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Review

Identification of meat origin in food products—A review

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ABSTRACT

Recently, falsified meat products have become a serious problem. Many issues such as public health, fair trade, and religious consideration are directly influenced by adulterations of meat. To overcome this problem, various analytical methods, based on physical, chemical, anatomical, histological, and biological approaches are being utilized to identify meat species. Nevertheless, by virtue of their inherent limitations, most of these methods have been replaced by more accurate and sensitive detection methods, such as DNA-based molecular techniques. This review highlights the most extensive and updated overview of meat species identification based on DNA hybridization techniques. It will be demonstrated that the DNA-hybridization method is a highly sensitive method in analyzing the similarity of DNA strands, where the limit of detections was reported to be from 0.1% to less than 0.01%, depending on the meat species.

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1. Introduction

Meat is one of the best nutritional sources of protein for human consumption, and due to its appreciated flavor and taste, is being largely consumed all over the world (Soares, Amaral, Oliveira, & Mafra, 2014). Due to the increasing price and decreasing availability of meat, meat producers may be tempted to commit fraud. In this context, adulteration of meat products has become a serious issue in the past three decades (Hsieh, 2006).

It has been claimed that precooked meat products, such as raw ground types, is more at risk of being adulterated, especially with cheaper meat species in the manufacturing process such as hamburger recipes compared to fresh meat (Hsieh, 2006; Mousavi et al., 2015). This growing phenomenon is mostly due to the lack of the reliable and efficient analytical methods to identify the specific species of the cooked meats (Hsieh, 2006).

There are several reports on the fraudulent substitution of

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higher-value meats with either lower value meat species (Fajardo et al., 2008b; Soares, Amaral, Oliveira, & Mafra, 2013), or by the use of vegetable proteins, such as soybean, instead of muscle proteins (Belloque, García, Torre, & Marina, 2002). The presence of undeclared species in meat products has been reported by other researchers as well (Ayaz, Ayaz, & Erol, 2006; Özpinar, Tezmen, Gökçe, & Tekiner, 2013). Moreover, using undeclared ingredients, such as infected neurological tissues, might be a reason for health complications, examples being the usage of bovine, ovine, and porcine in deer products (Zha, Xing, & Yang, 2010) and bovine spongiform encephalopathy (BSE) in heated meat products (Sultan et al., 2004). Allergic reactions such as gluten enteropathy and lactose intolerance have been diagnosed in some consumers due to the usage of certain non-meat ingredients, such as eggs, vegetables, or milk proteins, which illustrate the need of legal regulations for proper labelling to support fair-trade practices (Ballin, Vogensen, & Karlsson, 2009; Colmenero, 2000). Another serious aspect, which should also be taken into account in meat adulteration is religious beliefs; the consumption of dog meat is forbidden in Islam and Buddhism (Rahman et al., 2014; Soares, Amaral, Mafra, & Oliveira, 2010), while the consumption of pork is forbidden in Islam and Judaism (Nakyinsige, Man, & Sazili, 2012; Soares et al., 2010). Apart from religious considerations, the horse meat adulteration scandal in commercial food products across Europe in 2013 led to a series of product recalls. The detection of horse DNA in food items that were marketed as containing 100% beef has created a need to identify applicable methods for verifying meat authenticity (Ali, Razzak, & Hamid, 2014; Cai et al., 2014; Druml, Hochegger, & Cichna-Markl, 2015; Hou et al., 2015; Lin et al., 2014; Okuma & Hellberg, 2015; Schmutzler, Beganovic, Böhler, & Huck, 2015; Soares et al., 2014). The substitution of fraudulent meats in some meat and meat products were also reported elsewhere (Ayaz et al., 2006; Flores-Munguia, Bermudez-Almada, & Vázquez-Moreno, 2000; Mousavi et al., 2015; Özpinar et al., 2013).

To date, numerous identification methods for meat species detection have been developed, with conventional methods, which include physical, sensory analysis, anatomical, and histological, chemical, biochemical, chromatographic, spectrophotometric, electrophoretic, immune sera diffusion, immunological, and immunoelectrophoretic techniques (Hou et al., 2015; Kumar et al., 2013; Singh & Neelam, 2011).

During past years, the detection of species-specific proteins for food involved the determination of the source of material used in consumption. The varieties of electrophoretic and immunological methods have been used, but they were limited in certain aspects. These methods have commonly been applied to raw meat products due to their success rates being dependent upon the stability of the proteins in foodstuffs (Hsieh, 2006; Lockley & Bardsley, 2000). Table 1 detail the different detection methods based on the range of meat species. Thus, the development of simple and quick method for species identification of meat products has increasingly turned towards DNA-based techniques in overcoming the limitations of existing methods. DNA-based methods are the most specific and sensitive techniques for species identification, because they are extraordinarily quick compared to protein-based methods (Murugaiah et al., 2009). DNA has relatively higher stability in harsh conditions compared to many proteins. Thermo-stability and the ubiquitous presence of DNA molecules in the majority of biological tissues render DNA to be the most favorable molecule for the identification of component in food authentication tests (Ali et al., 2015; Hamzah, Mutalib, & Babji, 2013; Lin et al., 2014; Lockley & Bardsley, 2000; Murugaiah et al., 2009). Keeping that in mind, current studies have focused on the application of the DNA based method as a more effective approach to detect and identify meat sources (cattle, chicken, pig, goat, deer, horse …).

DNA-hybridization is one of the promising technique in meat species identification to realize the best properties via a combination of two or more materials within one system. The idea of hybridization of DNA into the solid surface was first described by Denhardt (1966), thereafter, the development of this method resulted in a significant insight for the identification of sequences in the genomic DNA, which is now referred to as biosensor technologies (Denhardt, 1966). We will discuss DNA-based methods and highlight DNA-hybridization techniques in this review.

2. Meat species identification methods

A considerable number of analytical methods have been developed to detect the origin of species in food products (Hsieh, 2006; Lockley & Bardsley, 2000). DNA and Protein-based methods have been introduced to identify meat species, where the former include hybridization and polymerase chain reaction (PCR) (Hsieh, 2006; Lockley & Bardsley, 2000). Protein-based methods include chromatography, spectroscopy, electrophoresis, and immunoassays (Hsieh, 2006; Nakyinsige et al., 2012). However, they might have their own limitations or weaknesses, including denaturation during thermal processing, laborious or time consuming method, and the requirement of expensive equipment. Both DNA and protein-based techniques consist of several subclasses, as detailed in Table 2.

2.1. DNA-based methods

Over the past two decades, DNA-hybridization and Polymerase chain reactions (PCR) are the two main DNA-based molecular techniques that help identify meat species (Lockley & Bardsley, 2000) in fraudulent food products. Some of the unique characteristics of DNA include stability against high temperatures, availability in most of an organism's cells, and potentially allowing for the extraction of exact information of a proper sample from the identical source regardless of the tissues of origin (Lockley & Bardsley, 2000).

2.1.1. DNA-hybridization technique

DNA-hybridization is key towards controlling the function of DNA-based materials in nanoscience (Dohno & Nakatani, 2011). The DNA-hybridization concept was first described in the late 1950's and early 1960's (Tullis & Streifel, 2002). Since then, the detection of DNA-hybridization has been at the heart of many recent studies in bioanalyses, including pathogen identification, genetic profiling, and single-nucleotide polymorphism (Han, 2015). It was first introduced for meat species identification in 1987 by (Baur, Teifel-Greding, & Liebhardt, 1987). They used absolutely simple methods, where labeled DNA probes were hybridized to food samples of genomic DNA covalently linked to membranes made out of nylon; a format slot- or dot-blot was then duly selected (Broll, 2013).

In recent years, reports have focused on the identification of DNA based on the hybridization systems between a targeted DNA and its complementary probe, either in solution or on solid support forms (Sassolas, Leca-Bouvier, & Blum, 2008). DNA biosensor and DNA microarray are the best specific detection systems that offer promising techniques allowing for fast, reusable, continuous, selective, and sensitive detection methods (Sassolas et al., 2008). Both DNA biosensors and microarrays uses the preferential binding of complementary single-stranded nucleic acid sequences. This structure generally depends on the immobilization of a single-stranded DNA (ss-DNA) probe onto a transducer surface to attach to its complementary target DNA sequence via hybridization (Fig. 1).