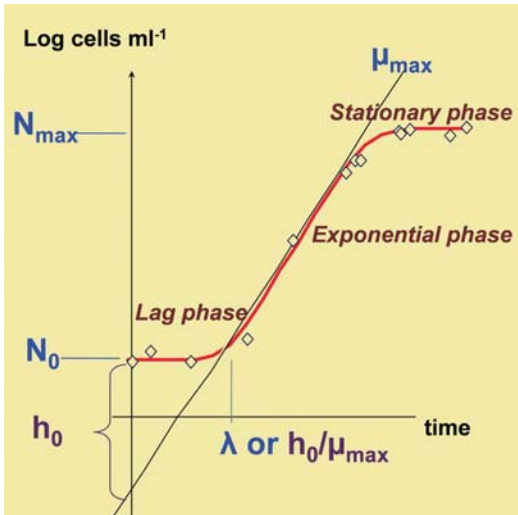


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## Pathogens: Physiology and Predictive Ecology

The microbiological safety of foods is important to everyone in the UK. The Food Standards Agency estimates there are 1.3 million cases of food poisoning each year in England and Wales, costing £1,500 million. Food poisoning can be mild, but it can also mean time off work, require hospitalisation or, in very rare cases, be fatal. New food processes and products are continuously being developed; the current trend is to reduce or remove preservatives, and chilled ready meal ranges are being extended. New products create new niches and opportunities for pathogen growth. In order to reduce food poisoning and ensure that new products are safe, we need to understand the behaviour of food poisoning microorganisms, and predict the conditions in which they grow.

In the pathogen physiology and predictive ecology programme, we contribute to the prevention of emerging bacteriological food safety problems, by advancing understanding of the behaviour of bacterial pathogens in food and improving prediction of their response to food environments. Our multidisciplinary research team combines a variety of microbiological and mathematical skills. Our work focuses on three important areas of food microbiology:

- *Clostridium botulinum*
- Modelling food microbial systems
- Food-borne hazards and risk assessment



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## *Clostridium botulinum*

*Clostridium botulinum* is an anaerobic spore forming organism that produces a lethal neurotoxin. As little as 30ng of toxin or 0.1g of food in which the organism has grown can cause severe illness or even death. Although rare, the severity of the disease makes its control in food very important.

IFR has well established niche expertise in anaerobic microbiology, especially in *C. botulinum*. We blend both fundamental and applied research to understand how *C. botulinum* behaves in different environments and thus provide a platform for its control.

### Current projects

#### Distribution, growth and survival

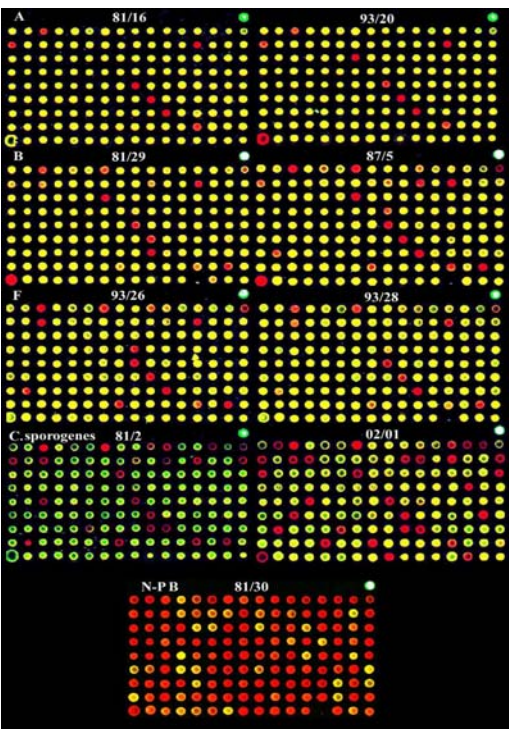
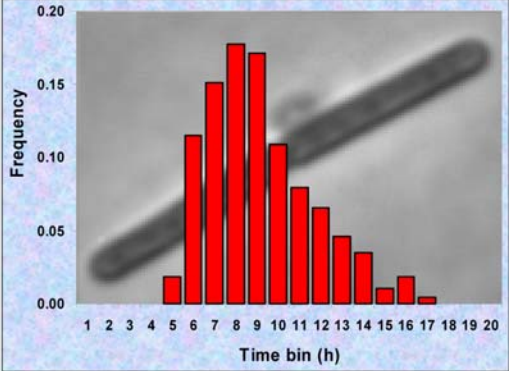
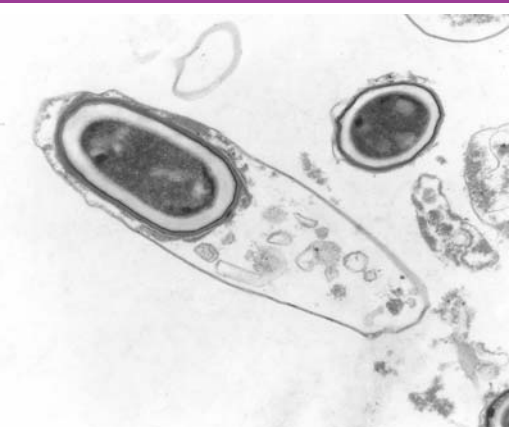
We support industry and regulators by quantifying how spore distribution, strain variability, processing conditions and combinations of environmental conditions effects the growth of *C. botulinum* in foods. These data are used in predictive modelling and quantitative risk assessment.

#### Molecular biology

We have pioneered the molecular genetic study of *C. botulinum*. *C. botulinum* is a group of organisms defined by their ability to produce neurotoxin. Two organisms, proteolytic and non-proteolytic *C. botulinum*, are usually responsible for food-borne botulism. We are contributing to genome sequencing and have built the first DNA microarrays for these organisms. These allow comparative genetic indexing and diversity calculations; and the activities of all genes can be monitored simultaneously. This research will identify potential targets and mechanisms to prevent growth and/or toxin production in foods.

#### Lag time from individual spores

*C. botulinum*, if present in a food, is likely to be at very low concentrations. Lag time from low starting numbers is very variable and very difficult to predict. We have been measuring how environmental conditions affect distinct lag stages and relationships between the stages. Knowledge of the distributions of times for germination and growth and quantification of biovariability improve predictions of growth and help estimate the risk of botulism associated with a food.



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## Modelling food microbial systems

At IFR we have been pioneering a quantitative approach to food microbiology, applying advanced mathematical, statistical and computational tools to food microbiological research. Research is in four main areas:

### ComBase - [www.combase.cc](http://www.combase.cc)

The ComBase initiative makes data and predictive tools on microbial responses to food environments freely available via web-based software. The ComBase Database contains over 35,000 growth and survival curves, accessible through the ComBase browser. ComBase Predictor uses these data for numerous microbial models, providing a useful tool for industry, academia and regulators.

### Improved control of *Clostridium perfringens*

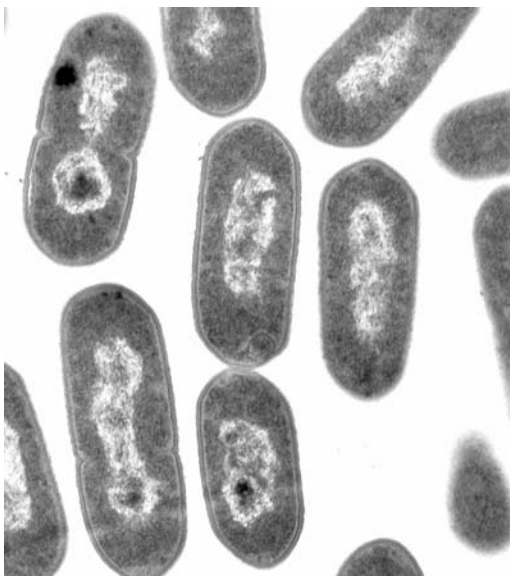
IFR has developed a user-friendly software tool that describes growth of *Clostridium perfringens* during the dynamic heating and cooling of meat products. "Perfringens Predictor" is available within the ComBase package.

### Lag time modelling

Lag phase is difficult to model as quantitative data are lacking and lag depends not only on the current environmental conditions but also cell history and the initial physiological state of the cell. Stochastic approaches have been developed to model the variation in distributions of lag times as a function of the history, initial physiological state and growth environment of the cells.

### Systems biology

The lag time of an individual cell depends on the intracellular activity needed to adjust the system-cell environment and initiate the division cycle. A systems biology approach is being applied to study intracellular activity during the lag time and to characterise the processes involved. The mechanism by which cells get ready to grow is explored by the analysis of a transcriptional network imbedding operon composition and functional relations.



**ComBase Predictor**

Temperature input:  Static  Changing temperature

Water activity:  NaCl  Aw

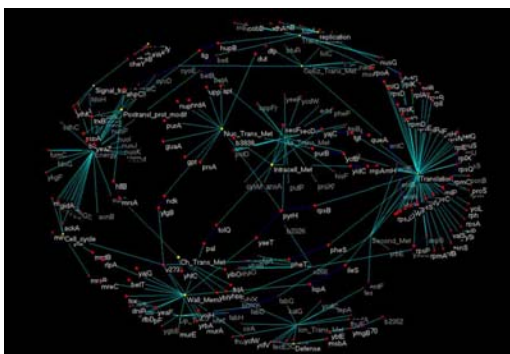
Observation duration: Time (h) 336.00

Initial level	Phys. state	T (°C)	pH	NaCl(%)	Max. rate (log.cou/h)	DM time (h)
1	0.000037	15	6.5	0.5	0.27	1.10
1	0.000037	10	6.5	0.5	0.09	3.42
1	0.000037	5	6.5	0.5	0.05	6.08
1	0.000037	5	6.5	0.5	0.02	16.45

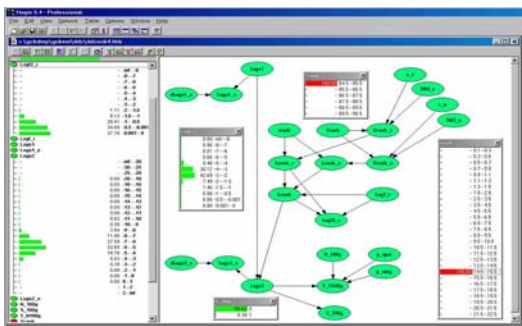
**Predict**

Time (h) conc. (log10 cfu/g)

0.00	1.00	1.00	1.00	1.00
0.00	1.00	1.00	1.00	1.00
4.72	1.00	1.00	1.00	1.00
13.44	1.07	1.00	1.00	1.00
20.16	2.10	1.00	1.00	1.00
24.88	3.90	1.00	1.00	1.00
33.60	5.67	1.01	1.00	1.00
40.32	6.83	1.05	1.00	1.00
47.04	7.03	1.18	1.00	1.00
53.76	7.04	1.48	1.01	1.00



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## Foodborne hazards and risk assessment

Quantitative risk assessments for complex food-borne hazards requires quantification of uncertainties, understanding of complexities and support for communication and management of information.

At IFR we have been developing strong mathematical descriptions for, and improving quantitative understanding of, the hazards and risks that are associated with food consumption. Such data have been used to construct a consistent framework, and a range of user-friendly tools, that facilitates strong communications between IFR food safety research expertise and appropriate stakeholders.

For further details see Risk and Choice display.

