

Dietary microbial exposure: Relation with allergies?

Keywords: allergies, nutritional micro-organism load, food habits

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Project duration: BSc and MSc - 3-6 months

Project description:

Background:

Declining microbial exposure is suggested as a major cause for the increase in allergic disease in recent decennia. This concept has been based on the "hygiene hypothesis" in which it is hypothesized that frequent infections in early childhood could be protective for the development of allergic disease. Over the years, the focus on microbial exposures has widened from the influence of pathogenic microbes causing infections towards non-pathogenic types of strains (commensals and environmental strains) and components of microbes such as bacterial endotoxins by farm living. In parallel with the potential association of microbial load and the increase in the prevalence of allergic disease in the past decennia, food habits have changed dramatically. However, there are no data available on the total microbial exposure of our diet. In earlier theses, we identified foods contributing to 95% of the total microbial load and developed a food frequency questionnaire (FFQ) for assessment of the dietary microbial content of the diet.

To follow-up these studies, we aim to:

1. Study factors influencing on minimum and maximum microbial contents and to incorporate these factors into the FFQ;
2. Evaluate the FFQ on the individual level;
3. To qualitatively describe differences between our actual food habits and those of several decennia ago, and the suspected effect on the dietary microbial exposure;
4. To quantitatively compare the microbial load of the Dutch National Food Consumption Survey 2003 with the diet used several decennia ago.

Activities:

Literature research, recruitment of participants, development and validation of an instrument by sampling and analysis of duplicate foods, statistical analyses using SPSS, report and presentation.

How heat resistant are microorganisms?

Keywords: meta-analysis, heat treatment experiments *D*- and *z*-value, variability

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Project duration: BSc and MSc – 4-6 months

Project description

Numerous thermal inactivation studies have been done for foodborne pathogens and spoilage microorganisms to determine their thermal resistance. However, the results of the thermal inactivation studies vary because of the differences between used inactivation method, strain, inactivation medium, physiological state of the cells, etc. To determine the global thermal inactivation parameters of a pathogen, such as the *D*-value and *z*-value, a meta-analysis study can be initiated (1). In a meta-analysis study, a vast number of thermal inactivation data of a foodborne pathogen are collected, and the global thermal inactivation parameters, as well as the factors influencing thermal resistance can be extracted. In this way, the differences found in many studies can be explained and the sources of variability can be listed and quantified. This information is critical to realistically predict inactivation of microorganisms in foods.

After the first meta-analysis initiative in 2006 for pathogens (1), more and more thermal inactivation studies of foodborne pathogens have been published. Thus, there is a need to incorporate those recent publication data into the existing database, especially for the pathogens for which only few studies were available at that time. The extension of this database is expected to result in more reliable information on the thermal inactivation profile of the pathogen in question. Furthermore, we want to extend the data base with information on spoilage organisms.

Also you will perform heat inactivation experiments with several strains from a same species (e.g. *Salmonella*, spores of *B. subtilis*) to compare strain variability to the variability found in literature (2). This will help us to understand how strain variability affects thermal inactivation efficiency.



1. van Asselt, E. D., and M. H. Zwietering. 2006. A systematic approach to determine global thermal inactivation parameters for various food pathogens. *International Journal of Food Microbiology*. 107:73-82.

2. Aryani D.C., den Besten H.M.W., Hazeleger W.C., Zwietering M.H. 2015. Quantifying variability and the effect of growth history on thermal resistance of *Listeria monocytogenes*. *International Journal of Food Microbiology* 193, 130-138

What are the kinetics of toxin formation of *Bacillus cereus*?

Keywords: meta-analysis, toxin production, variability

Supervisors: Heidy den Besten (heidy.denbesten@wur.nl)
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Project duration: BSc and MSc – 4-6 months

Project description

Numerous studies have been done to determine toxin production of *Bacillus cereus*. However, the results of these studies vary because of the differences between used method, strain, medium/food product, level, physiological state of the cells, etc. To determine the global kinetics of toxin production and main factors that control the formation, a meta-analysis study can be initiated (1). In a meta-analysis study, a vast number of data are collected, and the global kinetic parameters, as well as the factors influencing this can be extracted. In this way, the differences found in many studies can partly be explained and the sources of variability can be listed and quantified. This information is critical to realistically get insight in toxin formation.

After the first meta-analysis initiative in 2006 for pathogens, more and more meta-analyses of foodborne pathogens have been published.

Also you will perform some experiments with several strains in media and in some food products to compare strain variability to the variability found in literature. This will help us to understand how strain variability affects toxin formation.



1. Heidy M.W. den Besten, Marcel H. Zwietering. 2012. Meta-analysis for quantitative microbiological risk assessments and benchmarking data. Trends in Food Science and Technology 25: 34-39

Risk assessment of *Listeria monocytogenes*

Key words: exposure assessment, risk assessment, maximum dose, competitive flora, ready-to-eat products

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Project duration: MSc only – 3-6 months

Project description:

Listeria monocytogenes has caused foodborne disease with major public health consequences, mainly in the elderly. The organism is known to grow in a variety of ready-to-eat products at refrigeration temperatures. Various authors have estimated the risk of listeriosis and the risk of ingesting a certain number of *Listeria* has been assumed to depend on time and refrigeration temperature; higher temperatures being associated with higher maximal doses and lower temperatures with lower maximal doses. The maximum number of organisms that can be reached forms an essential parameter in exposure assessment of *L. monocytogenes*.

Recent experimental research suggests that the maximal number of *L. monocytogenes* that can be present in ready-to-eat food products is higher than previously assumed. The objective of this research is to update existing an existing risk assessment model with recently obtained data on the maximum concentration of *L. monocytogenes*. The work will include literature search, computer-based modelling and laboratory work.

Prediction of spoilage of fresh poultry meat under dynamic temperature regimes

Keywords: *shelf life fresh poultry meat, Pseudomonas ssp., cold chain, temperature abuse*

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Project duration: MSc thesis project- 6 months or
practical training – 6 months

Project description:

To control the spoilage of fresh poultry meat, it is of importance to control the temperature in the chain starting from production and distribution to storage at home of consumers. Predictive models could help to understand the impact of temperature on shelf life of products. Moreover, it allows prediction on the effect of interventions on the shelf life. This project aims to develop a predictive shelf life model for fresh poultry meat as a function of temperature. The project will be executed in collaboration with a Dutch producer of fresh poultry meat.



The following activities are foreseen in the project:

1) *Construction of a predictive shelf life model for fresh poultry meat*

Models that predict the growth of the spoilage microorganisms *Pseudomonas* sp. on fresh poultry meat as a function of temperature will be constructed.

2) *Validation of the predictive models*

The predictive shelf life model for fresh poultry meat will be validated in practice. The predicted shelf life of fresh poultry meat stored at different temperature regimes will be compared to the observed shelf life.

3) *Effect of interventions on the shelf life of fresh poultry meat*

Using the model developed under 1) the effect of interventions aiming for reduction of initial on shelf life can be predicted. Intervention that can be included are for example altered cleaning and disinfection regimes, use of UV or pulsed light treatment. Depending on the availability of literature data, relevant input data can be obtained from literature, historical data present of the producing industries or should be experimentally determined.

Project duration

This project could be executed as a MSc thesis project (6 months) at Food and Biobased Research or as a practical training (6 months) at Food and Biobased Research. In the latter case, a stay at the poultry meat producing industry is an option.

References:

Bruckner et al. (2013). A predictive shelf life model as a tool for the improvement of quality management in pork and poultry chains. *Food Control* 29: 451-460.

Sylvain Dabadé et al. (2015). Prediction of shelf life of tropical shrimp (*Penaeus notialis*) under dynamic temperature regimes. *Int. Journal of Food Microbiology* 210: 121-130.