

## Food Traceability : How microbial ecology can help

Jean-Christophe MEILE, PhD  
Food Safety Group  
UMR Qualisud - Cirad  
Montpellier  
France  
[meile@cirad.fr](mailto:meile@cirad.fr)

### Food Traceability requirements

Following various food crises such as the mad cow disease or the recent fraud in the beef meat market, European consumers are more and more perceptible to the quality and the origin of foodstuffs they buy, and food safety became one of their main concerns (Lairon, 2010). As a response to safety, sociologic and economic problems and within the framework of the globalization, the European regulation relative to the sanitary quality of foodstuffs had to be strengthened. The Food Law (European regulation CE No.178/2002), applied since January 2005, imposes to all food processing companies of the European Union (EU) to keep consumers informed about the nature of the product and any sanitary problems. Moreover, it imposes the traceability of foodstuffs at all steps of the food production.



According to the International Organization for Standardization (ISO 9000-2000), traceability is a risk management tool which allows tracing the progress of foodstuffs (“from the farm to the fork”). Traceability became a constant and compulsory concern for all actors of the food chain: producers, transformers and distributors have to identify and solve critical points, realize self-monitoring, but also, inform consumers about the nature of food products (UE regulation 178/2002). It permits a quicker crisis management and a fast removal of potentially dangerous food from the market. Traceability is one of the main tools that ensure both the effective responsibility of foodstuffs

manufacturers, farmers to industry of the food sector and the quality of the end product and also to improve risk estimation and manage effectiveness (Raspor, 2004).

### **And in practical ?**

However, there is, at the moment, no real analytical tool for food traceability allowing authentication of the product origin or the farming type in a simple, fast and inexpensive way. Currently, various modern analytical techniques allow determining the origin of food with a certain precision (Peres et al., 2007). These methods can be classified in two categories:

- i) Physico-chemical techniques such as Magnetic Nuclear Resonance (MNR), Near Infra-Red Spectroscopy (NIRS) or Stable Isotope Ratio Analysis (SIRA)
- ii) Biological techniques (biochemical or molecular biology involving DNA, RNA, proteins or biological molecules analyses).

Whereas physico-chemical methods require heavy, costly equipment and the construction and maintenance of databases, biological techniques are of great potential to develop rapid, cost-effective methods to screen, identify and detect (biological) markers that are specific to a variety, geographical location, and/or to a mode of production of foodstuffs.

For example, the skin of fresh foods (vegetables, fruits) is not sterile and carries microorganisms or their fragments. The presence of various microorganisms depends on the external environment of the food matrices (soil ecology, spoilage, insects, diseases), but also microorganisms brought by human activity. Previous works showed that there is a link between the geographical origin of food and the structure of the food microbial flora of wild and farm fish (Le Nguyen et al., 2008; Tatsadjieu et al., 2010), fruits (El Sheikha et al., 2009, 2011) and, more recently, marine salts (Dufossé et al., 2013). This was performed using a molecular biology method based on the extraction, PCR amplification and DGGE separation of microbial DNA (PCR-DGGE). Usually, 16S and 26S or 28S rDNA coding regions are used to study bacterial and fungal communities, respectively

Evidences suggest that there is a specific signature of food origin at the microbial ecology level that can be determined by molecular techniques (based on PCR amplification). Appropriate statistical methods applied to molecular signatures comparison can help reveal significant differences between samples and extract biological (DNA/RNA) markers that are specific of a region or a mode of production. Recent work showed that, by using appropriate statistical methods, it was possible to distinguish organic from conventional nectarines by analyzing the microbial ecology of their skin (Bigot et al., 2015). This kind of study opens the way to search for biological markers which detection can be for fraud detection, and authentication controls in food (biosensors).

### **Perspectives on food traceability tools using microbial ecology approaches**

As methodologies in molecular biology evolve very fast, reducing analysis time and cost, there is no doubt that these methods will be soon routinely applied in food microbiology analyses (Bokulich and Mills, 2012). Methods based on High Resolution Melting of PCR amplicons was recently

applied to characterize and authenticate greek feta cheese (Ganopoulos et al., 2013) and to monitor food fermentation (Lina and Gänzle, 2014). This rapid and cost-effective method will probably become a powerful tool for food samples characterization and authentication controls.

The number of studies describing the use of Next-generation sequencing (NGS) methods in food analysis has dramatically increased the past few years. Recent technological advances and the use of NGS in metagenomics approaches allow a comprehensive description of the microbial content in a given sample by generating up to  $10^9$  sequences reads per run (i.e. analysis). NGS methods have been mostly applied to study various fermented foods from different origin (for a review see Van Hijum et al., 2013). So far, metagenomics approaches constitute an ideal tool for an in-depth search of molecular markers in food.

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