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Scientific Integrity

Scientific Integrity Principles and Best Practices: Recommendations From a Scientific Integrity Consortium

Kretser A, Murphy D, Bertuzzi S, Abraham T, Allison DB, Boor KJ, et al. *Sci Eng Ethics*. 2019 Feb 27. doi: 10.1007/s11948-019-00094-3. [Article Link](#)

Significance: The Scientific Integrity Consortium developed a set of recommended principles and best practices for scientific integrity that can be used broadly across scientific disciplines and will better equip scientists to operate in a rapidly changing research environment.

A Scientific Integrity Consortium developed a set of recommended principles and best practices that can be used broadly across scientific disciplines as a mechanism for consensus on scientific integrity standards and to better equip scientists to operate in a rapidly changing research environment. The two principles that represent the umbrella under which scientific processes should operate are as follows: (1) Foster a culture of integrity in the scientific process. (2) Evidence-based policy interests may have legitimate roles to play in influencing aspects of the research process, but those roles should not interfere with scientific integrity. The nine best practices for instilling scientific integrity in the implementation of these two overarching principles are (1) Require universal training in robust scientific methods, in the use of appropriate experimental design and statistics, and in responsible research practices for scientists at all levels, with the training content regularly updated and presented by qualified scientists. (2) Strengthen scientific integrity oversight and processes throughout the research continuum with a focus on training in ethics and conduct. (3) Encourage reproducibility of research through transparency. (4) Strive to establish open science as the standard operating procedure throughout the scientific enterprise. (5) Develop and implement educational tools to teach communication skills that uphold scientific integrity. (6) Strive to identify ways to further strengthen the peer review process. (7) Encourage scientific journals to publish unanticipated findings that meet standards of quality and scientific integrity. (8) Seek harmonization and implementation among journals of rapid, consistent, and transparent processes for correction and/or retraction of published papers. (9) Design rigorous and comprehensive evaluation criteria that recognize and reward the highest standards of integrity in scientific research.

This work was conducted by the Scientific Integrity Consortium, which comprises 4 U.S. government agencies, 3 Canadian government agencies, 11 professional societies, 6 universities and 3 non-profit organizations. ILSI North America is a member of the Consortium.

Foodborne Pathogens



Prevalence of *Listeria monocytogenes* in Select Ready-to-Eat Foods—Deli Meat, Soft Cheese, and Packaged Salad: A Systematic Review and Meta-Analysis

Churchill KJ, Sargeant JM, Farber JM, O'Connor AM. *J Food Prot*. 2019 Feb;82(2):344-357. doi: 10.4315/0362-028X.JFP-18-158. [Article Link](#)

Significance: This systematic review and meta-analysis found that heterogeneity between existing studies is too high to use global summary prevalence estimates for risk assessment for *L. monocytogenes* in ready-to-eat foods.

Listeria monocytogenes is the cause of listeriosis, an important foodborne disease. Contaminated ready-to-eat foods are common sources of *L. monocytogenes*, yet no global estimates exist for prevalence and levels in high-risk ready-to-eat foods. Our objective was to estimate the prevalence and levels of *L. monocytogenes* in deli meat, soft cheese, and packaged salad. We searched Medline, Web of Science, Agricola, Conference Proceedings Citation Index-Science, Science.gov, ScienceResearch.com, and OpenGREY for studies on *L. monocytogenes* prevalence and/or levels, with no restriction on publication date. We used

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a priori study selection, data extraction, and risk of biases processes. Results were synthesized with random-effects meta-analyses and meta-regressions to evaluate heterogeneity between studies. We included in the review 100 studies with a sample size restriction of ≥ 100 , and we estimated *L. monocytogenes* prevalence in deli meat at 2.9% (95% confidence interval [CI], 2.3 to 3.6%), in soft cheese at 2.4% (95% CI, 1.6 to 3.6%), and in packaged salad at 2.0% (95% CI, 1.2 to 3.1%). High heterogeneity was present in all food groups, and meta-regressions did not reveal consistent explanations for heterogeneity. Pathogen level was not reported consistently or in the format required for synthesis, so meta-analyses of this variable were not performed. The high heterogeneity between studies indicates that use of global summary prevalence estimates for risk assessments are not advisable, but awareness of risk and the heterogeneity of the risk is relevant for education and further risk assessment.

Predictable and Unpredictable Survival of Foodborne Pathogens During Non-Isothermal Heating

de Jonge R. *Int J Food Microbiol.* 2019 Feb 16;291:151-160. doi: 10.1016/j.ijfoodmicro.2018.11.018. [Article Link](#)

Significance: The results from this study show that attachment to meat contributes to an increased level of heat resistance in *Salmonella* Typhimurium and *Campylobacter jejuni*.

In previous work, extreme survival of various bacterial species during cooking was reported when attached to chicken meat. In this paper the effects of an extremely high challenge temperature on survival of *Salmonella* Typhimurium and *Campylobacter jejuni*, attached to chicken breast fillets or pork to test for matrix effects are reported. Survival was predicted, using standard D- and z-values from the literature, and compared to experimentally obtained data. Attached to meat, both *S. Typhimurium* and *C. jejuni* survived longer than predicted, longer when attached to chicken meat than when attached to pork. Additionally, the effect of non-isothermal heating on survival of *Salmonella* in buffer is described. In buffer, when slowly heated, *Salmonella* died off as predicted. When *Salmonella* was heated in buffer according to a heating profile mimicking that of the surface of meat in boiling water, it appeared that cells died off much slower than predicted. It is shown that the thermal characteristics of *Salmonella* surviving the first 35 s of fast heating had changed. After these 35 s, remaining *Salmonella* survived for minutes, even at a challenge temperature of 90 °C. During heating, cell size decline was observed. A loss of intracellular water during cooking might have resulted in smaller, dehydrated cells, in cells with altered thermal resistance characteristics. This could explain why the use of standard D- and z-values did not allow the correct prediction of survival of *Salmonella* during fast heating in buffer, or during cooking, being attached to the surface of meat. Many factors affect the level of heat resistance of bacteria. The results of this and a former study show that attachment to meat contributes to an increased level of heat resistance of bacteria. A fast heating process further contributes to the increased level of heat resistance possibly as the result of changed thermal characteristics due to a loss of water.

Insights From Genome-Wide Approaches to Identify Variants Associated to Phenotypes at Pan-Genome Scale: Application to *L. monocytogenes*' Ability to Grow in Cold Conditions

Fritsch L, Felten A, Palma F, Mariet JF, Radomski N, Mistou MY, et al. *Int J Food Microbiol.* 2019 Feb 16;291:181-188. doi: 10.1016/j.ijfoodmicro.2018.11.028. [Article Link](#)

Significance: This study used combined bioinformatics approaches and whole-genome sequencing to associate genotypes with specific phenotypes in *L. monocytogenes*.

Intraspecific variability of the behavior of most foodborne pathogens is well described and taken into account in Quantitative Microbial Risk Assessment (QMRA), but factors (strain origin, serotype, ...) explaining these differences are scarce or contradictory between studies. Nowadays, Whole Genome Sequencing (WGS) offers new opportunities to explain intraspecific variability of food pathogens, based on various recently published bioinformatics tools. The objective of this study is to get a better insight into different existing bioinformatics approaches to associate bacterial phenotype(s) and genotype(s). Therefore, a dataset of 51 *L. monocytogenes* strains, isolated from multiple sources (i.e. different food matrices and environments) and belonging to 17 clonal complexes (CC), were selected to represent large population diversity. Furthermore, the phenotypic variability of growth at low temperature was determined (i.e. qualitative phenotype), and the whole genomes of selected strains were sequenced. The almost exhaustive gene content, as well as the core genome SNPs based phylogenetic reconstruction, were derived from the whole sequenced genomes. A Bayesian inference method was applied to identify the branches on which the phenotype distribution evolves within sub-lineages. Two different Genome Wide Association Studies (i.e. gene- and SNP-based GWAS) were independently performed in order to link genetic mutations to the phenotype of interest. The genomic analyses presented in this study were successfully applied on the selected dataset. The Bayesian phylogenetic approach emphasized an association with "slow" growth ability at 2 °C of the lineage I, as well as CC9 of the lineage II. Moreover, both gene- and SNP-GWAS approaches displayed significant statistical associations with the tested phenotype. A list of 114 significantly associated genes, including genes already known to be involved in the cold adaption mechanism of *L. monocytogenes* and genes associated to mobile genetic elements (MGE), resulted from the gene-GWAS. On the other hand, a group of 184 highly associated SNPs were highlighted by SNP-GWAS, including SNPs detected in genes which were already likely involved in cold adaption; hypothetical proteins; and intergenic regions where for example promoters and regulators can be located. The successful application of combined bioinformatics approaches associating WGS-genotypes and specific phenotypes, could contribute to

improve prediction of microbial behaviors in food. The implementation of this information in hazard identification and exposure assessment processes will open new possibilities to feed QMRA-models.

Thermal Inactivation of *Salmonella* and *Listeria monocytogenes* in Peanut Butter-Filled Pretzels and Whole Wheat Pita Chips

Kottapalli B, Nguyen SPV, Perez T, Cunningham A. *J Food Prot.* 2019 Feb;82(2):238-246. doi: 10.4315/0362-028X.JFP-18-231. [Article Link](#)

Significance: This study validates a thermal inactivation procedure for *Salmonella* and *L. monocytogenes* in peanut butter-filled pretzels and whole wheat pita chips.



Recent recalls and outbreaks due to foodborne pathogens in thermally processed low-moisture foods highlight the need for the food industry to validate their thermal process. The purpose of this study was to validate baking as an adequate lethality step in controlling *Salmonella* and *Listeria monocytogenes* during the production of peanut butter (PB)-filled pretzels and whole wheat (WW) pita chips. Two dough types, PB-filled pretzel and WW pita chip with varying water activities (0.96 to 0.98), were inoculated (target level, ~108 to 10⁹ CFU/g) with a multistrain cocktail of *Salmonella* and *L. monocytogenes* in separate trials and were baked at 300°F (148.9°C) and 350°F (176.6°C) for 0, 5, 10, 17, 25, and 30 min. Following baking, samples were rapidly cooled and analyzed for *Salmonella* and *L. monocytogenes* by the pour plate method. Uninoculated samples were analyzed for total viable aerobic plate count (APC) and Enterobacteriaceae counts. Water activity analysis was also performed. The experiment was replicated three times. Nonlinear regression was used to estimate the baking times required to achieve a minimum of 4- and 5-log reduction in APC, *Salmonella*, and *L. monocytogenes*. A 4- and 5-log reduction in APC was predicted following a treatment at 350°F for 3.3 and 5.6 min in WW pita chip product, respectively. Following a treatment of 350°F for 10 and 25 min, Enterobacteriaceae and APC counts were below the detection limit (<1 log CFU/g), respectively, in all of the PB-filled pretzel samples. *Salmonella* and *L. monocytogenes* counts decreased with increasing baking time regardless of the temperature used. Significant reductions (≥5-log reduction) were estimated in *Salmonella* and *L. monocytogenes* in product baked at 350°F for 15.5 and 17.5 min in WW pita chip dough and PB-filled pretzel dough, respectively. Both pathogens were below the detection limit (<1 log CFU/g) in PB-filled pretzel and WW pita chip products under baking conditions of 350°F for 25 and 30 min, respectively. This study demonstrates that PB-filled pretzel and WW pita chip products, when baked to saleable quality, will not present a public health risk from the standpoint of *Salmonella* or *L. monocytogenes*.

Pathogen Detection

Evaluation of PCR-Based Methods for the Identification of Enteroaggregative Hemorrhagic *Escherichia coli* in Sprouts

Rotundo L, Amagliani G, Carloni E, Omiccioli E, Magnani M, Paoli G. *Int J Food Microbiol.* 2019 Feb 16;291:59-64. doi: 10.1016/j.ijfoodmicro.2018.11.011. [Article Link](#)

Significance: This study demonstrates the efficacy of real-time PCR for specific and sensitive detection of enteroaggregative hemorrhagic *Escherichia coli* in sprouts.

In this study real-time PCR assays were evaluated for the detection of enteroaggregative hemorrhagic *Escherichia coli* (EAHEC) O104:H4 in artificially contaminated mung bean and alfalfa sprouts inoculated with 1, 10, and 100 CFU of EAHEC O104:H4 per 25 g sample (20, 10, and 2 replicates respectively). After selective culture enrichment the samples were tested using commercial real-time PCR kits detecting *aggR/aaiC*, *stx/eaec*, and *wzxO104*. Using the commercial real-time PCR kits, the artificially contaminated samples were detected in the range of 75-80% positive results when contaminated with approximately 1 CFU, and 100% at 10 and 100 CFU. Microbiological detection employing O104-specific immunomagnetic capture and plating onto chromogenic media (modified Rainbow Agar and CHROMagar STEC) and confirmation by latex agglutination and PCR gave similar results (Cohen's kappa value between 0.61 and 1). In addition, the real-time PCR assay targeting the *aggR* and *aaiC* genes, indicative of enteroaggregative *Escherichia coli* (EAHEC), was tested against a panel of 60 bacterial strains and demonstrated 100% exclusivity (54 strains) and 100% inclusivity (6 strains). This study demonstrates the efficacy of the real-time PCR assays for the specific and sensitive detection of EAHEC from sprouts.

A Loop-Mediated Isothermal Amplification (LAMP) Assay for the Rapid Detection of Toxigenic *Fusarium temperatum* in Maize Stalks and Kernels

Shan L, Abdul Haseeb H, Zhang J, Zhang D, Jeffers DP, Dai X et al. *Int J Food Microbiol.* 2019 Feb 16;291:72-78. doi: 10.1016/j.ijfoodmicro.2018.11.021. [Article Link](#)

Significance: A loop-mediated isothermal amplification assay is described for the rapid detection of *Fusarium temperatum*.

Fusarium temperatum is an emerging maize pathogen that causes maize ear and stalk rot diseases and produces various mycotoxins including moniliformin, beauvericin, enniatins and fumonisin B1, which poses a potential risk to the human food or animal feed supply chains. Early detection of *F. temperatum* is crucial to prevent its derived mycotoxins from entering the food chain, and is also a useful tool in disease management practices. Here, we describe a loop-mediated isothermal amplification (LAMP) assay for rapid diagnosis of *F. temperatum*. The 28S ribosomal DNA sequences (28S rDNA) of *F. temperatum* were used to design a set of six primers. The reaction conditions were optimized for developing a fast assay with high specificity and sensitivity, and were able to detect the presence of less than 10 pg of target DNA per reaction within 60 min. Furthermore, the resulting amplicons were visualized by adding SYBR Green I to the reaction tubes. Suspected *F. temperatum* infected maize stalk samples collected from Yunnan province, China were identified using the developed LAMP assay. In conclusion, the method not only provides a rapid and specific screening for the existence of *F. temperatum* in a bulk of maize samples without using sophisticated equipment, but also is potentially useful for other agriculturally important toxigenic fungi.

Mycotoxins

A Systematic Review of Plant-Conjugated Masked Mycotoxins: Occurrence, Toxicology, and Metabolism

Zhang Z, Nie D, Fan K, Yang J, Guo W, Meng J, et al. *Crit Rev Food Sci Nutr*. 2019 Feb 26:1-15. doi: 10.1080/10408398.2019.1578944. [Article Link](#)

Significance: This review summarizes country-specific natural-occurrence data for masked mycotoxins.

Masked mycotoxins are biologically modified phase II metabolites formed by plant defense mechanisms through glucosylation catalyzed by uridine diphosphate-glucosyltransferases. Most of the current reports focus on the occurrence of masked mycotoxins in Europe, America, Africa, and cover other geographic regions, e.g. China and Japan. High proportions of masked mycotoxins co-occurring with their parent forms in various cereal-based food and feedstuff could clearly increase total exposures and pose additional health risks to humans and animals. In contrast to the parent mycotoxins, the data on the toxicity of masked mycotoxins are still scarce, however, the poor existing information showed that masked mycotoxins generally exhibit significant *in vitro* and *in vivo* toxicities lower than those of their parent forms, especially for deoxynivalenol-3-glucoside, which is the only thoroughly investigated masked mycotoxin. Although the lower toxicity level of masked mycotoxins, these are probably hydrolyzed into their free forms by intestinal microorganisms in the digestive tract of mammals and thus contribute to unpredicted toxicity. The metabolic characteristics of reported masked mycotoxins are species-specific. The most relevant animal model of human sensitivity, the pig, is most sensitive to masked mycotoxins. This review focuses on updates in the current knowledge on country-specific natural-occurrence data in global surveys, as well as *in vitro* and *in vivo* toxicology and metabolic investigations of masked mycotoxins.

Aflatoxin B1: A review on Metabolism, Toxicity, Occurrence in Food, Occupational Exposure, and Detoxification Methods

Rushing BR, Selim MI. *Food Chem Toxicol*. 2019 Feb;124:81-100. doi: 10.1016/j.fct.2018.11.047. [Article Link](#)

Significance: This review highlights the need for detoxification methods to reduce the global burden of aflatoxin B1 toxicity.



Aflatoxins are a class of carcinogenic mycotoxins produced by *Aspergillus* fungi and are known to contaminate a large portion of the world's food supply. Aflatoxin B1 (AFB1) is the most potent of these compounds and has been well-characterized to lead to the development of hepatocellular carcinoma (HCC) in humans and animals. This review focuses on the metabolism of AFB1, including epoxidation and DNA adduction, as it concerns the initiation of cancer and the underlying mechanisms. The link between AFB1 consumption and HCC is also discussed including synergistic interactions with the hepatitis B virus. Toxic effects of AFB1, including growth suppression, malnutrition, and immunomodulation, are also covered. This review also describes recent reports of AFB1 occurrence in global food supplies and exposures in occupational settings. Furthermore, a summary of recent detoxification methods is included to indicate the present state of the field in developing aflatoxin control methods. This information shows that AFB1 occurs frequently in food supplies at high concentrations, particularly in maize. Regarding detoxification methods, chemical control methods were the fastest methods that still retained high detoxification efficacy. The information presented here highlights the need to implement new and/or existing detoxification methods to reduce the global burden of AFB1 toxicity.

Food Processing Safety

Effect of Atmospheric Pressure Plasma on *Listeria monocytogenes* Attached to Abiotic Surfaces

Alessandria V, Rantsiou K, Cavallero MC, Cocolin LS. *J Food Prot.* 2019 Feb;82(2):233-237. doi: 10.4315/0362-028X.JFP-18-228. [Article Link](#)

Significance: The effectiveness of cold atmospheric pressure plasma treatments against *Listeria monocytogenes* biofilms is presented.

Listeria monocytogenes can be introduced into food processing plants via raw material of animal or plant origin and can establish endemic populations through formation of biofilms. Biofilms are a continuous source of contamination for food products, and *L. monocytogenes* cells in biofilms are more resistant to stress and sanitizing agents than are planktonic cells. The use of gas-discharge plasmas may offer a feasible alternative to conventional sanitization methods. Plasmas are a mixture of charged particles, chemically reactive species, and UV radiation and can be used to destroy microorganisms. The purpose of this study was to measure the effectiveness of cold atmospheric pressure plasma (APP) treatments against bacteria attached to a solid surface and to evaluate the individual susceptibility of various *L. monocytogenes* strains. Attention was focused on the state of the cells after treatment, combining detection by viable counts and quantitative PCR (qPCR). Most of the culturable cells were inactivated after APP treatment, but the qPCR assay targeting the 16S rRNA revealed the presence of injured cells or their entrance into the viable but nonculturable state. These results were at least partly confirmed by a resuscitation experiment. After APP treatment, *L. monocytogenes* cell suspensions were incubated in brain heart infusion broth; some cells grew in the medium and therefore had survived the treatment. An understanding of the effects of APP on *L. monocytogenes* can inform the development of sanitation programs incorporating APP for pathogen removal. Methods other than those based on the culturability of the cells should be used to monitor pathogens in food processing plants because cultivation alone may underestimate the actual microbial load.

Heavy Metals

Occurrence and Bioaccessibility of Mercury in Commercial Rice Samples in Montreal (Canada)

Lin H, Santa-Rios A, Barst BD, Basu N, Bayen S. *Food Chem Toxicol.* 2019 Feb 5;126:72-78. doi: 10.1016/j.fct.2019.02.006. [Article Link](#)

Significance: Estimates of dietary mercury exposure from rice in a typical Canadian population are below the current provisional tolerable weekly intake guidelines.

The objective of this study was to increase the understanding of mercury exposure via rice commonly consumed in a major North American city. Rice samples were collected from Montreal markets ($n = 89$) between 2016 and 2017 and analyzed for total mercury (THg) content. THg content ranged from 0.7 ± 0.1 to 9.3 ± 0.5 ng g⁻¹ dw. Significant differences ($p < 0.05$) were recorded among the various rice types and countries of origin. Overall, cooking had little effect on the THg concentrations in rice. Thiols play a major role in the fate of Hg, therefore thiol contents in rice were measured, and a weak but significant relationship between thiol and THg contents in rice ($p < 0.05$) was observed. An *in vitro* gastro-intestinal digestion method was used to assess the bioaccessibility rate of THg in cooked rice samples, and less than 44.5% of THg from the initial rice samples was bioaccessible after *in vitro* digestion. Dietary exposure to Hg through rice consumption was calculated for the typical Canadian population and values were all below current provisional tolerable weekly intake guidelines. This study improves our understanding of Hg exposures via rice in a large North American city.

Cadmium, Lead and Mercury in Muscle Tissue of Gilthead Seabream and Seabass: Risk Evaluation for Consumers

Renieri EA, Safenkova IV, Alegakis AK, Slutskaya ES, Kokaraki V, Kentouri M, et al. *Food Chem Toxicol.* 2019 Feb;124:439-449. doi: 10.1016/j.fct.2018.12.020. [Article Link](#)

Significance: A risk evaluation of cadmium, lead and mercury exposure from gilthead seabream and seabass found that consumption of the studied species is safe for these metals.

Cadmium (Cd), lead (Pb) and mercury (Hg) presence was investigated in the muscle tissue of gilthead seabream and seabass, collected from various aquaculture sites of the Aegean and Cretan Sea as well as from the fish market (fisheries). Risk for the Greek population through consumption of these species was estimated using two approaches: Target Hazard Quotient (THQ) and Hazard Index (HI). All heavy metal levels in the fish tissue were below the established safe limits for consumption. Metal accumulation was found to differ amongst mode of production, species, location and seasonality. Seabass demonstrated higher Hg and lower Cd concentrations than seabream, Hg and Pb seem to be more accumulated in closed seas and Pb values displayed a linear increasing trend from warmer to colder periods. Regression analysis revealed that the main contributing factor to Cd accumulation is species (beta: -0.28, 95%CI: -0.48 to -0.09); lead is predominately affected by seasonality (beta: 0.44,

95%CI: 0.29 to 0.59), Hg accumulation is mainly affected by location (beta: -0.32, 95%CI: -0.61 to -0.03) while wild seabream accumulates greater levels for Hg and Pb than farmed. Risk analysis demonstrated that consumption of the studied species, is safe for all metals (HI < 0.460 and TTHQ < 0.299).

Food Packaging

Risk Assessment for Migration of Styrene Oligomers Into Food From Polystyrene Food Containers

Gelbke HP, Banton M, Block C, Dawkins G, Eisert R, Leibold E, et al. *Food Chem Toxicol.* 2019 Feb;124:151-167. doi: 10.1016/j.fct.2018.11.017. [Article Link](#)

Significance: This risk assessment found that dimers and trimers in polystyrene food packaging present a low risk for consumers.

Regulation EU 10/2011 requires a risk assessment of Non Intentionally Added Substances (NIAS) migrating into food for food contact plastics within the EU. Styrene oligomers are important potential components of NIAS in polystyrene used for food packaging and so far only dimers and trimers have been identified. They are not genotoxic in vitro, and there is good evidence that they are not endocrine disruptors. Hazard characterization to establish "safe" exposure levels is based on 1. The No Adverse Effect Level (NOAEL) of 1 mg/kg bw/d in an oral rat study during pregnancy and lactation and 2. The concept of Threshold of Toxicological Concern (TTC). Likely human exposure is derived from 1. the concentrations of dimers and trimers in food simulants or 2. in food and 3. the probabilistic FACET exposure estimation based on dimer and trimer concentrations in polystyrene and their potential for migration. The Margin of Safety as the relation of potential consumer exposure and the "safe" exposure level was always above 1 (apart from migration with 95% ethanol which is no longer recommended as an official food simulant for overall migration into fatty food) demonstrating that dimers and trimers in PS food packaging present a low risk for consumers.

Food Allergy

Defining the Targets for the Assessment of IgE-Mediated Allergenicity of New or Modified Food Proteins

Houben G, Blom M, Alvito P, Assunção R, Crevel R, Fæste CK, et al. *Food Chem Toxicol.* 2019 Feb 28. pii: S0278-6915(19)30096-1. doi: 10.1016/j.fct.2019.02.036. [Article Link](#)

Significance: An inventory of health outcome-related assessment parameters and criteria potentially important for risk management decision-making for new or modified food proteins is presented.

Many food innovations rely on the introduction and use of new or modified proteins. New or modified food proteins may lead to major health risks due to their inherent potential to cause food allergy. Currently, the pre-market allergenicity assessment for new or modified food proteins and protein sources relies on methods for identifying allergenic hazards based on characteristics of known allergens. However, there is no general consensus on the allergenicity parameters to use and the criteria that should apply for the evaluation and decisions to be made. In this paper, we propose that the strategy for allergenicity risk assessment of new or modified food proteins and the methodologies applied should be governed by the risk management questions to be answered, reflected in the information needed by risk managers to enable their informed decision making. We generated an inventory of health outcome-related assessment parameters and criteria potentially important for risk management decision-making and we discuss the implications of selecting different optional criteria (e.g. cut-off values) for what could be accepted as safe with regards to the health outcomes in the (at risk) population. The impact of these various options on both method development and risk management practices was investigated.

Mechanisms That Define Transient Versus Persistent Food Allergy

Berin MC. *J Allergy Clin Immunol.* 2019 Feb;143(2):453-457. doi: 10.1016/j.jaci.2018.12.991. [Article Link](#)

Significance: Recent findings and knowledge gaps related to persistent versus transient food allergy are discussed.

Currently, we have a poor understanding of why some food allergies are outgrown and others are not. Deciphering the immune basis of the natural resolution of food allergy will likely provide critical information for developing new therapies for the treatment of persistent food allergies. There are limited cohort studies that have followed children with food allergy over time, but information generated from such cohorts points to features of innate and adaptive immunity, as well as environmental differences (microbiome) that discriminate those with persistent versus transient food allergy. Studies from mouse models highlight the importance of novel subsets of memory B cells rather than plasma cells combined with antigen re-exposure and T-cell help in the maintenance of IgE. In this review we discuss these findings from human cohorts and experimental systems and discuss existing gaps in our knowledge.