

# Proteomics in Food Safety

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#### Introduction

Each year thousands of foodborne illnesses are detected all over the world jeopardizing the public health and causing loss in the food industry. 48 million Americans suffer from a foodborne illness every year and diarrhea causes **2,2 million** deaths worldwide per year<sup>1</sup>. Therefore, it is mandatory to invest more funds in the discovery of new techniques that allow for a rapid, automatic and accurate processing and characterization of the food samples in a routinely way. Proteomics, appear like a promising alternative to traditional methods

The aim of this review is to analyze the advantages and limitations of proteomics in food safety and look over the last applications of these techniques in food safety and quality, both in industry and research.

14.2% Campylobacter Clostridium perfringens, 2.2% monocytogenes 18.8% (\$1.8 billion) (\$2.7 billion) 'ersinia enterocolitica, 1.8% 10.1% (\$1.5 billi Toxoplasma gondii STEC non-O157, 0.2% 21.1%

Fig 1.Estimated cost in 2011 in EEUU based on disease incidence<sup>2</sup>.

#### Methods

Data displayed in this poster has been obtained from original research papers and reviews using the software Pubmed and Google Scholar. Key words: Proteomics; food safety; foodborne; MS.

# What is « Proteomics»?

Proteomics is the large-scale study of proteins. Initially aimed at the identification of proteins expressed by a genome, proteomics now involves a study of their structure, localization, modification, interactions and functions. Proteomics is largely taking advantage by progress in mass spectrometry<sup>5</sup>.

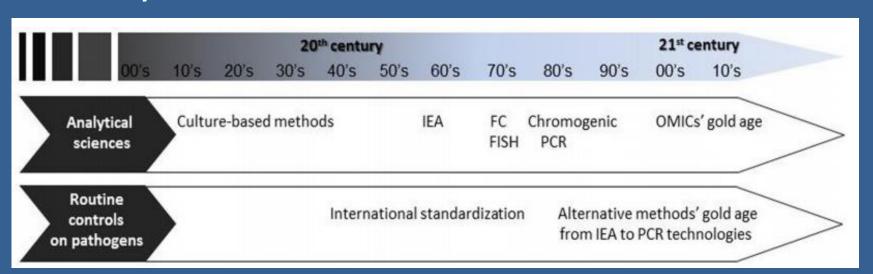


Fig 2.Evolution of analytical methods (modified from Sohier, D) 3

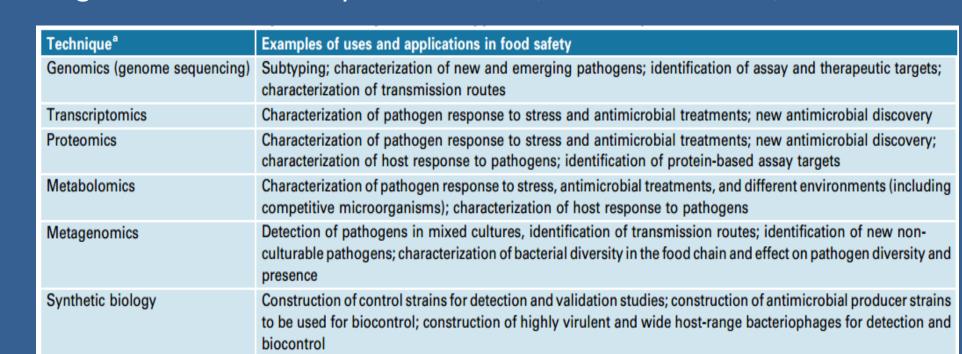


Fig 3.Selected omics techniques and examples of their application in food safety 4

## Mass Spectrometry as a Key Player in Food Safety

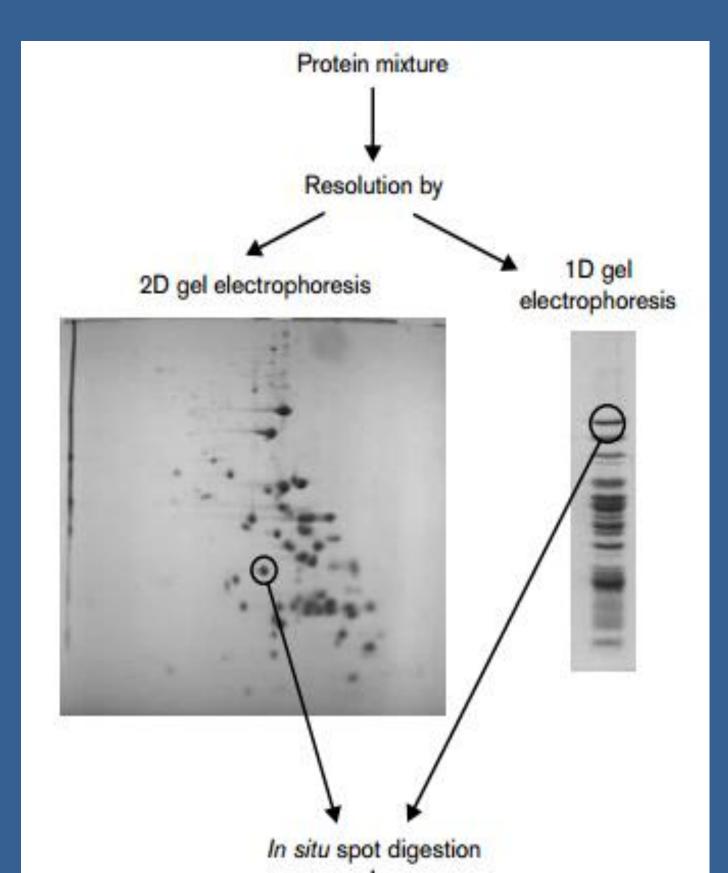


Fig 4. Main steps of proteomics strategy (modified from Washburm, M P) <sup>5</sup>

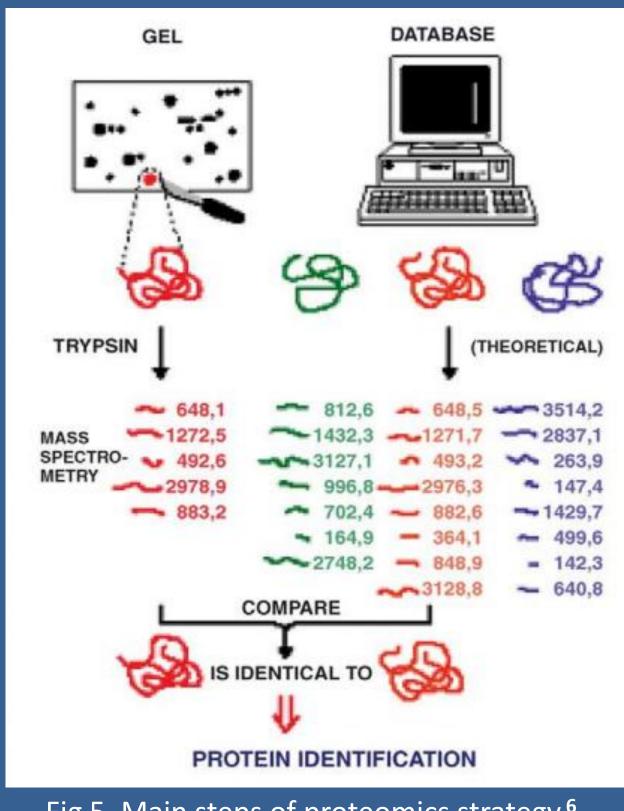


Fig 5. Main steps of proteomics strategy 6

#### The cucumber crisis

In 2011 central Europe experienced a large outbreak of Shiga-Toxigenic Escherichia Coli 0104:H4. Almost 4000 persons resulted infected in Germany. Even if the sequenciation of the genome and the identification of the pathogen were performed in a record time, the big amounts of samples highlighted the 🖁 0.15importance of fast and inexpensive typing procedures. Experimentally, MALDI-TOF MS strategy was applied for the identification of the causative pathogen. Specific peaks in the outbreak strain's spectrum were identified by comparative analysis of archived pre-outbreak spectra<sup>7</sup>.

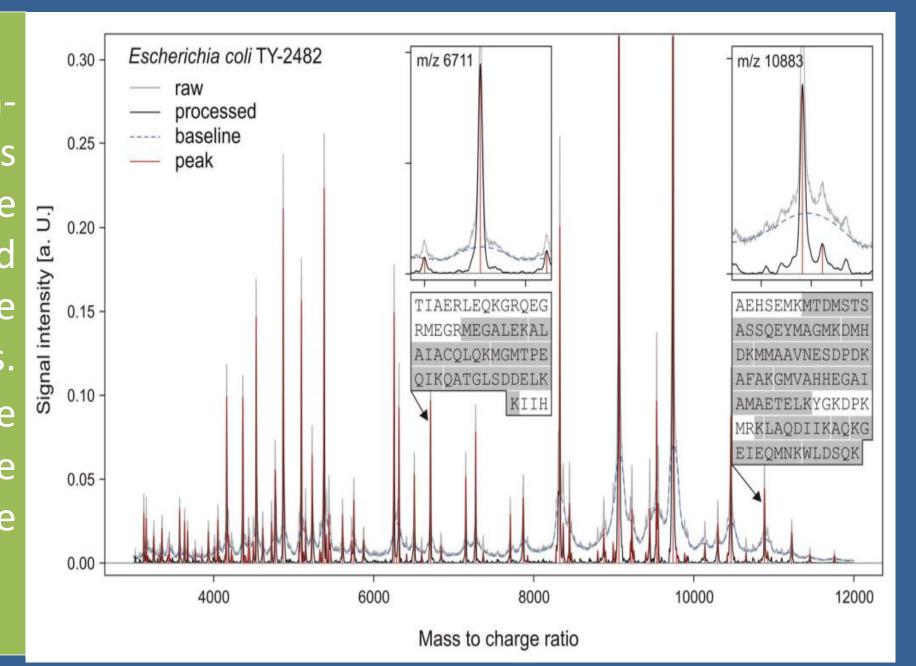


Fig 6. MALDI-TOF mass spectrum of *E.coli* outbreak isolate TY-2482 <sup>7</sup>

# The mad cow disease

In 1996 the first case of Sporadic Creutzfeldt-Jakob Disease (sCJD) was detected in humans and it wasrapidly associated with the Bovine Spongiform Encephalopathies (BSE). The disease was transmitted by the consumption of cattle meat containing PRP sc ,the pathologic isoform of PrP.. A diagnostic Kit was designed, but it was an inconvenience: It was only applicable in postmortem identification. Biomarkers in fluids were in very low concentration and therefore not detectable. **SELDI-TOF** could be a good tool in biomarker discovery<sup>8</sup>.

## Cholera

589854 cases of cholera were registered during 2011 in 58 countries and 7816 persons died. Cholera outbreaks are caused by 01/0139 strains, which are able to produce the cholera toxin. While colonizing humans, this strain expresses a membrane protein named Ompu that possesses good properties to work as a biomarker. MALDI-TOF MS enables the identification of a larger mass rank, whereby bigger proteins such as Ompu could be detected and used as biomarkers<sup>9</sup>.

# Milk Adulteration

Donkey and Goat's milk are commonly used in newborn feeding because they are less allergenic than other milk types. Consequently, it is mandatory to avoid adulteration and contamination by other milk allergens. At present, most milk quality controls use a chemical and immunological approach. Nevertheless, the fingerprints comparison of proteins such as α-lactalbumina and β-lactoglobulinasa in milk serum with MALDI-TOF MS would allow for the rapid detection of adulteration at levels of 0,5%<sup>10</sup>.

## Conclusions

The development of automated, accurate and little consuming time techniques, as proteomics, would improve the analysis in food safety. Moreover, for large amounts of samples, these methods result more economic than traditional ones. There is still a lot to do in this field, new approaches must be developed to increase the capacity of the procedures and they must be accompanied by the improvement of computers and data bases. Even so, we should not forget that the best results are obtained of the combination of traditional and new techniques.

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waves/2013-november/

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