

Data exchange for safer food

Increased collaboration and the use of internet technology is helping to bolster food safety research efforts.

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Microbiological food safety is a major issue for the food and beverage industry as well as for regulators, and much research effort is dedicated to ensuring that our food is safe. Despite this, there were an estimated 1.3 million cases of food-borne disease and 480 deaths in England and Wales, UK, in 2000, mainly due to *Campylobacter*, *Salmonella*, *Clostridium perfringens*, verocytotoxin producing *E. coli* (VTEC) O157 and *Listeria monocytogenes*¹. The financial implications of an outbreak of food-borne disease traced back to a commercial product are far from inconsequential. The US Agricultural Research Service (ARS) has estimated that the cost of a product-related outbreak of listeriosis or salmonellosis is \$12,000 per person infected. This includes product recall and healthcare costs, as well as damage to brand image. For an outbreak of botulism this rises to a staggering \$30m per person.

Analysing the adequacy of testing methods

Traditionally, the safety and shelf life of foods have been estimated by challenge tests or inoculated pack experiments. After storage, the food is tested to determine whether the organism of interest has multiplied, merely survived or lost viability. The test conditions often differ substantially from actual conditions during processing and storage, and this has led to questions over validity. Accelerated challenge tests, for example, might not accurately represent microbial growth at lower temperatures due to temperature dependent changes in microflora.

Microbiologists in industry, at research institutes and universities have produced large amounts of data evaluating the response of food-borne pathogens to the food environment (such as temperature, pH and salt). Despite this inexorable increase in the amount of challenge test data available, the need for a better understanding of microbial replication and death in the food environment has not abated. Every modification to a food process has the potential to impact on growth and death rates, novel foods are providing entirely new bacterial ecosystems, and emerging pathogens give rise to new challenges for both the food and the clinical microbiologist. Consumers desire food that is 'fresher' and more 'natural', whilst expecting it

to be free from pathogenic and spoilage bacteria, additives or contaminants. These demands require a sound understanding of microbial physiology and ecology in foods, as well as of microbial responses to food preservation methods.

Predictive microbiology

Based on the premise that bacteria respond to environmental conditions in reproducible ways, empirical data can be described and summarised in mathematical models to predict the microbiological ecology of a new environment. Predictive microbiology informs safe food processing at a number of levels. Understanding the microbiological consequences of changes to product formulation guides the rational design of new processes. It also empowers Hazard Analysis Critical Control Points (HACCP) by evaluating the consequences of processing, assessing critical control points (in association with stochastic modelling) and evaluating lapses at critical control points, from which appropriate remedial action can be identified.

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Microbiologists have long dreamed of being able to model the growth and death of microbes in foods; indeed the concept of predictive microbiology was suggested as early as 1937, but work did not begin in earnest until the 1980s, when sufficient funding and computing power became available. Because of the inherent complexity of food as a microenvironment, large quantities of data are necessary to develop mathematical models. However, incompatible data recording practices have been a major obstacle in the development of predictive microbiology.

The Institute of Food Research (IFR) developed a standard microbiology data recording protocol in the early 1990s. The protocol was initially used to enable data from any laboratory to be processed by IFR's modelling programs, DMFit and MicroFit. The UK Ministry of Agriculture Fisheries and Food (MAFF) adopted the same format to store the entire data set (10,000 microbial curves) generated during its £5m Predictive Microbiology Programme and the Food Standards Agency (FSA) have continued to support this format. One of the spin-offs of this programme was Food MicroModel, predictive software based on a subset of the whole dataset.

The USA Eastern Regional Research Center of the Agricultural Research Service (ARS-ERRC) also saw several advantages in a universal predictive microbiology database, including access to raw data, increased efficiency of data retrieval and analysis, and higher mobility of the data among users. It also used a standard recording protocol for the data underpinning their Pathogen Modelling Program (PMP). Thus, two large compatible databases of microbial responses to food environments were developed, each composed from thousands of microbial growth and survival curves that are the basis for numerous microbial models used by industry, academia and government regulatory agencies. Now, these two independent databases have been unified in a common database known as ComBase. Additional information has been submitted by the Center of Excellence in Microbial Modeling and Informatics (CEMMI) and further entries have been compiled from the scientific literature by IFR researchers.

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Creating a unified database

The rationale behind the database is that whilst microbial survival and death curves have been generated for a variety of purposes, they all represent microbial response to a specific environment around the cells. In mathematical terms, this is a mapping between two spaces, both of which can be characterised by one or more variables, depending on how detailed the description is intended to be.

The ComBase consortium (FSA and IFR in the UK, and the US Department of Agriculture and ARS-ERRC in the USA) had to consider which environmental conditions to include, and how each should be quantified. The structure of the database had to support common search requests; it needed to be user-friendly, but

sophisticated enough to help analyse questions on hazard and risk analysis. In addition, it needed to be sufficiently flexible to be able to include new types of data, or risk rapid obsolescence.

The result was a relational database with four major groups of fields: administrative (organism, data source and so on), environment (temperature, pH, additives, special properties and so on), response (change of cell concentration during the observation time, maximum specific rate, growth/no growth and so on) and comments (other experimental conditions, materials and methods, and notes on the quality of the record).

A major feature of the database is that an entry need not only be a single (numeric or alphanumeric) value in a field, but may also be a pointer to another table. In this way, an environment or response variable can take up a dynamic (time-dependent) profile. This makes it possible to record a whole growth or survival curve, possibly observed under fluctuating temperature, in accordance with the dynamic model of Baranyi and Roberts², for which this database structure was originally introduced.

Regulation and expansion

Quality control of uploaded information is regulated by IFR, and the web-interface of ComBase, developed by the US partners, is now freely available on the internet (www.ifr.ac.uk/combase). At present, it contains around 20,000 growth and survival curves, and 8000 records containing growth rates. The ComBase partners are inviting microbiology laboratories in academia, government and industry to submit relevant predictive microbiology data. This international effort will: avoid unnecessary repetition of experiments, thus increasing the efficiency of research efforts; improve predictive models, thus improving food safety and quality; and standardise the data sources for microbial risk assessors, thus decreasing potential trade disputes.

Work is now underway to use ComBase to produce a package of unified predictive models known as ComBase-PMP (Combined Database and Predictive Microbiology Program), which will supersede the various software packages currently supported by each of the ComBase partners. Funding from the European Commission is providing the opportunity for many EU institutions to add their own publicly available data into ComBase. This pooling of microbiology data represents a major breakthrough in the development of data exchange between the EU and the USA. Recent moves to extend the idea worldwide include negotiations with Australian and South American partners. ❖

References

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- 2 Baranyi J & Roberts TA. 'A dynamic approach to predicting bacterial growth in food'. *Int J Food Microbiol* 1994;23:277-94.