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POSTER ABSTRACTS

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The National Information System on Biosafety: An Online Public Source for Information on Activities Related to GMOs

Ariel Alvarez-Morales, Rosa Ines González-Torres, Sol Ortiz-García
Intersecretarial Commission for Biosafety and Genetically Modified Organisms (CIBIOGEM), Mexico
http://www.cibiogem.gob.mx

Mexico acknowledges in its national regulatory framework the right of society to have access to information. On this issue, the Law for Biosafety and Genetically Modified Organisms (LBGMO) offers an adequate response through its articles 108 and 109, which also address article 20 of the Cartagena Protocol. In accordance with the legal mandate, Mexico has implemented the *National Information System on Biosafety (NISB)*, which includes the National Register of GMOs. These are hosted within the Web Page of the Intersecretarial Commission for Biosafety and Genetically Modified Organisms (CIBIOGEM), and managed by its Executive Secretariat. The information in the NISB includes: the National Register of GMOs; statistical Information; information on restricted areas; documents and activities on biosafety; notice formats; permit applications available for public consultation; and reports and activities related to the special protection of maize. The National Register of GMOs includes information supplied to the Executive Secretariat by the national competent authorities on:

I. Applications for environmental release (Permits) and for the importation of GMOs as Food, Feed or for Processing (Authorizations);
II. Resolutions for both Permits and Authorizations issued by the corresponding competent authority;
III. Suspensions and Revocations;
IV. Submission of Notices for contained use of GMOs;
V. Requirements and additional measures; and
VI. Communications on accidental releases of GMOs.

This information also complements the information submitted to the BCH.

Besides the National Information System on Biosafety and the National Register of GMOs, which are both mandatory, additional information can be found in the Web Page addressing multiple issues directed to different publics. Among these can be found a section to provide information to researchers in biotechnology and biosafety regarding, for instance, the opening of a program by CIBIOGEM to provide funds to renew/update or improve infrastructure in containment research facilities, or to invite to submit research proposals on specific topics of biosafety or biotechnology, etc. There are also sections to find relevant information on applicable legislation (some translated into English, such as the Biosafety Law and its Bylaw), relevant scientific and technical information, frequently asked questions, a glossary, and a complete section on biotechnology for children as part of the efforts of CIBIOGEM to provide information starting from a very basic level that can be used by parents, teachers and school children of different ages. Of course, there is also a set of links to related and important sites such as those hosted by the Secretaries that integrate CIBIOGEM, the Cartagena Protocol on Biosafety and its Biosafety Clearing House, Codex Alimentarius, CERA, ISBR, EFSA, USDA, CFIA, and many others.

Repeated Sequences with Similar Physicochemical Properties May Account for Cross-Reactions between Peanuts and Tree Nuts

S. J. Maleki1, T. Charles, C.C. Grimm, B.K. Hurlburt, M. Chruszcz., H. Cheng, C. H. Schein3; 1US Dept. of Agriculture, New Orleans, LA, 3University of Texas Medical Branch, Galveston, TX

RATIONALE: Many peanut allergic individuals also have allergies to tree nuts. Our previous work has shown that the property distance (PD) scale in Structural Database of Allergenic Proteins (SDAP) can identify similar IgE binding areas that may be important for cross-reactivity between allergens.

METHODS: The specificity of six monoclonal antibodies against Ara h 2 was determined with SPOTs analysis, and the epitope regions mapped to the surface of the recent crystal structure. Western blots were used to compare the binding of these monoclonals to almond, cashew, peanut, pistachio, soy, green pea and walnut extracts, and purified recombinant Jug r 2 leader sequence, Jug r 1, Ara h 2 and Ara h 6. Proteins in the reactive bands were identified by mass spectrometry.

RESULTS: Searching the SDAP using the PD tool revealed many potential IgE epitopes in other nut allergens, including several 7S, 2S and 11S albumins, with similar physicochemical properties (low PD value) to known Ara h 2 epitopes. The anti-Ara h 2 monoclonal antibodies recognized many of these predicted vicillin, conglutinin, and glycinin nut allergens. All of the monoclonals recognized Jug r 1, and four were highly reactive with the Jug r 2 leader sequence, confirming the presence of similar antigenic regions.

CONCLUSIONS: Repeated sequences similar to known IgE epitopes are common to many different allergenic proteins from nuts and seeds. The importance of these regions for clinically relevant IgE cross-reactivity is indicated by these results.

Germfree and Conventional C3H/HeN Mice Used to Compare the Sensitizing Potential of Purified β-Lactoglobulin and Whey Protein

NL Marsteller[1,2], K Andoh-Kumi[1], DA Peterson[3], RE Goodman[1], JL Baumert[1]

[1]Food Allergy Research and Resource Program, Dept. of Food Science and Technology, University of Nebraska, Lincoln, NE

[2] School of Biological Sciences, University of Nebraska, Lincoln, NE

[3]Dept. of Pathology, Johns Hopkins University, Baltimore, MD

The connection between gastrointestinal microbiota, sensitization, and elicitation of allergic symptoms to various allergenic foods or purified allergens, in and out of the context of natural food matrices, has yet to be conclusively defined. This study was performed to investigate the connection between route of sensitization, microbial status and food matrix on elicitation of allergic response in mice, and to develop/test an animal model to evaluate the sensitization and eliciting properties of novel proteins. Conventional and GF C3H/HeN mice were sensitized with BLG or whey protein either 5x orally or 3x by intraperitoneal injection (IP) on weekly intervals in the presence of cholera toxin or alum adjuvant, respectively. One week following the final sensitization an oral challenge of 60mg BLG was given. One hour post-challenge clinical scores were assigned and body temperatures recorded. BLG serum specific IgE and mast cell protease concentrations were determined using ELISA. Removing the microbial signals normally present in the gut resulted in a skewing of the immune response to a more allergenic profile. Germfree mice may be a more predictive model of food allergy sensitization and elicitation due to lower variability in responses than conventional mice.

Characterising Microbial Protein Test Substances and Establishing Their Equivalence with Plant-produced Proteins for Use in Risk Assessments of Transgenic Crops

Alan Raybould[1], Peter Kilby[1], Shuang Song[2] and Gerson Graser[2]

1. Syngenta, Jealott's Hill International Research Centre, Bracknell, Berkshire RG42 6EY, UK
2. Syngenta Biotechnology Inc., 3054 E. Cornwallis Rd, P.O. Box 12257, Durham, NC 27709, USA

Most commercial transgenic crops are genetically engineered to produce new proteins. Studies to assess the risks to human and animal health, and to the environment, from the use of these crops require grams of the transgenic proteins. It is often extremely difficult to produce sufficient purified transgenic protein from the crop. Nevertheless, ample protein of acceptable purity may be produced by over-expressing the protein in microbes such as *Escherichia coli*. When using microbial proteins in a study for risk assessment, it is essential that their suitability as surrogates for the plant-produced transgenic proteins is established; that is, the proteins are equivalent for the purposes of the study. Equivalence does not imply that the plant and microbial proteins are identical, but that the microbial protein is sufficiently similar biochemically and functionally to the plant protein such that studies using the microbial protein provide reliable information for risk assessment of the transgenic crop. Equivalence is a judgment based on a weight of evidence from comparisons of relevant properties of the microbial and plant proteins, including activity, molecular weight, amino acid sequence, glycosylation and immuno-reactivity. We describe a typical set of methods used to compare proteins in regulatory risk assessments for transgenic crops, and discuss how risk assessors may use comparisons of proteins to judge equivalence.

Leveraging Non-Targeted Metabolite Profiling via Statistical Genomics

Miaoqing Shen [1,2,6], Corey Broeckling [3], Elly Y. Chu [1,2], Gregory Ziegler [4,5], Ivan R. Baxter [4], Jessica E. Prenni [3], and Owen A. Hoekenga [2,7]

[1] Boyce Thompson Institute for Plant Research, Cornell University, Ithaca NY

[2] USDA-ARS, Robert Holley Center for Agriculture and Health, Ithaca NY

[3] Colorado State University, Proteomics and Metabolomics Facility, Fort Collins CO

[4] USDA-ARS, Plant Genetics Research Unit, St. Louis MO

[5] Donald Danforth Plant Science Center, St. Louis MO

[6] Current address: Advion, Inc. Ithaca NY

[7] Presenting and corresponding author: Owen.Hoekenga@ars.usda.gov

One of the challenges of systems biology is to integrate multiple sources of data in order to build a cohesive view of the system of study. Here we describe the mass spectrometry based profiling of maize kernels, a model system for genomic studies and a cornerstone of the agroeconomy. Using a network analysis, we can include 97.5% of the 8,710 features detected from 210 varieties into a single framework. More conservatively, 47.1% of compounds detected can be organized into a network with 48 distinct modules. Eigenvalues were calculated for each module and then used as inputs for genome-wide association studies. This allows us to determine the genetic bases for particular facets of maize grain composition. Nineteen modules returned significant results, illustrating the genetic control of biochemical networks within the maize kernel. Our approach leverages the correlations between the genome and metabolome to mutually enhance their annotation and thus enable biological interpretation. This method is applicable to any organism with sufficient bioinformatic resources. We use four case studies in maize grain quality that utilize our systems biology approach, leveraging genetics, genomics and metabolomics to describe aspects of protein quality, pathogen resistance, iron nutritional quality and seed weight.

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