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Editorial

A Brief Summary about Analytical Laboratory Methods of Food Microbial Pathogens

R. García-Fernández

Centro de Estudio de Proteínas, Facultad de Biología, Universidad de la Habana, Calle 25 No. 455, CP 10 400 Ciudad de la Habana, Cuba

(E-mail: rossana@fbio.uh.cu)

Food-borne pathogens are the leading causes of illness and death especially in developing countries followed by the consumption of contaminated foods. Hence, to achieve food safety and quality, the ability of detecting pathogens in food is a necessity. This task faces many challenges, among them i) the wide variety of food products, ii) the native microflora, e.g. in raw foods, can interfere with detection and isolation of a pathogen, iii) pathogens in foods are generally present at lower levels and their infectious doses may be as low as a few cells, iv) sample preparation procedures usually requires dilution of solid samples and the detection limit is affected by sample size and assay volume. Moreover, many techniques traditionally used to extract and purify pathogens and toxins in foods suffer poor recovery rates, resulting in reduced assay sensitivity and efficiency.

Together with the traditionally used microbiological methods in food analysis, i.e., light microscopy, culture and colony counting, different methods have been conventionally employed. The polymerase chain reaction (PCR) and immunology-based methods have advantages of acceptable sensitivity, specificity and rapidity (Byrne et al., 2009; Lazcka et al., 2007). In the last years, several kinds of biosensors, using different biological recognition elements (bioreceptors) such as antibodies, enzymes, nucleic acids, cells, non-enzymatic proteins, biomimetics or bacteriophages have been described (Velusamy et al., 2010). Recent researches also revealed the significance of metabolomics, genomics, transcriptomics and proteomics about this issue (Bergholz et al., 2014). The former results in characterizing the diversity in food systems and analysis of new emerging pathogens and whole genomes sequencing may be effective in detection of food-borne outbreak. In the past decade, many investigations have analyzed transcriptomes and/or proteomes of bacteria under conditions simulating of a pathogen may experience on a food, thus providing information to develop new control strategies. Such "omics" technologies have resulted in the accessibility of various datasets that can let identifying molecular targets for achieving new antimicrobial agents. New insights into food-borne pathogens are gained with the discovery of novel toxin genes. The analysis of these increasing data sets through bioinformatics, providing a more detailed scenario that underlies the mechanisms of pathogenicity as well as diseases (Bierne and Cossart, 2007; Metris et al., 2011; Mondal et al., 2012).

Finally, X-ray crystallography and also electron microscopy have provided information about structure and molecular mechanisms of toxins from these organisms (Lee et al., 2013; Stiles et al., 2014). Such data have been increasing in the last years, and certainly will allow developing structure-based drug approaches for control of pathogenic microorganisms.

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