific issues related to human health, toxicology, risk assessment and the environment. It is widely recognized among scientists from government, industry and academia as an objective, science-based organization within which important issues of mutual concern can be discussed and resolved in the interest of improving public health. As part of its public benefit mandate, HESI's activities are carried out in the public domain, generating data and other information for broad scientific use and application, and include participation from government, industry, and academic scientists.



Professor Dr. James Gibson
East Carolina University