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Research Article

How to Visualize Depth of Interface Between Risky and Safety in the Food-Driven Intoxication?

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Introduction

Food intoxication is common environmental related health issue that it could trigger health imparities linked to autoimmune disease, infection, and metabolic disorders due to molecular re-wiring in homeostasis reflects skewed immune malfunction and oxidative stress to neuronal network, such as interruption development of brain, and cognitive function in early children [1]. Food borne illness caused by bacteria, viruses and parasites are one of the most common burdens in the world. Food borne illness is also one of the most prevalent causes in the United States [2-5]. It is estimated approximately one million diseases a week in the United States could be related to a pathogen. Microbial Genomics is the study of a viruses or bacteria's genome with the purpose to increase identification time and therefore decrease a delay in treatment. Additionally, many individuals in the United States struggle with food allergies. Food allergies are very serious towards public health since there is no current cure and treatment is for symptoms only [6].

Allergies, especially food allergies, are a common health concern, and it is important to research the best strategies to reduce illness because of the consequences of exposure to certain allergens. Omics technologies are methodologies related to DNA, RNA, proteins and metabolites [7,8]. The public has become more aware of this and other allergens and considerations have been made to prevent exposure. There is still more we can do to improve quality of life and treatment for people with food allergies, and prevent food-borne illness. The purpose of this perspective is to identify the economic impact of food borne illness/ food allergies in the United States and the use of advanced predictive methodology structured by various Omics platform combined with bioinformatics in the scope of detection of the potential pathogen in disease specific

pattern, identification of pathogen with symptomatic, and risk assessment based on the pathogen's genomic, and functional analysis reflecting immunogenicity using protein level compare to traditional methodology

Methods

We conducted a literary search in Pubmed. Key word search consisted of "Omics and Food Borne Illness", "Omics and Microbial Genomics" and "Biomarkers and Food Allergy." An initial search was limited to articles which have been peer reviewed from 2010 or more recent. We identified several different peer reviewed articles and digest them with discussing the concept and potential use of Omics as a potential detection tool and prevention earlier by setting pertaining to food borne illness or health intoxication. In addition to peer reviewed articles we also reviewed government databases used in risk assessment and the identification of pathogens may have been linked to a food illness/poisoning outbreak. These databases were generated using PulseNet 2016, CDC) and Genome Trakr (FDA) [9,10].

Result

Food borne illness continues to be a major problem in the United States. It is estimated, one is six Americans suffer from a food related pathogen in one year. Which equals to approximately 48 million people every year with an estimated economic burden of approximately $152 billion dollars annually? [11] Molecular-based detection method was implemented to address this public health issues, for example the Center for Diseases Control and Prevention (CDC) uses Pulsed-Field Gel Electrophoresis (PFGE) to produce a pathogen's DNA finger print. This method has been considered the gold standard for risk assessments pertaining to

food borne illnesses since the 1990s. There are some limitations to PFGE. Some strains cannot be identified using this method, it is time consuming, there is a potential a sample may change due to human error, and PFGE cannot separate isolates as efficiently as whole genome sequencing [9,12].

There are multiple different omics methods used in assessing bacteria and food borne illness. The some of the selected omics were Genomics, Transcriptomics, Proteomics, Metabolomics, and Metagenomics [8]. Genomics is the study of the genome. Transcriptomics, proteomics, metabolomics and metagenomics is the study of a pathogen and how it responds to stress and transmission routes. Transcriptomics pertaining to food borne illness looks into how bacteria or pathogens can become stressed when the cell is exposed to environmental situations causing the pathogen to leave homeostasis. One way a bacteria cell can become stress is by being exposed to antimicrobial or antibacterial treatments [8]. Metabolomics reviews the way the host might respond to the pathogen and how competitive microorganisms may influence the disease pattern. Proteomics is used comparatively to find similarities in proteins [13], while metagenomics focuses on mixed cultures and bacteria diversity.

Moving forward U.S. Food and Drug Administration (FDA) created a database where scientists and researchers from forty labs from all over the United States can add information about pathogens they have studied. According to the FDA's website, Genome Trakr has reviewed and stored over a 175 genomes and 129,000 sequences ("Whole Genome Sequencing (WGS) Program - GenomeTrakr Fast Facts", 2017). Genome Trakr identified the top pathogens in food outbreaks as *Salmonella, Listeria, E. coli/ Shigella, Campylobacter* and *V. parahaemolyticus* ("Whole Genome Sequencing (WGS) Program - GenomeTrakr Fast Facts", 2017) [12]. In addition to the collection of the genome, data associated with the pathogen sample is also collected. This data includes the individual's name who collected it, where the sample was collected and what food item the sample is from. The more data added the more likely public health officials can start using the Genome Trakr to start reviewing probability trends regarding the risk of specific food items and pathogens [11].

In addition to being able to predict trends pertaining to specific food sources or pathogens, sequencing the entire genome through Metagenomics can start linking cases to each other. This will allow public health officials to see more of the impact a particular pathogen or outbreak has on public health. As of right now one of the more commonly used tests can be compared to Metagenomics is a Culture-Independent Diagnostic Tests (CIDTs), which uses nucleic acid and antigen-based tests to determine the pathogen present [14]. Standard culture-based methods are more likely to take longer than an Omics based strategy due to standard culture/ microbio taxonomy and culture processes of testing and retesting. Metagenomics is likely to be faster and more comprehensive.

However, there are several drawbacks to Metagenomics. It is expensive in comparison to traditional techniques. One of the reasons for the increase in cost is the requirement of a fast high powered computer. The cost of the computer-equipped bioinformatics matrix may be worth the gain in time due to the ability for Metagenomics to test and rule out DNA sequences of bacteria, archaea, eukaryotes, parasites, and viruses at the same time [14].

The majority of this research paper up until this point has focused on food poisoning/food borne illness. However, food allergies are another prevalent public health concern which this paper will discuss at this time. The prevalence for food allergies is slightly ambiguous due to the tendencies for individuals to self-report food intolerances as food allergies but there is an estimated 5-8% in children and 5% in young adults/ late adolescence [6]. Food allergies have a longer chronicity than food borne illness. Some children are able to outgrow food allergies but many do not. This causes additional economic impact since care givers may need to take time off of work to take care of their sick child. The estimated economic cost of food allergies in the United States, including lost wages is approximately $24.8 billion per year. The ultimate goal in using Food Omics and Proteomics is to determine predictable biomarkers to determine which foods are more likely going to cause allergies in the general population based off of food contaminants, food origins, and how close the food product's genome is to its original genome, additives present and the type of processing the food product endures prior to reaching the consumer's home [15-17].

Zhou et al. [18] identified 13 peanut allergens, which come from 7 protein families. The linear epitopes sequences and the corresponding genes of the peanut allergens have been identified. The authors describe characteristics such as structure of the proteins and the percentage of the allergic population they affect. As a result of this understanding, the authors were able to identify chemical methods of reducing allergenicity of peanuts. For example, they described how tannic acid interrupts the interaction between epitopes and antibodies, and therefore reduces allergenicity. According to the CDC (2015), there are six different *E. coli* pathogen associated with sickness. Due to the diversity of these bacteria, it is important to know the process of the infection cycle as well as how the bacteria interact with a potential host. One study led by Hua et al. [19], they found that *E. coli* gene expression was significantly influenced by nutrient conditions which could be associated with alteration of gene expression pattern due to glucose limitation. Similarly, other group in food science produces support results like impact of glucose in their own experimental model utilize E coli regarding to underlying mode of action during a food poisoning outbreak.

A common method of conducting a risk assessment for food allergies is probabilistic risk assessment. Probabilistic risk assessment is a computer based statistical method is used to calculate

potential outcomes through identifying the minimum eliciting dose for a specific allergen [20]. Proteomics has been useful when it comes to studying allergies. Proteomics is the study of proteins and an allergy is caused by the body lacking the necessary enzyme. A data base (allergen.org) was created as a way to maintain and transport allergen information to researchers and health care professions. However, this data base is limited due to the amount of proteins are linked to allergies and the abundance of specific proteins present. Protein library is important in proteomics when using peptide epitope because redundancy and abundance of a specific protein can produce from mass spectrometry to be misread [17].

Translating omics based strategies out of the research lab and into the clinical setting has been more of a challenge. Specimen collection, FDA Standards and lengthy clinical trials are all barriers widespread omics strategies must overcome prior to being consistently used in a clinical setting [14]. However, biomarkers are used consistently in oncology for screening for disease and predicting treatment and prognosis. Additionally, there has been success in identifying potential drug resistances which can accelerate treatment for several individuals by decreasing the number of drug trials prior to successful medication therapy [21].

Conclusions

The use of multi-dimensional to define interface between safety and risky in food allergy/food poisoning and prediction as a health care assessment has benefit by increasing identification of a pathogen or hazardous contamination and empower treatment option. This concept sounds assessment procedure but ideal to develop key molecule driven from innate or delayed immune response to adaptive or differentiated immune machinery in the human body. If the multiple data from human specimen's bases around the world continue to grow, making identification of a strand more likely, then public health officials could predict the likelihood of a disease outbreak, cancers, and the probability that a treatment will work under one networking such as e-surveillance for safety in patients and clinic level. Being able to arrest these problems prior to the start, structuring of bioinformatics has the potentiality to greatly diminish the current health care economic burden. However, the implementation in the clinical setting may take time from lab to bench; the product will be worth the wait. In the future, it is likely that a majority of our treatment and care for patients will be based on an omics strategy to visualize stratification of pathogen or environmental contamination in single molecule level.

Future Perspective

Breaking barrier by identifying macromolecules and their network with functionality such as immunogenicity or food insensitivity to niche of microflora in organ specific pattern have the empower to prevent metabolic malfunctions or indulgence of network between neural and digestive system by adopting integrate fields such as predictive food safety derived from toxicology and genomics by visualizing each module of omics to identify relationships between the two and multiple interactions (e.g. DNA to protein vs. RNA to protein) or between organisms and toxins (e.g., SNP vs. sensitivity to toxin) and create treatments utilize targetable molecular/receptor- specific interaction (e.g. immune cell surface molecule to food intoxication) and sequential of cognitive and behavioral action between body to brain in signaling crosstalk (i.e., reward circuit to food addiction vs. stress).

Acknowledgement

References

1. Gupta R, Holdford D, Bilaver L, Dyer A, Holl JL, et al. (2013) The economic impact of childhood food allergy in the United States. JAMA Pediatr 167: 1026-1031.

2. Wells JM, Bennik MH (2003) Genomics of food-borne bacterial pathogens. Nutr Res Rev 16: 21-35.

3. Kirk MD, Pires SM, Black RE, Caipo M, Crump JA, et al. (2015) World Health Organization Estimates of the Global and Regional Disease Burden of 22 Foodborne Bacterial, Protozoal, and Viral Diseases, 2010: A Data Synthesis. PLoS Med 12: e1001921.

4. Nony E, Le Mignon M, Brier S, Martelet A, Moingeon P (2016) Proteomics for Allergy: from Proteins to the Patients. Current Allergy and Asthma Reports 16: 64.

5. Bergholz TM, Moreno Switt AI, Wiedmann M (2014) Omics approaches in food safety: fulfilling the promise?. Trends Microbiol 22: 275-281.

6. Boyce JA, Assa'ad A, Burks AW, Jones SM, Sampson HA, et al. (2010) Guidelines for the Diagnosis and Management of Food Allergy in the United States: Report of the NIAID-Sponsored Expert Panel. J Allergy Clin Immunol 126: 1-58.

7. Blum K, Oscar-Berman M, Barh D, Giordano J, Gold M (2013) Dopamine Genetics and Function in Food and Substance Abuse. J Genet Syndr Gene Ther 4: 1000121.

8. Center for Disease Control and Prevention. CDC 24/7: Saving Lives, protecting people (2015) *E. coli* (*Escherichia coli*).

9. Center for Disease Control and Prevention. CDC 24/7: Saving Lives, protecting people (2016) Pulsed-field Gel Electrophoresis (PFGE).

10. Allard MW, Strain E, Melka D, Bunning K, Musser SM, et al. (2016) Practical Value of Food Pathogen Traceability through Building a Whole-Genome Sequencing Network and Database. J Clin Microbiol 54: 1975-1983.

11. Wiwanitkit V (2013) Utilization of multiple "omics" studies in microbial pathogeny for microbiology insights. Asian Pac J Trop Biomed 3: 330-333.

12. O'Connor JP, Aboagye EO, Adams JE, Aerts HJ, Barrington SF, et al. (2017) Imaging biomarker roadmap for cancer studies. Nat Rev Clin Oncol 14: 169-186.

13. Forbes JD, Knox NC, Ronholm J, Pagotto F, Reimer A (2017) Metagenomics: The Next Culture-Independent Game Changer. Front Microbiol 8: 1069.

14. Bucholska J, Minkiewicz P, Darewicz M, Iwaniak A (2018) Databases and Associated Bioinformatic Tools in Studies of Food Allergens, Epitopes and Haptens - a Review Pol. J Food Nutr Sci 68: 103-113.

15. Boehmer JL (2011) Proteomic analyses of host and pathogen responses during bovine mastitis. J Mammary Gland Biol Neoplasia 16: 323-338.

16. Ortea I, O'Connor G, Maquet A (2016) Review on proteomics for food authentication. J Proteomics 147: 212-225.

17. Zhou Y, Wang JS, Yang XJ, Lin DH, Gao YF, et al. (2013) Peanut Allergy, Allergen Composition, and Methods of Reducing Allergenicity: A Review. Int J Food Sci 2013: 909140.

18. Hua Q, Yang C, Oshima T, Mori H, Shimizu K (2004) Analysis of gene expression in *Escherichia coli* in response to changes of growth-limiting nutrient in chemostat cultures. Appl Environ Microbiol 70: 2354-2366.

19. Crevel RW, Baumert JL, Baka A, Houben GF, Knulst AC, et al. (2014) Development and evolution of risk assessment for food allergens. Food Chem Toxicol 67: 262-276.

20. U.S. Food and Drug Administration (2017) Whole Genome Sequencing (WGS) Program - Genome Trakr Fast Facts.

21. McShane LM, Cavenagh MM, Lively TG, Eberhard DA, Bigbee WL, et al. (2013) Criteria for the use of omics-based predictors in clinical trials. Nature 502: 317-320.