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Food microbiology: the challenges for the future

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Abstract

Food microbiology has become a mature science in the twentieth century and has made great advances. While recognising these achievements, it is also necessary to consider how the science may need to change. This paper addresses this by reference to three areas. These are possible changes in foodborne diseases of concern and the impact of molecular and genetic techniques on our current methodology. The recognition of the role of food and associated microbial contaminants in chronic diseases could become a major concern. New developments in our understanding of microbial genetics could affect our concepts of bacterial taxonomy. The current methodologies we use, based upon genotypically identical populations, may need to be addressed. If the trends indicated here are realised, they indicate a major challenge and opportunity for the food microbiologist.

1. Introduction

The twentieth century has seen the maturing of food microbiology as a science. In particular, the last thirty years of the century has seen the subject go up the social and regulatory agenda. This is particularly true in the industrialised World, where living standards are high and society is becoming increasingly complex and demanding. These conditions place demands upon our lifestyles, the environment and our expectations for quality of life.

We enjoy increased health and longevity and take as our right the safety of the foods and beverages we consume. These foods are becoming increasingly international, prepared to give convenience and variety. In addition, the consumer is now able to express a view clearly on food safety (Cowan, 1998). The task of delivering the convenience and variety is carried out by the Food Industry with a high degree of regulatory control and monitoring. With increasing population growth and the increased demands for health and quality from our foods, the food microbiologist is an important contributor to our quality of life.

Historically, food microbiology grew out of medical microbiology to become a subject in its own right. As a result of its history, it has recognisable characteristics. Practitioners use techniques which rely upon concentrating high numbers of genotypically and (as far as is possible) phenotypically identical units for study. The standard techniques used through the twentieth century have followed this pattern, whether in Research or Measurement Science. It is not surprising, therefore, that our understanding of the subject is based upon such ‘populations’. Even now, when biotechnology is giving us so many new and exciting tools, we still adhere to the same basic experimental tools.

If we talk about food microbiology we talk about food enhancement (e.g. fermentation), food spoilage

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or food poisoning. Our technical struggle has been to satisfy the demands of society for good quality foods without causing poisoning. This is an area where we have been peculiarly successful, and should be proud of the achievements of workers in food microbiology. Unfortunately, during the twentieth century, so far new microbial threats have always been a surprise. Operating globally leads to a set of conditions which often conspire against the best intent of the food microbiologist (Wilson, 1997). These conditions can be categorised as the increased vulnerability of the population (including ageing, immunosuppression, environmental exposure to pollutants, chemicals, poverty and crowding); technological advances (including antimicrobials and pesticides, land usage and agricultural change and urbanisation); the human impact of increased travel and contact of different cultures and customs, genetic make-up and 'cultural vectors' (Ewald, 1996).

As we enter the next millennium, it is a good time to ask what the future holds. None of us know, but there are a few issues that can be addressed which might signpost the way forward. The rest of this paper addresses some of these issues.

2. Food poisoning

The overwhelming majority of work and thinking about microbial food poisoning is centred around acute poisoning. Undoubtedly, new issues will arise and the concern with acute poisoning will remain a major topic for us into the next millennium. Acute poisoning has a high impact because it is relatively easy to associate cause and effect, especially where outbreaks occur within a community. It can take a very long time to obtain clear evidence of cause and effect for long-term diseases (for example, consider the time to taken to get a consensus on the relationship between beef and nv-CJD).

There is increasing evidence that microbial contaminants of food may cause other, chronic health problems (Bunning et al., 1997). Already, potential candidates for such diseases are being identified (Table 1). During the next century, we can expect to see increasing concern about such diseases. Basically, there are three routes by which such diseases could occur:

Table 1
Some examples of diseases which may have a food-borne microbial involvement[a]

·	Septic arthritis
·	Aseptic arthritis
·	Inflammatory bowel disease
·	Autoimmune diseases
·	Polycystic kidney disease

[a] After Bunning et al., 1997; Miller-Hjelle et al., 1997.

1. Cells, alive or dead, could carry specific antigens which contribute to the disease
2. Live cells could infect the gut and either (a) migrate and cause secondary infections, or (b) provide specific antigens contributing to the disease
3. The food itself alters the ecosystem in the gut that leads to a flora change.

In order to deal with such challenges, the food microbiologist will need to develop new skills. Interest in the ecology of the gut flora will become mainstream. One important consequence for the food microbiologist is that he will need to work with communities rather than the rather limited populations in his test tubes and on his petri dishes.

Food poisoning will also be affected by the ecological changes we see in the world. Such factors as climate change, population density and Internationalisation, will have profound affects upon us, including in our foods. A major consideration is the management of water, a finite resource that, if not a food itself, is a prime ingredient of them. Already, we see increasing concern about water-borne pathogens in the food chain, including parasites (Neumann and Foran, 1997). For the next millennium, we should already be preparing for the foreseeable threats to society.

3. Methodology

As already indicated, the food microbiologist deals primarily with populations of identical 'cells'. The majority of techniques used to manipulate the microorganism results in reduced genetic variability (Table 2). Researchers expect to obtain a homogeneous population of a large enough biomass to produce

Table 2
Some examples of common techniques which lead to production of genotypically similar populations

·	Enrichment/pre-enrichment
·	Environmental control (e.g. temperature/pH/a_w)
·	Plating and colony selection
·	High amplification of numbers

signals in whatever experimental technique they are using. Indeed, it has been the ability of the 'cell' to amplify enough to give a signal that has made our Science possible, and so far a success.

The only premise for such manipulation techniques is that the organisms behave the same as those that exist naturally; that is, this same genotype is a constant and consistent part of the ecosystem we are studying. Of course, if we were in another science (for example, toxicology) we might claim the reverse. Take for example a study on mice. The researchers will attempt to obtain as identical a genotype as possible for research. This is done to control variability so that comparison of tests becomes easier and cheaper. What the toxicologist will not do is to claim that the mouse has any relevance to the environment from which it was derived. The question is, if the microbiologist uses a 'strain' to do comparative tests, we may learn something about the different tests, but do we have any right to extrapolate this result to the ecosystem (e.g. a food preservation system) in which we are interested?

If we wish to understand the role of microorganisms in food safety and preservation, can we continue to use techniques that guarantee that the biomass that we are studying may not truly represent the ecosystem of interest? Rather, the much used term, but little used Science of Microbial Ecology will need to become a full part of the food microbiologist's armoury. It is fundamental that we have a proper understanding of the impact of an environmental selective pressure anywhere in the food chain on the microbial flora. We understand how common genetic transfer occurs amongst the groups of concern to the food microbiologist, and so it is imperative that we develop techniques which allow this to happen rather than deliberately preventing it. Producing techniques to deliver this is a major challenge to the food microbiologist.

4. Taxonomy

Linneaus developed a protocol to name eukaryotes which was quickly adapted by the microbiologist for prokaryotes. This gave a uniformity and logic to nomenclature within the biological sciences The definition of a species as an organism which is, and remains, distinct because it does not normally interbreed with other organisms (Gray, 1967) is not a particularly good description for a bacterial 'species'. As a consequence, classification was largely based upon phenotypic characteristics as measured under laboratory conditions. Various methods of differentiation were then overlaid onto this (Table 3) and eventually aspects of the genetic material itself were included. Taxonomy has been a very active field, with different systems being proposed over the years.

The basis of all such taxonomic efforts revolves around the notion that the 'cell' in the test tube has some taxonomic significance. Of course, in the test tube it is a single phenotype and will remain so while kept in the laboratory. Such an organism can then be a 'type' and is available while we provide it with the appropriate life support systems. Such taxonomic systems have served us well during the twentieth century, but will they be adequate for the next millennium?

If bacteria share genetic material in their normal habitat as freely as they do in the test tube, it is conceivable that this is the normal lifestyle for them. As such, they have no species status when in our test tubes, and it is questionable whether an individual bacterial 'cell' can be considered as a an organism in its own right. Rather, it may be part of a continuum of like, or related, organisms sharing genetic material to respond rapidly to exploit a new habitat. The story with emerging pathogens is one of change in the environment producing a new selective pressure with the probability that a new pathogen will arise (Miller

Table 3
Examples of differentiating characteristics

·	Phage typing
·	Serotyping
·	Metabolite characterisation (e.g. toxins)
·	Antimicrobial resistance (e.g. antibiotics)
·	Physical limits for growth

et al., 1998). Indeed, the question has to be asked whether *E-coli O157:H7* is a new pathogen, or is the 'newness' merely due to its recognition in humans (Armstrong et al., 1996). The likely source of these organisms is recombinants from the wild genetic pool. It is also clear that these recombinants occur across the classical taxons that we currently use (Dietsch et al., 1997). This is illustrated by the *Citrobacter freundii* gastroenteritis case in children (Tschape et al., 1995) where genes shared between the *C. freundii* and *Escherichia coli* was the most likely scenario. Such sharing of genetic material becomes even more of a threat when we accept the idea of 'pathogenicity islands' as particular regions of the genome which are easily transferred (Hacker et al., 1997) (Table 4).

Against this background, there is also the possibility that our 'test tube' biotype may have been a recombinant obtained by the selective pressure we apply in our recovery techniques. If this should be true, then we have a real potential for self-delusion from results with our laboratory strains, for example when developing preservation systems or modelling kinetics.

This implies a change of attitude which could lead to different avenues for research and perhaps help us to tackle some of the more important issues, such as emerging pathogens (see Table 5, based on Smith and Fratamico, 1995). Perhaps *E. coli O157* would be a good case to consider. This is an organism that appeared to arrive in the last twenty years as a fully formed 'type'. At the same time, we are well aware that part of its capability (and genetic code) is common to its relatives. In some cases, related types showing varying biochemical capabilities, and hence bearing different names, are known to give rise to the self same syndrome. Such cultures look different in our test tubes but does this justify a different taxon?

Historically, the Linnaean nomenclature has been convenient and has served us well, enabling communication between scientists. During the next millennium, it may be a good time for the microbiologist to take a step back from this nomenclature. This may require the redefining of prokaryotes with a classification suitable to their nature and of more use to the practitioners trying to provide practical solutions to problems and understand what the effect of the next change in practices in the food chain will be on food safety. We know that there are many changes occurring globally affecting our foods and these have been categorised (Smith and Fratamico, 1995). Furthermore, we have some clear ideas on risk factors involved in food-borne disease (Bryan, 1988). There is a great challenge to rethink attitudes towards microbial ecology and to carry out structured Risk Assessment based upon our existing knowledge. This can be used as a springboard for predicting future trends.

Table 4
Some factors involved in developing taxons for bacteria

· Morphology (including colonial morphology and motility)
· Biochemical capability
· Antigenic properties
· G&C ratios
· Numerical taxonomy
· Genetic typing

Table 5
Foodborne pathogens which have emerged in the past 20 years[a]

Campylobacter jejuni
Infant botulism
Escherichia coli O157:H7
Listeria monocytogenes
Salmonella enterititidis
Vibrio cholerae
Vibrio vulnificus
Yersinia enterocolitica
Norwalk and Norwalk like viruses

[a] After Smith and Fratamico, 1995.

5. Conclusions

By giving the three examples above, I hope to have demonstrated that the uniformity of approach and technique in the twentieth century has enabled the food microbiologist to make major steps in our science and to achieve so much in a relatively short time. There is no doubt that food microbiology is a successful and relevant scientific discipline with excellent practitioners in it. The science is now mature and operates to a set of understood rules that govern experimental design.

The challenge for the next millennium is to now review our current pre-conceptions. I have illustrated some areas where, in my opinion, we need to rethink our approaches and attitudes in order to take our

science on to the next phase. Science never stands still and today's certainties always become tomorrow's myths. Food microbiology is an important discipline. Everyone must eat, everyone wishes to enjoy eating without being poisoned, yet the need is to feed more and more people with finite resources. Demands upon us will increase in the next few years and it would be nice if we stopped becoming the 'victim' of the next organism which we did not see coming and were able to pro-actively take steps to deal with threats in the food chain.

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