



European Symposium on Food Safety

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Programme



In Collaboration with ILSI Europe and with the
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11.6, 5.3, and 2.3 QALY loss per 1000 human campylobacteriosis cases, respectively. Inflammatory bowel disease and irritable bowel syndrome were omitted, in line with a WHO opinion. The overall, discounted health burden per case was calculated as 0.0152 QALY loss (versus the assumed 0.0389 DALYs). The combined application of currently available control measures of low/medium consumer impact were found to generate both cost saving in the EU-27 and health benefits, even when using the adjusted, conservative model input parameters. Value based pricing of a control measure under development will also be presented in two EU countries.

S5 Strain and Population Diversity; Implications for Food Safety and Food Spoilage

It is a well-recognized problem within the field of food quality and safety assurance that microorganisms behave very diversely with respect to their robustness. Efficacy of control is challenged by diversity in robustness of strains belonging to same species, diversity within microbial populations, and the physiological state of micro-organisms. Food processing environments and food preservation measures can impose significant selection forces on foodborne microorganisms, and thereby possibly selecting for the most robust microorganisms. These robust survivors can cause food safety or food spoilage problems, or can become domestic flora in factories. This symposium will focus on robustness diversity of relevant food spoilage organisms (both bacteria and fungi) and foodborne pathogens. We will address these issues with leading experts in the field, discussing single-cell based approaches to investigate population heterogeneity, giving insight in mechanisms contributing to selection of persisters upon food processing, and the importance of quantification of microbial diversity to make prediction of microbial behaviour along the food chain more realistic.

Strain Variability in Growth and Inactivation Parameters: Relevance for Pathogens and Spoilage Organisms

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The actual behaviour of microorganisms can differ from the prediction of microbial growth and inactivation models. Various factors might contribute to this difference, including strain variability and variability between experiments. Therefore, apart from quantifying the impact of strain variability on growth rate and thermal resistance, also biological variability was determined to prioritize their importance.

The impact of strain variability on the μ_{max} was found to be comparable to biological variability as function of pH, a_w , temperature, and undissociated lactic acid concentration for *L. monocytogenes*. The integration of strain variability in the prediction of growth of *L. monocytogenes* caused easily a difference of about 2–3 log, depending on the conditions and type of food product, between the most and least robust strains.

In contrast to the results for growth rate, strain variability in thermal resistance of *L. monocytogenes* was found to be four times higher than biological variability. Strain variability in thermal resistance was also comparable to the effect of growth history, which was mainly determined by the effect of growth phase. Strain variability alone explained about ¾ of the variability in thermal resistance of *L. monocytogenes* found for a large variety of data in literature. Although with bias, the effect of both strain and growth history explained all the variability from literature. Strain variability in thermal resistance of a spoilage microorganism, *Lactobacillus plantarum*, was also found to be larger than biological variability. Thus, it may be suggested that strain variability is the most important aspect to be considered for designing an appropriate thermal process.

Single Cell Variability: Relevance for Fungal Spoilage Processes

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Most of the available studies on fungal behaviour in foods deal with monitoring growth of mycelia originated from a large number of spores. In practice however, the contamination of food with fungal spores is often associated with very low numbers. This presentation provides an overview of the recent studies on the variability of the germination time and mycelium growth kinetics of single fungal spores with examples for *Penicillium expansum* and *Aspergillus niger*. The methodology for taking into account single spore variability in modeling fungal behavior in foods is described. A large number of data on the germination and the lag time of mycelia originated from single spores at various storage temperatures is presented together with time-lapse microscopy videos on single spore germination and mycelium growth. In addition, the relation between germination and lag time of single spores is discussed. The importance of single spore variability is demonstrated through a quantitative risk assessment study of yogurt spoilage by *Aspergillus niger*. In this study a stochastic modelling approach was applied based on *Aspergillus niger* mycelium growth model taking into account the important sources of variability such as time-temperature conditions during the different stages of chill chain and individual spore lag time. By combining the output of the model with the mould prevalence, estimated by the industry using challenge tests, the probability distribution of the number of cups in which a visible mycelium of *A. niger* is formed at the time of consumption can be estimated. The risk assessment model which takes into account variability can lead to a more effective risk-based quality management of yogurt and support the decision making in yogurt production.

Causes and Consequences of Heterogeneity in Stressed Populations of Foodborne Pathogens

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Comprehensive insights into how foodborne pathogens exactly perceive, react, respond and adapt to the many stresses and selection pressures they encounter throughout the food production chain are elementary for a proper understanding of their resulting behavior and evolvability. In this context, the implementation of live cell biology approaches to study (stressed) bacterial populations with increased intra- and intercellular resolution is yielding an increasingly detailed view on the causes and consequences of population heterogeneity, which are likely to become indispensable in our efforts to mechanistically explain and better anticipate the mechanisms and strategies behind the inactivation, survival and resistance development of foodborne pathogens.

S6 Virus Testing, Interpretation and What Do I Do with a Positive Result

Enteric viruses, particularly human noroviruses (NoVs) are the most common cause of food borne disease, responsible for up to 50% of all outbreaks and cases per year worldwide. Viruses enter the food supply across the farm-to-fork chain by exposure to contaminated waters, surfaces, and/or human hands. A number of high profile outbreaks