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Culture independent methods to assess the diversity and dynamics of microbiota during food fermentation

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Abstract

Culture independent methods first appeared in the food microbiology field at the end of the 90s and since then they have been applied extensively. These methods do not rely on cultivation and target nucleic acids (DNA and RNA) to identify and follow the changes that occur in the main populations present in a specific ecosystem. The method that has most often been used as a culture independent method in food microbiology is denaturing gradient gel electrophoresis (DGGE). The number of papers dealing with DGGE grew exponentially in the late nineties and, by analysing the studies available in the literature, it is possible to describe a trend in the subjects that have been investigated. DGGE was first used as a tool to monitor the ecology of fermented food, such as fermented sausage, cheese and sourdough, and later it also showed its potential in microbial spoilage process. In the last few years, the main application of DGGE has been to study fermented food from Asia, Africa and South America.

The information collected using DGGE has made it possible to confirm the existing knowledge on food fermentation and spoilage. However, in some cases, new evidence that helps scientists to fully comprehend a specific microbial ecosystem has emerged.

In this review, the roadmap of culture independent methods in food microbiology will be summarized, focusing on the DGGE technique. Examples of how this approach is useful to obtain a better understanding of microbial diversity are reported for several kinds of fermented food, such as fermented sausage, cheese and wine.

The future of culture independent methods in food microbiology, with the increasing availability of next generation sequencing techniques, is also discussed.

Key-words: culture independent methods; DGGE; food fermentation; food spoilage; microbial ecology.

1. Introduction

The last 30 years have been characterized by a significant change in the approaches used for the microbiological examination of food. The invention of PCR (Mullis et al., 1986) has led to new strategies to study food-borne microorganisms. Although, in the past, synthetic media, which were used to cultivate microorganisms, were the only way of conducting a microbiological analysis of food, with the arrival of PCR it has become possible to investigate microorganisms without any cultivation. In its early stages in food microbiology, PCR was mainly used as a detection method (Rossen et al., 1991). At the end of the 90s, a number of techniques were developed and, coupled with PCR, these techniques offered scientists the possibility of studying the ecology of complex microbial ecosystems. In this context, the term "culture-independent techniques" was coined. This term indicates the use of methods that are not based on cultivation to study microorganisms in a specific ecosystem. Undoubtedly, culture-independent methods offer a number of advantages over culture-dependent methods. Microorganisms are studied not because they are able to grow on a specific microbiological medium, but because they possess DNA, RNA and proteins, which are the preferred targets for such approaches. Moreover, the physiological status of the microbial cell does not affect the outcome of the investigation. In traditional microbiological examinations, cells that are stressed and injured are often not able to grow on synthetic media that contain agents, such as antibiotics, to make them selective towards a specific microorganism, and this can lead to false-negative results. Finally, populations that are numerically less important are not detected by means of traditional methods, because they are masked on the plates. Most of these issues can be solved by culture-independent methods (Cocolin and Ercolini, 2008).

The introduction of culture-independent methods allowed scientists to understand the limitation of microbial cultivation and, in 1998, Hugenholtz et al. published a paper in which it was stated that “our knowledge of the extent and character of microbial diversity has been limited, however, by reliance on the study of cultivated microorganisms. It is estimated that >99% of microorganisms observable in nature typically are not cultivated by using standard techniques”. Such evidence encouraged researchers to use culture independent methods in different fields of microbiology. In food microbiology, the late 90s – early 20s represents a key period for the application of these approaches and the first papers, dealing with the study of microbial ecology of fermented foods, started to appear in scientific journals. One of the aspects that was immediately highlighted by these pioneer studies was the presence of non culturable populations in food systems, and these outcomes were in agreement with results obtained in other branches of microbiology, such as environmental and intestinal microbiology. Since they had never been detected by traditional methods, these populations were described for the first time by culture independent methods. This state, defined as viable but not culturable (VBNC), was defined by Oliver (1993) as “a cell which is metabolically active, while being incapable of undergoing the cellular division required for growth in or on a medium normally supporting growth of that cell”, can be considered as a survival strategy and response to adverse environmental conditions (e.g. starvation or acid stress) (Rowan, 2004) that can easily be found in food fermentation and processing. The VBNC state is of concern when associated to food-borne pathogens, because there is a general lack of knowledge on the risks from VBNC cells. It cannot be assumed that such cells will not emerge from this state after entering the human body and cause disease. Moreover, a possible impact in food fermentation can be considered if the VBNC cells are responsible for biochemical activities involved in the formation of the final characteristics of the product.

In the field of food microbiology, culture-independent techniques, used as tools to profile microbial ecosystems, have been used more in the food fermentation and food spoilage fields, although, in a few cases, they have also been exploited to study the ecology of food-borne pathogens (Cocolin et al., 2002b, 2005).

2. Culture-independent methods used in food microbiology

Most of the techniques used for culture independent analysis are PCR-based. After amplification of the nucleic acids extracted directly from the food matrix, the PCR product is subjected to specific analyses that are able to highlight differences in the amplified DNA sequences.

One of the most important aspects that should be considered, in order to properly profile microbial populations in food ecosystems, is the selection of the DNA region that has to be amplified. The target gene has to have two basic characteristics: (i) it should be present in all members of the microbial group that is under consideration, (ii) it should have conserved regions, in which universal primers can be designed, and variable regions, in which differentiation is possible. Genes encoding for ribosomal RNA (rRNA) fall into this category. Various regions of the 16S rRNA coding gene have been used in bacteria, while the 26S rRNA coding gene is commonly the target in yeasts. One important advantage of the use of these two genes is that large sequence databases exist. On the other hand, one drawback of the use of rRNA coding genes is the inherent sequence heterogeneity within the same species, which is the result of multi-copies of the genes with small differences in the sequence (Fogel et al., 1999). These multi-copies often result in multi-signals, which complicate the analysis. The *rpoB* gene, encoding for the β-subunit of the RNA polymerase, has been proposed as an alternative, but its application is still limited (Dahllof et al., 2000; Rantsiou et al., 2004)

In post amplification analysis, the goal is to detect DNA sequence heterogeneity. Such a goal is reached using denaturing/temperature gradient gel electrophoresis (D/TGGE) and single strand conformation polymorphism (SSCP) through the study of the electrophoretic mobility of completely or partially denatured PCR products, respectively, or by using restriction endonucleases in terminal restriction fragment length polymorphism (TRFLP).

D/TGGE consists of an electrophoretic separation of PCR products in a polyacrylamide gel containing a gradient of chemical (urea and formamide in DGGE) or physical (temperature in TGGE) denaturants. As the DNA molecule encounters the appropriate denaturant gradient, a sequence-dependent, partial denaturation of the double strand occurs. This change in the conformation of the DNA structure causes a reduced migration rate of the molecule. When the method is used for microbial profiling, after amplification, the complex mixture of the DNA molecules can be differentiated and characterized. Bands visible in D/TGGE gels represent components of the microbiota. They can be excised and, after re-amplification, can be sequenced in order to obtain the corresponding microbial species. Using these methods, it is possible not only to profile the microbial populations, but also to follow their dynamics over time. It should be noted that these methods are not quantitative (Ercolini, 2004a).

In the case of SSCP, the differentiation is based on the mobility of single strands of DNA. Small changes in the sequence can be detected because the single strand may create intrastrand base pairing, which results in loops and folds that give the single strand a unique 3D structure, and this affects its mobility through a gel. In SSCP analysis, the amplified product is denatured to a single-stranded form and subjected to non-denaturing polyacrylamide gel electrophoresis. In the last few years, SSCP methods have been based on amplification with fluorescein-labelled primers and detection of the signals by fluorescence.

When SSCP is used to profile a complex microbial ecosystem, a robust database should be created in order to be able to identify each single component by comparing the retention time of each signal with a reference time in the database. If matching does not occur, identification cannot be obtained (Hayashi, 1992)

Finally, in T-RFLP, one of the PCR primers is labelled with fluorescent dye and used to amplify a selected region of a gene of interest by means of PCR. The resulting PCR fragment is digested with one (or more) restriction endonuclease(s) and the resulting fragments are separated by means of an automated DNA analyser. Microbial diversity in a community can be estimated by analysing the number and peak heights of patterns. T-RFLP is an effective tool for characterizing the dynamic changes that occur in complex microbial ecosystems over time. However, the technique is best suited for microbial communities with low to intermediate richness (Sibley et al., 2012).

These PCR-based assays all suffer from amplification bias. Appropriate primer selection is essential, but it must be noted that a perfect universal primer set does not exist for community profiling. Usually they are reproducible, however low number populations signals may not always be detected if multiple runs of the same sample are carried out. Regarding the sensitivity it has been recognized that these methods are able to detect as low as 1% of the total community, however this limit depends on the composition of the microbial ecosystem and on the detection strategy (gel based or by using fluorescent dyes in capillary electrophoresis). For DGGE analysis the limit of detection has been described to be about 10^3 colony forming units (cfu)/ml or g (Cocolin et al., 2001a; Cocolin et al., 2001b).

Among the culture-independent methods, one of the few that do not rely on PCR amplification is fluorescence in situ hybridization (FISH). This technique is based on the hybridization of fluorescein-labelled probes to specific sequences of the rRNA. Target cells

are immobilized on a microscope glass and then subjected to a permeabilisation step in order to allow the probe to penetrate into the cell. After hybridization, the results are visualized under a UV microscope (Bottari et al., 2006). FISH has not been used intensively in food microbiology, although it has the great potential of being able to localize microbial populations in a solid food matrix (Ercolini et al, 2003).

Considering the wide application of DGGE and its extensive literature in the field of food microbiology, this review will be focused on this method.

3. DGGE applications in food microbiology: a temporal evolution

As reported above, DGGE is the culture-independent technique that has been used most often in food microbiology. The first paper to exploit the potential of DGGE, by Muyzer et al., was published in 1993. They investigated the microbial ecology of mats taken from different depths and bacterial biofilms isolated from aerobic and anaerobic wastewater treatment reactors. Only in the late 90s, was DGGE introduced into food microbiology and since then an extensive number of studies, exploiting DGGE as a method to profile microbial ecology in food, have been reported (Table 1). It is interesting to note that DGGE has been applied to all areas of food microbiology, such as food fermentation, food spoilage and food safety, the former being the richest in terms of scientific literature. DGGE is most suitable for the study of the microbial ecology of spontaneous fermentations. Wine, meat and meat products, milk and dairy products are the most frequently studied kinds of food, both in terms of fermentation and spoilage processes, while sourdough and vegetables have been investigated to a lesser extent using culture-independent methods. DGGE has been the subject of several review papers, some of which have focused on its general aspects and applications (Ercolini 2004a), while others have dealt with specific reviews in the dairy sector

(Jany and Barbier, 2008; Quigley et al., 2011), meat fermentations (Rantsiou and Cocolin, 2006; Cocolin et al., 2011b), grape surface in relation to wine production (Barata et al., 2012), wine and beer fermentation (Cocolin et al., 2011a; Bokulich et al., 2012) and spoilage of meat (Doulgeraki et al., 2012).

A search conducted in Scopus (www.scopus.com) in December 2012, using DGGE and food as keywords, resulted in more than 400 hits, with the first one dating back to 1999 (Ampe et al., 1999). The trend presented in Figure 1 has been obtained considering the number of papers published each year, from 1998 up to now. As it can be observed, three time spans can be distinguished. Period 1, from the late 90s to 2004, is characterized by a slight, but steady increase in the number of papers published. This is followed by the second period, from 2005 to 2008, in which the studies exploiting DGGE almost triplicate in just 4 years. The number of DGGE papers reaches a peak in the third period (2009-present), in 2010, after which a decrease can be observed.

Analysing the temporal evolution of the use of DGGE in food microbiology, it is worth noticing that a correlation exists between the subjects considered in the papers and their distribution in the three time spans described above. In the first years of application, DGGE was mostly used to study well established food fermentations in industrialized countries. Fermented sausage (Cocolin et al., 2001a), cheese (Ercolini et al., 2001) and wine (Cocolin et al., 2001b) were the first products to be investigated, although studies focusing on the ecology of Mexican pozol (Ampe et al., 1999; Ben Omar and Ampe, 2000) were also published. The portfolio of food investigated by means of DGGE expanded in the following years, when studies on sourdough (Meroth et al., 2003a), whisky (van Beek et al., 2002) and raw milk ecology (Lafarge et al., 2004) became available.

A remarkable increase in the number of DGGE papers can be observed for the following time period. This could be correlated to an intensification of the studies on the fermented products described above (especially fermented sausage and cheese), but also to the exploitation of DGGE to follow the dynamic changes that occur during food spoilage. The first examples of DGGE application to investigate spoilage organisms date back to 2004, when two papers, one focusing on the late blowing of cheese (Cocolin et al., 2004a) and the other on fresh sausage storage at refrigeration temperatures (Cocolin et al., 2004b) were published. An important contribution to the increasing trend of DGGE papers in this period was given by the spoilage studies from 2006, when, for the first time, DGGE was applied to investigate the microbiota of fresh meat during refrigerated storage under different packaging conditions (Ercolini et al., 2006).

The growing trend observed in Figure 1 until 2010 could be due to the increase in studies in which DGGE was used as a tool to study the ecology of different kinds of fermented food from the ones described above. Kimchi (Lee et al., 2005) and cocoa (Nielsen et al., 2005) were among the first products to be investigated, and these have been followed in recent years by soybean-based foods (Kim et al., 2009, 2010; Park et al., 2009; Lee et al. 2010). The decrease in the number of studies should be considered carefully, and it is necessary to consider that information related to the 2012 papers will only become available at the beginning of 2013.

4. What have we learnt from the application of DGGE in food microbiology?

The results obtained by applying DGGE as a culture-independent method to food fermentation have generally confirmed previous knowledge obtained through traditional microbiological methods. Members of lactic acid bacteria (LAB) were found to be the main

microorganisms active in food fermentation, but also involved in spoilage processes together with *Pseudomonas* spp. and *Enterobacteriaceae* (Table 1). From this point of view, the novelties introduced by the application of DGGE are related not so much to the discovery of new microbial species, but to a new way of globally investigating the ecology of food during microbial transformations.

4.1 DNA versus RNA DGGE analysis

One of the potentials of DGGE is that it offers the possibility of performing ecological studies that target both nucleic acids, that is, DNA and RNA. It should be underlined that these two molecules have completely different biological meanings, since DNA contains hereditary messages, and RNA has a direct involvement in its translation into proteins. Moreover, DNA shows remarkable stability in the environment, as can be seen from the recovery of DNA, and the successful amplification by PCR, from archaeological and paleontological samples, which can be thousands of years old (Landweber, 1999), while RNA, and more specifically messenger RNA (mRNA), persists for short periods of time in actively growing bacteria cells, with an average half-life measured in minutes (Arraiano et al., 1988). Studying the DNA of a microbial ecosystem in ecological studies allows the microbial ecology and diversity to be defined, while RNA analysis is able to better highlight the microbial populations that are metabolically active, and thereby contribute to the microbial process. Since the number of intact ribosomes approximately reflects the rate of protein synthesis, ribosomal RNA (rRNA) can be used as a marker for general metabolic activity (Gosalbes et al., 2011), although it must be accepted that these molecules are characterized by a much higher level of protection, than mRNA (sometimes even weeks). Another strategy to detect viable population is the use of ethidium monoazide (EMA) and propidium monoazide (PMA), DNA-

intercalating agents able to selectively penetrate the membranes of dead cells and form stable DNA monoadducts upon photolysis, resulting in DNA which cannot be amplified by PCR. While this approach has been frequently used to differential live and dead cells of pathogenic microorganims (Rudi et al., 2005), its perfromances in complex microbial ecosystems has been tested.

RNA has not been used extensively in DGGE studies, but, when targeted, it has allowed some new evidence to be highlighted, especially in food fermentation. In dairy fermentation, the differentiation between starter LAB (SLAB), mainly *Lactococcus* spp., *Streptococcus thermophilus* and several *Lactobacillus* spp., and non-starter LAB (NSLAB), belonging to *Lactobacillus* spp., *Leuconostoc* spp. and *Pediococcus* spp. (Fox et al., 2004), is generally scientifically accepted. The former are responsible for the acidification of milk and curd in the early stages of cheese manufacturing, while NSLAB are considered as secondary microbiota, associated with the organoleptic development of cheese during ripening. Studies conducted on different types of cheese (Dolci et al., 2008, 2010; Rantsiou et al., 2008) have confirmed this switch in LAB populations through traditional methods. However, they have also highlighted the presence of stable signals of *L. lactic* and *S. thermophilus* at an RNA level in the late stages of ripening. This new information leads to the conclusion that SLAB are not only involved in the acidification process and in the proteolysis that results from their production of proteolytic enzymes, but may also play a role in the development of the organoleptic characteristics of cheese during the ripening period. Recently, it has been demonstrated that, during ripening, *L. lactis* may be involved in several pathways, such as carbohydrate and amino acids metabolisms, protein degradation and lipolysis (Desfossés-Foucault 2012).

Apart from the detection of a metabolically active population, RNA targeted DGGE has recently shown another advantage, compared to DGGE, when analyzing DNA. In a study performed by Dolci et al. (2012) on the surface microbiota of Fontina, a smear cheese from the Aosta Valley region, North Italy, it was noticed that when subjected to an image analysis, the DGGE profiles obtained from the RNA extracted from the surface of the cheese, were clustering apart from the respective DNA samples. This result allowed the authors to speculate that RNA molecules may be a better target to describe the microbial ecology of complex microbial ecosystems, such as the rind of smear cheeses. This evidence could be due to the high number of ribosomes that metabolically active cells possess. In these circumstances, the PCR amplification should also be able to pick out microbial populations that are numerically low, but metabolically active, and should allow their specific signals to be detected in the DGGE gels. This outcome has also recently been described for table olive fermentation (Cocolin 2012, personal communication).

4.2 DGGE is a useful tool to assess product-specific microbial biodiversity

Food fermentations are microbial transformations in which a large number of microorganisms, belonging to different species and genera, compete to establish their supremacy. DGGE has been demonstrated to be able to follow the dynamic changes that occur during food fermentation and highlight dominant microbial populations. Its potential has been demonstrated by Cocolin et al. (2007) in a study in which an optimisation of the DGGE procedures was carried out to study different sets of primers that are often used in DGGE analysis, denaturing gradients and electrophoretic conditions. When the optimised protocol was applied to fresh and ripened meat as well as dairy products, the ecological pressure exerted by certain microbial groups, namely LAB, during the fermentation process,

became evident. The fresh produce was characterized by higher biodiversity, as observed from the complex patterns, while ripened products presented just a few bands, corresponding to the species that were able to dominate the microbial ecosystem. In the specific sector of meat fermentation, the main products that were investigated by DGGE were sausages from Italy, Argentina and Portugal (Table 1). LAB and coagulase negative cocci (CNC) are the main microbial groups responsible for fermentation and transformation, and this evidence was confirmed through an analysis of the DGGE profiles obtained in the above-mentioned studies. However, it should be noted that microbial competition occurs in the very early stages of fermentation, since, as demonstrated by Cocolin et al. (2001a), already at the third day, the signals of *Lb. sakei* and *Lb. curvatus*, the main species involved in sausage fermentation, became predominant. In studies conducted on fermented sausage ecology it has often been highlighted how DGGE profiles could be used to differentiate products from different geographic regions and production plants. This result was obtained for Argentinian sausages (Fontana et al., 2005a), and also for sausages produced in North-East Italy (Rantsiou et al., 2005). More specifically, in the latter study, the microbial changes that occurred during fermentations of the three products, with a ripening period of 28, 45 and 120 days, respectively, were investigated. Through a cluster analysis of the DGGE profiles, it was demonstrated that sausages at the beginning of the fermentation (from 3 to 7 days) present DGGE patterns that do not show any similarity with other samples, while from day 10 onwards the different types of sausages started to group together in a product-specific clustering manner.

4.3 DGGE analysis highlights hidden populations

As already mentioned above, one of the main criticisms that is currently directed towards traditional microbiological methods concerns the impossibility of detecting microorganisms in low numbers in complex ecosystems with dominant populations. DGGE has partially overcome this limitation, having a limit of detection of about 10^3 cfu/ml or g (Cocolin et al., 2001a; Cocolin et al., 2001b).

In several food fermentation sectors, the DGGE technique has been able to highlight populations that may have an important impact on the final characteristics of the product, but which were not well described by means of traditional methods. An interesting example, in this context, is the application of DGGE to wine fermentation. The ecology of wine yeasts has been the focus of a large amount of literature, starting from the 80s, which has indicated *Saccharomyces cerevisiae* as the main responsible for alcoholic fermentation (Fleet and Heard, 1993), which is able to dominate over other yeast species, collectively called non-*Saccharomyces*. This last group is usually of concern in the wine making sector, since it contains yeasts that are detrimental to the quality of wine. There is scientific consensus on the capability of *S. cerevisiae* to take over the wine fermentation process. However, the role of non-*Saccharomyces* is still under debate. The use of DGGE during wine fermentation has often demonstrated an active participation of non-*Saccharomyces* yeasts in the fermentation process, and their persistence is longer than what was previously believed. Ecological studies on a sweet wine produced in California (USA), called Dolce, produced from botrytized grapes, highlighted multiple bands in DGGE profiles that, after sequencing, were identified as putative *Candida stellata*. These bands were present from the very beginning of the fermentation and remained stable throughout the fermentation process (Cocolin et al., 2001b). In another study conducted the following year (Mills et al., 2002), the active participation of this *Candida* sp. was confirmed and it was demonstrated, by RNA dot blot

analysis, that viable populations of at least 10^6 cfu/ml were present at the end of the fermentation. This species was classified as a new member of the *Candida* genus and it was given the name *C. zemplinina* by Sipiczki in 2003 and it is nowadays considered as a possible fermentation partner of *S. cerevisiae* in mixed fermentations to reduce the acetic acid content in sweet wines (Rantsiou et al., 2012a). The concept of mixed fermentations is not new in wine making, however the results obtained by means of culture-independent methods support the idea of exploiting some positive contributions of non-*Saccharomyces* yeasts to obtain wines with more complex organoleptic profiles.

5. Conclusions and future perspective

The application of culture-independent methods to food microbiology is relatively new and the last 15 years have been particularly exciting for those working in the field of microbial food ecology. For the first time in the history of microbiological food examination, scientists have had methods at hand that do not rely on cultivation, and which are able to study microbial populations that had not been detected previously on synthetic media, because they had been overgrown with the dominant microbiota, or because they had been in VBNC states. DGGE, as the most representative technique in this context, has been used extensively and a large amount of literature has been written for different types of fermented food and for food spoilage processes.

The last couple of years have seen the introduction of new methodologies in microbial food ecology and these are expected to increase in number over the next few years. Next generation sequencing (NGS) has a great advantage over DGGE. In the latter case, only intense and well separated bands can be sequenced in the profiles, and as a consequence, only a partial fraction of the microbiota in that specific food sample can be assessed and identified, but with NGS a

massive quantity of sequences are generated from a single sequencing run, and the analysis of this run offers the possibility of obtaining a large amount of information in a relatively short time. When applied to microbial ecology studies, NGS makes it possible to determine how many reads of different operational taxonomic units (OTUs) occur in a template and therefore to have an estimation of the percent of occurrence of different OTUs in a specific ecosystem. This modern molecular approach has been used in the field of applied food microbiology to study the ecology of pearl millet slurries (Humblot and Guyot, 2009), the microbiota of different kinds of cheese (Alegría et al., 2012; Quigley et al., 2012; Ercolini et al., 2012; Masoud et al., 2011), the microbial diversity of Brazilian kefir grains (Leite et al., 2012) and the fermentation dynamics of different Asian foods (Nam et al., 2012a,b; Park et al., 2012). However, NGS offers the even more interesting possibility of studying the occurrence and abundance of microbial genes in a given ecosystem and of establishing how these genes are expressed. Metagenomic and metatranscriptomic studies represent the future for the study of the microbial ecology of food. In a few years, detailed data on the ecology of microbial transformations in food will become available, allowing scientists to fully comprehend the role and impact of specific microorganisms in defined food sectors. It is expected that new information will become available which will be used to improve food quality and safety.

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Figure 1. Trend in the publication of papers using DGGE as culture-independent method. The data were obtained from the Scopus database (www.scopus.com) in December 2012, using the keywords "DGGE and food"

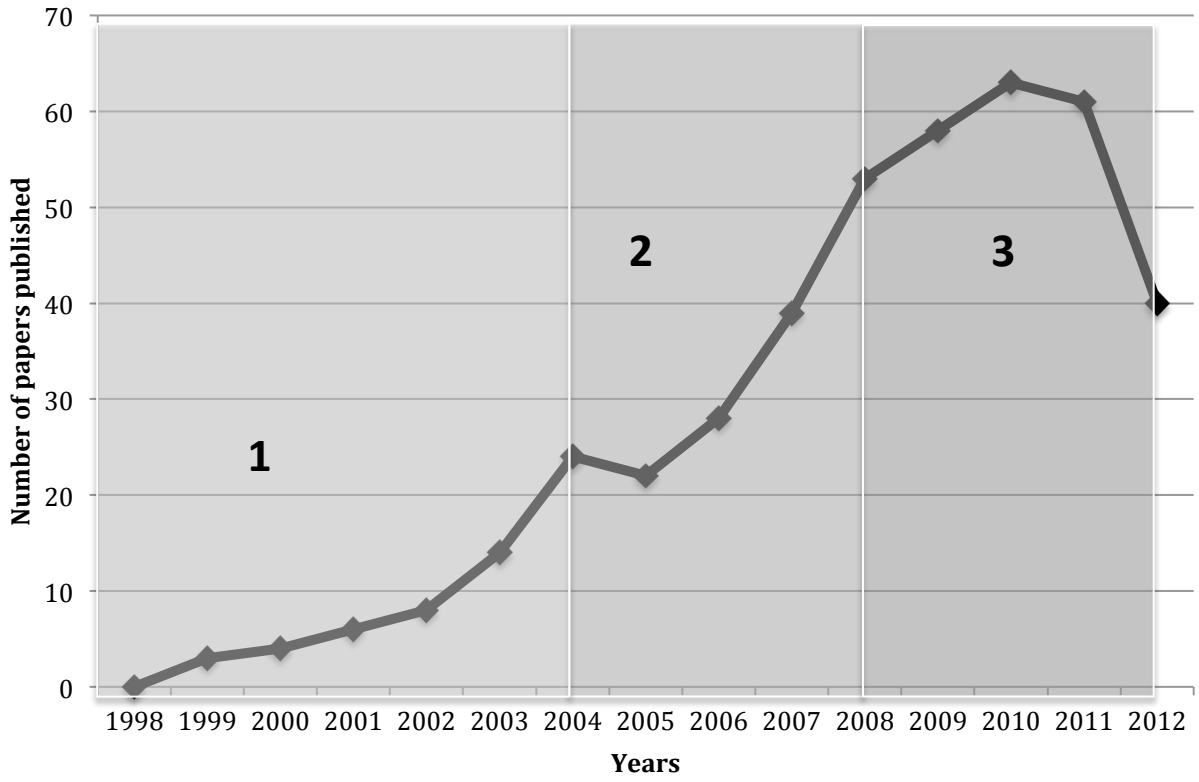

Table 1. Studies exploiting the DGGE technique to study the microbial ecology of various food products.

Food products	Country	Microbial species identified	Target gene(s)	Reference
Milk and dairy products				
Flemish artisan raw milk Gouda-type cheese	Belgium	*Enterococcus faecalis, Lactobacillus parabucheri, Lactobacillus gallinarum*	16S rRNA gene	Van Hoorde et al., 2008
Gouda-type cheeses		*Lactococcus lactis, Lactobacillus plantarum, Lactobacillus casei, Leuconostoc pseudomesenteroides*	16S rRNA gene	Van Hoorde et al., 2010
Capo Verde cheese	Capo Verde Islands	*Lactococcus lactis subsp. lactis, Lactobacillus helveticus, Kocuria rhizophila, Escherichia coli, Delphinella strobiligena, Saccharomyces cerevisiae, Filobasidium elegans*	16S and 26S rRNA genes	Alessandria et al., 2010
Yoghurt	China	*Streptococcus thermophilus, Lactobacillus delbrueckii, Lactobacillus crispatus, Lactobacillus rhamnosus*	16S rRNA gene	Ma et al., 2009
Calenzana cheese	Corsica	*Lactococcus lactis ssp. lactis,* coryneform bacteria	16S rRNA gene	Casalta et al., 2009
Domiati cheese	Egypt	*Leuconostoc mesenteroides, Lactococcus garvieae, Aerococcus viridans, Lactobacillus versmoldensis, Pediococcus inopinatus, Lactococcus lactis, Kocuria rhizophila, Kocuria kristinae, Arthrobacter sp., Brachybacterium tyrofermentans*	16S rRNA gene	El Baradei et al., 2007
Zabady fermented milk		*Streptococcus thermophilus, Lactococcus garvieae, Lactobacillus raffinolactis, Leuconostoc citreum*	16S rRNA gene	El Baradei et al., 2008
Different cheeses	France	*Lactococcus lactis, Streptococcus thermophilus, Lactobacillus buchneri, Corynebacterium variabile, Lactobacillus plantarum*	16S rRNA gene	Ogier at al., 2004
Raw milk during refrigeration		*Lactococcus lactis, Staphylococcus warneri, Staphylococcus epidermidis, Klebsiella pneumoniae, Kocuria rosea, Listeria spp., Arthrobacter sp.*	16S rRNA gene	Lafarge et al., 2004

Table 1. continued

Fermented milk	Ghana	*Lactobacillus acidophilus, Streptococcus salivarius, Lactobacillus delbrueckii subsp. delbrueckii, Streptococcus thermophilus*	16S rRNA gene	Obodai and Dodd, 2006
Feta cheese	Greece	*Streptococcus thermophilus, Lactobacillus delbrueckii subsp. bulgaricus, Kluyveromyces lactis, Pichia membranifaciens, Pichia fermentans*	16S and 26S rRNA genes	Rantsiou et al., 2008
Caciocavallo Silano	Italy	*Lactobacillus delbrueckii, Lactobacillus helveticus, Streptococcus thermophilus, Lactococcus lactis*	16S rRNA gene	Ercolini et al., 2008
Caciotta cheese		*Leuconostoc mesenteroides, Lactobacillus fermentum, Lactobacillus sakei/curvatus*	16S rRNA gene	Aquilanti et al., 2011
Castelmagno cheese		*Lactobacillus plantarum, Streptococcus agalactiae, Lactococcus lactis subsp. lactis, Lactococcus lactis subsp. cremoris, Lactobacillus kefiranofaciens*	16S rRNA gene	Dolci et al., 2008
		Lactococcus lactis, Lactobacillus helveticus, Streptococcus agalactiae	16S rRNA gene	Dolci et al., 2010
Fontina cheese rinds		*Lactococcus lactis subsp. lactis, Streptococcus thermophilus, Arthrobacter nicotianae, Brevibacterium casei, Corynebacterium glutamicum, Debaryomyces hansenii, Candida sake*	16S and 26S rRNA genes	Dolci et al., 2009
Fontina cheese		*Streptococcus thermophilus, Enterococcus faecium, Lactococcus lactis, Macrococcus caseolyticus, Chryseobacterium spp.*	16S rRNA gene	Giannino et al., 2009
Gorgonzola rinds		*Arthrobacter sp., Staphylococcus sp.*	16S rRNA gene	Cocolin et al., 2009a
Parmigiano Reggiano cheese		*Lactobacillus fermentum, Lactobacillus casei, Lactobacillus paracasei, Lactobacillus helveticus, Lactobacillus delbrueckii subsp. lactis*	16S rRNA gene	Gala et al., 2008
Pecorino Siciliano cheese		*Streptococcus bovis, Lactococcus lactis*	16S rRNA gene	Randazzo et al., 2006
		Streptococcus thermophilus, Enterococcus durans, Lactobacillus rhamnosus, Lactobacillus casei	16S rRNA gene	Randazzo et al., 2008

Table 1. continued

Ragusano Cheese	Italy	*Streptococcus thermophilus, Lactococcus lactis, Lactobacillus delbrueckii, Enterococcus faecium*	16S rRNA gene	Licitra et al., 2007
		Leuconostoc sp., Lactococcus lactis, Macrococcus caseolyticus, Streptococcus thermophilus, Lactobacillus delbrueckii, Lactobacillus fermentum	16S rRNA gene	Randazzo et al., 2002
Raw milk		*Candida spp., Kluyveromyces spp.*	26S rRNA gene	Cocolin et al., 2002a
Robiola di Roccaverano		*Lactococcus lactis subsp. lactis, Geotricum spp., Kluyveromyces lactis*	16S and 26S rRNA genes	Bonetta et al., 2008
Surface microbiota of Taleggio, Gorgonzola, Casera, Scimudin and Formaggio di Fossa Italian cheeses		*Psychrobacter celer, Psychrobacter aquimaris, Micrococcus luteus, Staphylococcus equorum*	16S rRNA gene	Fontana et al., 2010
Taleggio cheese		*Arthrobacter spp., Brevibacterium spp., Pseudoalteromonas agarivorans, Brevibacterium linens*	16S rRNA gene	Feligini et al., 2012
Tosela cheese		*Lactobacillus paracasei, Streptococcus macedonicus, Lactobacillus rhamnosus*	16S rRNA gene	Settanni et al., 2011
Water-Buffalo Mozzarella Cheese		*Streptococcus thermophilus, Lactococcus lactis, Lactobacillus delbrueckii, Lactobacillus crispatus*	16S rRNA gene	Ercolini et al., 2004b
Tarag cheese	Mongolia	*Lactobacillus helveticus, Lactococcus lactis subsp. lactis, Lactobacillus casei*	16S rRNA gene	Liu et al., 2012
Oscypek cheese	Poland	*Lactococcus lactis, Lactobacillus plantarum, Leuconostoc citreum, Streptococcus vestibularis, Debaryomyces hansenii, Candida pararugosa*	16S and 26S rRNA genes	Alegría et al., 2012
Bukuljac cheese	Serbia	*Leuconostoc mesenteroides*	16S rRNA gene	Nikolic et al., 2010
Cabrales Spanish blueveined cheese	Spain	*Lactococcus garvieae, Lactococcus lactis subsp. lactis, Lactobacillus raffinolactis, Penicillium roqueforti, Geotrichum candidum*	16S and 26S rRNA genes	Flórez and Mayo, 2006
Casín cheese		*Streptococcus thermophilus, Lactococcus lactis, Streptococcus parauberis, Lactobacillus plantarum, Geotrichum candidum, Kluyveromyces lactis*	16S and 26S rRNA genes	Alegria et al., 2009
Kefir grains	Taiwan	*Lactobacillus kefiranofaciens, Lactobacillus kefiri, Lactococcus lactis*	16S rRNA gene	Chen et al., 2008

Table 1. continued

Taiwanese ropy fermented milk	Taiwan	*Lactococcus lactis subsp.lactis, Leuconostoc mesenteroides subsp. mesenteroides, Lactobacillus fermentum*	16S rRNA gene	Wang et al., 2011b
Tibetan Kefir	Tibet	*Pseudomonas sp., Leuconostoc mesenteroides, Lactobacillus helveticus, Lactobacillus kefiranofaciens, Lactococcus lactis, Lactobacillus kefiri, Lactobacillus casei, Kazachstania unispora, Kluyveromyces marxianus, Saccharomyces cerevisiae*	16S and 26S rRNA genes	Zhou et al., 2009
Kefir grains and kefir beverages	Turkey	*Lactobacillus kefiranofaciens, Lactococcus lactis*	16S rRNA gene	Kesmen and Kacmaz, 2011
Fermented meats				
Fermented sausages	Argentina	*Lactobacillus sakei, Lactobacillus plantarum, Staphylococcus saprophyticus*	16S rRNA gene	Fontana et al., 2005a
		Lactobacillus plantarum, Lactobacillus sakei, Staphylococcus saprophyticus, Corynebacterium variabilis, Brochothrix thermophacta	16S rRNA gene	Fontana et al., 2005b
	Italy	*Lactobacillus plantarum, Staphylococcus carnosus, Lactobacillus curvatus*	16S rRNA gene	Cocolin et al., 2006b
		Lactobacillus plantarum, Lactobacillus curvatus, Lactobacillus sakei	16S rRNA gene	Cocolin et al., 2001a
		Penicillium farinosum, Debaryomyces hansenii, Penicillium viridicatum, Mucor racemosus	26S rRNA gene	Cocolin et al., 2006a
		Enterococcus faecalis, Pediococcus acidilactici, Lactobacillus rhamnosus, Enterococcus faecium, Enterococcus durans, Lactobacillus sakei	16S rRNA gene	Gazzola et al., 2012
		Lactobacillus curvatus, Lactobacillus sakei, Brochothrix thermosphacta, Macrococcus caseolyticus, Staphylococcus xylosus	16S rRNA gene	Rantsiou et al., 2005

Table 1. continued

Fermented sausages	Italy	*Lactobacillus plantarum, Lactobacillus curvatus, Lactobacillus sakei, Lactococcus lactis ssp. lactis, Staphylococcus xylosus, Debaryomyces hansenii*	16S and 26S rRNA genes	Aquilanti et al., 2007
		Lactobacillus curvatus, Lactobacillus sakei, Lactobacillus paraplantarum, Lactobacillus algidus, Leuconostoc mesenteroides/pseudomesenteroides, Staphylococcus saprophyticus	16S rRNA gene	Cocolin et al., 2009b
Soppressata of Vallo di Diano sausage		*Staphylococcus xylosus, Staphylococcus succinus, Staphylococcus equorum, Lactobacillus sakei, Lactobacillus curvatus, Debaryomyces hansenii*	16S and 26S rRNA genes	Villani et al., 2007
Alheira: traditional Portuguese fermented sausage	Portugal	*Brochothrix thermosphacta, Lactobacillus sakei, Leuconostoc lactis, Streptococcus lutetiensis, Lactobacillus curvatus, Lactobacillus brevis*	16S rRNA gene	Albano et., 2008
Fermented ham	Taiwan	*Lactobacillus sakei, Staphylococcus saprophyticus, Lactobacillus mesenteroides, Carnobacterium divergens, Brochothrix thermosphacta*	16S rRNA gene	Tu et al., 2010
Cereal-based foods				
Sourdoughs	Belgium	*Lactobacillus spicheri, Lactobacillus plantarum, Lactobacillus sanfranciscensis*	16S rRNA gene	Scheirlinck et al., 2009
		Lactobacillus frumenti, Lactobacillus panis, Lactobacillus pontis, Lactobacillus curvatus	16S rRNA gene	De Vuyst and Vancanneyt, 2007
		Lactobacillus sanfranciscensis, Lactobacillus paralimentarius, Lactobacillus plantarum, Lactobacillus pontis, Acetobacter sp.	16S rRNA gene	Scheirlinck et al., 2008
Rice sourdough	Germany	*Lactobacillus plantarum, Lactobacillus fermentum, Lactobacillus kimchii, Lactobacillus gallinarum, Lactobacillus pontis*	16S rRNA gene	Meroth et al., 2004
Sourdough		*Lactobacillus sanfranciscensis, Lactobacillus crispatus, Lactobacillus pontis, Lactobacillus johnsonii, Lactobacillus mindensis*	16S rRNA gene	Meroth et al., 2003a
		Saccharomyces cerevisiae, Candida humilis, Dekkera bruxellensis	26S rRNA gene	Meroth et al., 2003b
Panettone	Italy	*Lactobacillus sanfranciscensis, Lactobacillus brevis, Candida humilis*	16S and 26S rRNA genes	Garofalo et al., 2008

Table 1. continued

Sourdough	Italy	*Saccharomyces cerevisiae, Kazachstania unispora, Saccharomyces bayanus/Kazachstania sp., Candida humilis*	26S rRNA gene	Minervini et al., 2012
		Lactobacillus sanfranciscensis, Lactobacillus fermentum	16S rRNA gene	Randazzo et al., 2005
		Lactobacillus plantarum, Lactobacillus sanfranciscensis, Lactobacillus rossiae	16S rRNA gene	Settanni et al., 2006
Ting: fermented sorghum	South Africa	*Weissella cibaria, Lactobacillus curvatus, Lactococcus lactis*	16S rRNA gene	Madoroba et al., 2011
Maize fermentation	Mexico, Congo and Benin	*Lactobacillus plantarum, Lactobacillus delbrueckii, Lactobacillus fermentum*	16S rRNA gene PCR-DGGE	Ampe and Miambi, 2000
Fermented cassava	Congo	*Lactobacillus plantarum/pentosus, Lactobacillus plantarum/sanfrancisco, Lactobacillus fermentum, Lactobacillus delbrueckii, Clostridium acetobutylicum/butyricum*	16S rRNA gene	Miambi et al., 2003
Mexican fermented and maize dough pozol	Mexico	*Streptococcus bovis, Enterococcus saccharolyticus, Lactobacillus fermentum, Lactobacillus plantarum, Exiguobacterium aurantiacum*	16S rRNA gene	Ben Omar and Ampe, 2000
Pozol		*Lactobacillus plantarum, Lactobacillus fermentum, Streptococcus bovis, Weissella paramesenteroides*	16S rRNA gene	Ampe et al., 1999
Fresh and fermented vegetables				
Fuzhuan brick-tea	China	*Debaryomyces spp., Eurotium spp., Aspergillus niger*	26S rRNA gene	Xu et al., 2011
Fresh cut salad	Italy	*Pseudomonas siringae, Pantoae agglomerans, Pseudomonas rhodesiae, Erwinia persicinus*	16S rRNA gene	Randazzo et al., 2009
Sunki	Japan	*Lactobacillus fermentum, Lactobacillus plantarum, Lactobacillus delbrueckii*	16S rRNA gene	Endo et al., 2008
Kimchi	Korea	*Halococcus spp., Natronococcus spp., Natrialba spp., Lodderomyces spp., Trichosporon spp.*	16S rRNA gene	Chang et al., 2008
		Weissella confusa, Leuconostoc citreum, Lactobacillus sakei, Lactobacillus curvatus	16S rRNA gene	Lee et al., 2005

Table 1. continued

Dongchimi	South Korea	*Lactobacillus algidus, Lactobacillus plantarum*	16S rRNA gene	Park et al., 2008
Olives	Spain	*Gordonia sp., Pseudomonas sp., Sphingomonas sp., Halosarcina pallida, Lactobacillus sp., Saccharomyces cerevisiae, Lactobacillus pentosus/plantarum, Lactobacillus vaccinostercus/suebicus, Candida cf. apicola*	16S and 26S rRNA genes	Abriouel et al., 2010
Wine, vinegar and other beverages				
Caxiri, alcoholic beverage	Brazil	*Paenibacillus sp., Bacillus subtilis, Lactobacillus fermentum, Saccharomyces cerevisiae, Pichia membranifaciens, Rhodotorula mucilaginosa*	16S and 26S rRNA genes	Santos et al., 2012
Palm wine	Cameroon	*Saccharomyces cerevisiae, Saccharomycodes ludwigii, Zygosaccharomyces bailii, Hanseniaspora uvarum, Candida parapsilopsis, Candida fermentati, Pichia fermentans*	26S rRNA gene	Stringini et al., 2009
Hong Qu glutinous rice wine	China	*Janthinobacterium lividum, Bacillus subtilis, Bacillus amyloliquefaciens, Saccharomycopsis fibuligera, Rhizopus oryzae, Aspergillus flavus*	16S rRNA and 18S genes	Lv et al., 2012
Sauternes wines	France	*Saccharomyces cerevisiae, Candida stellata, Hanseniaspora uvarum, Botrytis cinerea*	26S rRNA gene	Divol and Lonvaud-Funel
Botrytis-affected wine fermentations	Greece	*Metschnikowia pulcherrima, Zygosaccharomyces bailii, Issatchenkia spp., Botrytis cinerea*	26S rRNA gene	Nisiotou et al., 2007
Botrytis-affected grapes and wine fermentations		*Klebsiella oxytoca, Citrobacter freundii, Enterobacter spp., Erwinia sp., Pantoea dispersa, Tatumella ptyseos* on grapes. *Lactobacillus plantarum* and *Enterobacter ludwigii* during fermentations	16S rRNA gene	Nisiotou et al. 2011
Balsamic vinegar	Italy	*Acetobacer pasteurianus/aceti*	16S rRNA gene	De Vero et al., 2006
		Acetobacer pasteurianus, Gluconacetobacter europaeus	16S rRNA gene	Gullo et al., 2009
Erbaluce wine		*Candida zemplinina, Metschnikowia fructicola, Hanseniaspora uvarum, Saccharomyces cerevisiae*	26S rRNA gene	Rantsiou et al., 2013
Picolit wine		*Saccharomyces cerevisiae, Aureobasidium pullulans, Candida zemplinina*	26S rRNA gene	Urso et al., 2008

Table 1. continued

Vinegard	Japan	*Aspergillus oryzae, Saccharomyces sp., Lactobacillus acetotolerance, Acetobacer pasteurianus*	16S and 26S rRNA genes	Haruta et al., 2006
Takju: Korean rice wines	Korea	*Lactobacillus paracasei, Lactobacillus plantarum, Leuconostoc pseudomesenteroides, Lactobacillus harbinensis, Lactobacillus parabuchneri*	16S rRNA gene	Kim et al., 2010
Mezcal, alcoholic beverage	Mexico	*Pediococcus parvulus, Lactobacillus brevis, Lactobacillus composti, Lactobacillus parabuchneri, Lactobacillus plantarum*	16S rRNA gene	Narváez-Zapata et al., 2010
Fruit juice	South Africa	*Alicyclobacillus acidoterrestris, Alicyclobacillus pomorum*	16S rRNA gene	Duvenage et al., 2007
Makgeolli	South Korea	*Lactobacillus crustorum, Lactobacillus brevis, Lactobacillus plantarum*	16S rRNA gene	Kim et al., 2012
Tempranillo wines	Spain	*Oenococcus oeni, Gluconobacter oxydans, Asaia siamensis*	16S rRNA gene	Ruiz et al., 2010
Kava beverages	Unites States	*Weissella soli, Lactobacillus spp., Lactococcus lactis*	16S rRNA gene	Dong et al., 2011
Botrytis-affected wine fermentations		*Hanseniaspora uvarum, Hanseniaspora osmophila, Candida zemplinina, Lachancea thermotolerans, Saccharomyces cerevisiae*	26S rRNA gene	Mills et al., 2002
Sweet wine fermentation		*Metschnikowia sp., Botrytis cinerea, Pichia anomala, Saccharomyces cerevisiae*	26S rRNA gene	Cocolin et al., 2001b
Fish products				
Chum salmon sauce	Japan	*Zygosaccharomyces rouxii, Candida versatilis, Aspegillus oryzae*	26S rRNA gene	Yoshikawa et al., 2010
Aji-narezushi and iwashi-nukazuke		*Lactobacillus acidipiscis, Lactobacillus versmoldensis, Lactobacillus plantarum,Tetragenococcus muriaticus, Tetragenococcus halophilus*	16S rRNA gene	An et al., 2010
Sea food	Korea	*Sulfolobus sp.,Thermocladium sp., Lactobacillus sp., Weissella sp., Salinivibrio sp.*	16S rRNA gene	Roh et al., 2010
Philippine fermented food products	Philippine	*Lactobacillus fermentum, Lactobacillus plantarum, Lactobacillus panis, Lactobacillus pontis, Acetobacter pomorum, Acetobacter ghanensis*	16S rRNA gene	Dalmacio et al., 2011

Table 1. continued

Cocoa and african foods				
Tayohounta: natural fermentation of baobab seed kernels	Benin	*Bacillus licheniformis, Bacillus pumilus, Bacillus subtilis, Bacillus thermoamylovorans, Lactobacillus fermentum*	16S rRNA gene	Chadare et al., 2011
Cocoa beans	Brazil, Ecuador, Ivory Coast, Malaysia	*Hanseniaspora sp., Pichia kudriavzevii, Saccharomyces cerevisiae, Hyphopichia burtonii, Meyerozyma caribbica*	26S rRNA gene	Papalexandratou and De Vuyst, 2011
	Ghana	*Hanseniaspora guilliermondii, Candida krusei, Candida zemplinina, Pichia membranifaciens*	26S rRNA gene	Nielsen et al., 2005
		Hanseniaspora guilliermondii, Candida diversa, Candida zemplinina, Pichia membranifaciens, Issatchenkia orientalis, Lactobacillus fermentum, Bacillus licheniformis, Acetobacter pasteurianus, Leuconostoc pseudoficulneum	16S and 26S rRNA genes	Nielsen et al., 2007
		Lactobacillus fermentum, Lactobacillus pseudomesenteroides, Lactobacillus plantarum, Weissella hanaensis	16S rRNA gene	Camu et al., 2007
Cocoa fermentation		*Lactobacillus fermentum, Leucnostoc pseudomesenteroides, Leuconostoc seudoficulneum, Acetobacter pasteurianus, Saccharomycopsis crateagensis, Hanseniaspora guilliermondii, Candida zemplinina*	16S and 26S rRNA genes	Nielsen et al., 2008
Processing of cocoa beans into cocoa powder	Netherlands	*Bacillus licheniformis, Bacillus subtilis*	16S rRNA gene	Lima et al., 2012
Cassava for gari production	Nigeria	*Issatchenkia scutulata, Candida rugopelliculosa, Candida maritime, Zygosaccharomyces rouxii, Galactomyces geotricum*	18S rRNA gene	Oguntoyinbo 2011

Table 1. continued

Cereal foods: kunu-zaki and ogi		*Weissella confusa, Lactobacillus fermentum, Lactobacillus amylolyticus, Lactobacillus delbrueckii subsp. bulgaricus, Bacillus sp., Lactococcus lactis subsp. lactis*	16S rRNA gene	Oguntoyinbo et al., 2011
Ugandan Ghee	Uganda	*Lactobacillus helveticus , Lactobacillus plantarum, Bifidobacterium sp., Enterococcus faecium, Lactobacillus brevis, Lactobacillus acetotolerans, Lactococcus raffinolactis, Acetobacter aceti, Acetobacter lovaniensis, Acetobacter pasteurianus, Brettanomyces custersianus, Candida silvae, Issatchenkia orientalis, Saccharomyces cerevisiae*	16S and 26S rRNA genes	Ongol and Asano 2009
Cassava for gari production	West Africa	*Lactobacillus plantarum, Lactobacillus fermentum, Lactobacillus pentosus, Lactobacillus acidophilus, Lactobacillus casei*	16S rRNA gene	Oguntoyinbo and Dodd, 2010
Soy-based products				
Chinese liquor	China	*Lactobacillus acetotolerans*	16S rRNA gene	Wang et al., 2008
Daqus		*Saccharomycopsis fibuligera, Pichia anomala, Aspergillus oryzae, Absidia blakesleeana*	18S rRNA gene	Wang et al., 2011a
Douchi		*Bacillus subtilis, Aspergillus oryzae*	16S and 18S rRNA genes	Chen et al., 2011a
		Lactococcus lactis, Staphylococcus lentus	16S rRNA gene	Chen et al., 2011b
		Bacillus subtilis, Bacillus amyloliquefaciens, Saccharomyces cerevisiae, Pichia farinosa	16S and 26S rRNA genes	Chen et al., 2012
Soy sauce	Japan	*Weissella cibaria, Staphylococcus gallinarum, Staphylococcus kloosii, Aspergillus oryzae, Zygosaccharomyces rouxii, Candida etchellsii, Candida versatilis*	16S and 26S rRNA genes	Tanaka et al., 2012
Chungkookjang	Korea	*Pantoea agglomerans, Bacillus subtilis, Pantoea ananatis, Bacillus licheniformis*	16S rRNA gene	Hong et al., 2012
Doenjang		*Leuconostoc mesenteroides, Tetragenococcus halophilus, Enterococcus faecium, Mucor plumbeus, Debaryomyces hansenii*	16S and 18S rRNA genes	Kim et al., 2009

Table 1. continued

Japanese and Chinese fermented soybean pastes	Korea	*Tetragenococcus halophilus, Staphylococcus gallinarum, Aspergillus oryzae, Zygosaccharomyces rouxii*	16S and 18S rRNA genes	Kim et al., 2010
Meju		*Enterococcus durans, Bacillus subtilis, Absidia corymbifera, Aspergillus sp., Candida rugosa*	16S and 18S rRNA genes	Lee et al., 2010
Kochujang	South Korea	*Bacillus ehimensis, Bacillus megaterium, Bacillus pumilus, Bacillus subtilis, Bacillus licheniformis*	16S rRNA gene	Park et al., 2009
Food spoilage				
Artisan-type cooked ham	Belgium	*Carnobacterium divergens, Brochothrix thermosphacta, Leuconostoc carnosum*	16S rRNA gene PCR-DGGE	Vasilopoulos et al., 2007
Packaged sliced cooked meat		*Lactobacillus sakei, Lactobacillus fuchuensis, Lactobacillus curvatus, Carnobacterium divergens, Leuconostoc carnosum*	16S rRNA gene PCR-DGGE	Audenaert et al., 2009
Raw milk	Canada	*Clostridium tyrobutyricum, Clostridium sporogenes, Clostridium disporicum*	16S rRNA gene PCR-DGGE	Julien et al., 2008
Broiler Meat	China	*Staphylococcus sp., Pseudomonas sp., Carnobacterium sp., Weissella sp.*	16S rRNA gene PCR-DGGE	Zhang at al., 2012
Chilled pork		*Pseudomonas sp., Lactobacillus sp., Brochothrix thermosphacta, Staphylococcus sp., Arthrobacter sp., Enterococcus sp., Moraxella sp.*	16S rRNA gene PCR-DGGE	Li et al., 2006
Packaged pork		*Pseudomonas sp., Pseudomonas fluorescens, Brochothrix thermosphacta, Achromobacter xylosoxidans*	16S rRNA gene PCR-DGGE	Jiang et al., 2011
Packed cooked ham		*Weissella viridescens, Leuconostoc mesenteroides*	16S rRNA gene PCR-DGGE	Han et al., 2011
		Weissella viridescens, Weissella minore	16S rRNA gene PCR-DGGE	Han et al., 2010
Prepared chicken products		*Acinetobacter sp., Carnobacterium sp., Pseudomonas sp., Brochothrix sp., Weissella sp.*	16S rRNA gene PCR-DGGE	Liang et al., 2012
Vacuum-packaged pork during chilled storage		*Carnobacterium sp./divergens, Lactobacillus sakei, Lactococcus sp./piscium*	16S rRNA gene PCR-DGGE	Jiang et al., 2010
Beef chops	Italy	*Brochothrix thermosphacta, Pseudomonas spp., Carnobacterium divergens*	16S rRNA gene PCR-DGGE	Ercolini et al., 2011

Table 1. continued

Beef stored in nisin activated packaging	Italy	*Pseudomonas spp., Carnobacterium spp., Carnobacterium divergens, Staphylococcus xylosus*	16S rRNA gene PCR-DGGE	Ercolini et al., 2010
Cheese in late blowing spoilage		*Clostridium butyricum, Clostridium tyrobutyricum, Clostridium sporogenes*	16S rRNA gene PCR-DGGE	Cocolin et al., 2004a
Fresh sausages		*Brochothrix thermosphacta, Lactobacillus sakei, Debaryomyces hansenii*	16S and 26S rRNA gene PCR-DGGE	Cocolin et al., 2004b
Freshly cut beefsteaks		*Rahnella aquatilis, Pseudomonas spp., Carnobacterium divergens, Lactobacillus sakei*	16S rRNA gene PCR-DGGE	Ercolini et al., 2006
Packaged Beef		*Lactobacillus sakei, Brochothrix thermosphacta, Leuconostoc spp.*	16S rRNA gene PCR-DGGE	Fontana et al., 2006
Spoiled wines		*Brettanomyces bruxellensis, Saccharomyces cerevisiae, Brettanomyces anomalus*	26S rRNA gene PCR-DGGE	Cocolin et al., 2004c
Wheat bread		*Bacillus subtilis, Bacillus licheniformis, Bacillus clausii, Bacillus firmus*	16S rRNA gene PCR-DGGE	Pepe et al., 2002
Packaged beef	New Zealand	*Carnobacterium spp., Clostridium spp.*	16S rRNA gene PCR-DGGE	Brightwell et al., 2009
Atlantic cod	Norway	*Photobacterium phosphoreum, Pseudomonas spp., Shewanella baltica, Shewanella putrefaciens*	16S rRNA gene PCR-DGGE	Hovda et al., 2007a
Farmed atlantic cod		*Pseudomonas spp., Photobacterium spp., Shewanella putrefaciens*	16S rRNA gene PCR-DGGE	Hovda et al., 2007b
Morcilla de Burgos	Spain	*Weissella viridescens, Leuconostoc mesenteroides, Weissella confusa, Gamma proteobacterium*	16S rRNA gene PCR-DGGE	Diez et al., 2008
Pasteurized milk	United States	*Pseudomonas sp., Streptococcus sp., Buttiauxella sp.,*	16S rRNA gene PCR-DGGE	He et al., 2009