The ComBase initiative

Introduction

Food safety professionals in industry, academia and regulatory agencies increasingly use computer modelling tools to improve food safety and shelf life (including the development of Hazard Analysis Critical Control Point (HACCP) plans) and to support microbial food safety risk assessments. Earlier this year, we conducted workshops in Melbourne and Sydney to introduce Australian scientists to one such tool, ComBase, and to provide training in its use.

ComBase is an internet-searchable database of microbial growth and inactivation responses that provides support for the use of 'predictive microbiology' approaches [1-3]. Predictive microbiology involves the systematic development of knowledge of microbial growth responses to environmental factors relevant to foods, and their summary as mathematical models. The models can be used to interpret the effect of processing and distribution practices on microbial growth in foods, or to design foods, or food processes, to meet required levels of shelf life/and or safety. Predictive microbiology models can provide precision in making decisions on the microbiological safety and quality of foods [2].

ComBase is based on the combined data resources of the Pathogen Modelling Programme (PMP), the now defunct Food MicroModel (FMM) and publicly available scientific literature. It includes tens of thousands of growth and inactivation rate data for food-borne pathogens and spoilage organisms.

History of ComBase

A database format for the purpose of collating and making accessible microbiological data produced by different laboratories was developed at the Institute of Food Research (IFR, Norwich, UK) and adopted by the UK Food Standards Agency for the data collected in their Predictive Microbiology Programme during 1985-1992. The United States' Department of Agriculture's Agricultural Research Service Eastern Regional Research Centre, in

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Philadelphia, USA (ARS ERRC) also joined the initiative, transforming the raw data behind their Pathogen Modelling Program (download from: http://www.arserrc.gov/mfs/pathogen.htm) into the same format.

The resultant database created ComBase, a COMmon relational dataBASE, which is accessible on-line (and free of charge) at: www.combase.cc. The FMM and PMP datasets have been supplemented with additional information submitted by members of the ARS ERRC Center of Excellence in Microbial Modelling and Informatics (CEMMI) and by that compiled from the scientific literature by the IFR, Norwich, UK, through the support of the UK Food Standard Agency.

With funding from the European Union, data from other European institutions have also been incorporated in ComBase, which now contains thousands of full bacterial growth and survival curves or their kinetic parameters. In addition, software routines are provided to facilitate the application of the data that can be obtained from the database.

In May, 2003, the USDA-ARS, its ERRC laboratory, the Food Standards Agency of the UK and the Norwich-based Institute of Food Research signed a 'Concordat' that established the ComBase Consortium. The aims of the Concordat are to support long-term collaboration in compatible database building and exchange, as well as data dissemination, in the interests of food safety and to support the development of quantitative microbial risk assessment.

The database was officially launched in June 2003, at the 4th International Conference on Predictive Modelling in Food, Quimper, France. At that time, it contained around 24,000 full viable count growth/survival curves and some 8,000 records on the growth/death rate parameters. Negotiations have begun between the ComBase Consortium and Australian Food Safety Centre of Excellence to incorporate the Centre's modelling database into ComBase and for long-term collaboration.

What is in ComBase?

Currently, two types of microbial responses are recorded in ComBase: full growth or survival/inactivation curves produced by viable count measurements; and specific growth/inactivation rates only, derived from viable count or other (e.g. optical density) measurements, as published by various authors, in refereed papers. As well as the most well-known pathogens, data describing the behaviour of spoilage organisms can be also found in the database.

Among pathogens, data on *Aeromonas hydrophila/sobria/caviae; Bacillus cereus* (spores and vegetative cells); *Clostridium botulinum; Clostridium perfringens; Escherichia coli* (O157 and also non-pathogenic *Escherichia coli* (NPEC); *Listeria monocytogenes/innocua; Staphylococcus aureus; Shigella flexneri; salmonellae;* and *Yersinia enterocolitica* are included.

Among data on spoilage organisms are those describing the microbial ecology of *Brochothrix thermosphacta*; psychrotrophic pseudomonads; lactic acid bacteria; enterobacteria; total spoilage flora and other psychrotrophic bacteria in foods.

Users can search by the database according to any combination of organism of interest, the type of food or other environment that the experiments were conducted in, the temperature, pH and water activity ranges of interest, and the source (authors or institution) of the data. Matching records are then displayed individually with the user able to scroll between records.

Depending on the specificity of the search parameters, more or fewer records will be retrieved, and it may be necessary for a user to attempt a few variations on the search criteria to obtain the desired number of records. The data displayed include the time vs. log CFU plot, raw data, source of the data and full details of the experimental methods used (Figure 1).

With funding from the UK Food Standards Agency, a software package to predict microbial growth in food environments, called Growth Predictor, has been developed at IFR and is available, also free of charge, at http://www.ifr.ac.uk/Safety/GrowthPredictor/ This software is intended to replace Food MicroModel, the former commercial predictive microbiology software package supported by the FSA.

The future of ComBase

An aim of the ComBase project is to produce a software environment with a robust database of information that will help the work of risk assessors, using standardised methods. In the new science-based paradigm of international trade in foods, the availability of such tools and methods, together with supporting data, will contribute positively to international food trade negotiations as well as to better management of microbial food safety.

Servicing, data analysis and predictive programmes are also being developed to maintain the quality of the database and to enable it to realise its full potential.

Roberts & Jarvis [4] challenged traditional methods of food quality and assurance testing, which they described as *"an expensive and largely negative science"* and formally introduced the concept of predictive microbiology. They advocated a more systematic and cooperative approach to microbial food safety assurance where individual workers and organisations would cooperate to generate quantitative data on the microbial ecology of foods, and thereby build up a quantitative database from which all could benefit, rather than duplicating the same data repeatedly.

Roberts [5] recounted their belief that *"models relevant to broad categories of foods would greatly reduce the need for ad hoc microbiological examination and enable predictions and quality and safety to be made more speedily with considerable financial benefit".* Roberts and Jarvis' vision may now be realised in ComBase, as highlighted by McMeekin [6], who considered that *"properly supported, the COMBASE initiative will be a watershed in the evolution of predictive modeling and its widespread application".*

Further detail on ComBase can be found in Baranyi & Tamplin [7] and Baranyi *et al.* [8].

Acknowledgements

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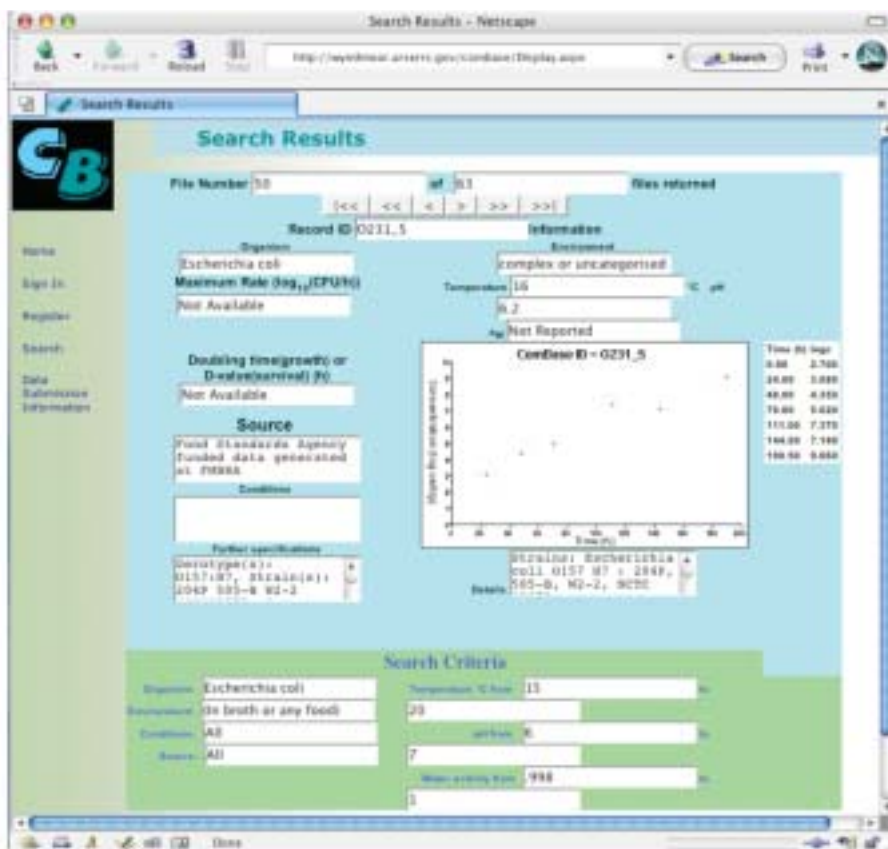

Figure 1. A example output screen from ComBase showing the search criteria (lower part of screen) and one of the records found. Near the top of the screen can be seen the specific record being viewed, the total number of records matching the search criteria, and the links for moving forward and backward between the records presented.