Review Article

Application of Proteomic Tools in Food Quality and Safety

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Abstract | The development in food science research aimed to achieve high nutritious, superior quality and safe food. The foodomics based research includes genomics, transcriptomics, epigenetics, proteomics, peptidomics, and/or metabolomics. The proteomics is study of proteins, and its characterization. Proteomics based study in food science research been applied in various food products such as milk, meat, agro-food and marine products. Mainly involves topics such as food quality, bioactive compounds, functional foods and nutraceuticals, molecular marker, integrated foodomics, allergic proteins, diagnosis, targeted treatment and vaccine/ drug development. This paper is a comprehensive overview on application of proteomic tools in food quality and safety research module which help to find some of the latest development in proteomics in relation to food science and animal research aspects.

Keywords | Foodomics, Milk and milk products, Meat and meat products, Animal science research, Marine food

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INTRODUCTION

In a changing scenario, growing population has increased requirement of food, which emphases on the development of advanced food production and processing techniques. Augmenting to the need of food science research which is focusing on improving foods' nutritional quality and food safety. The new novel techniques have been introduced to identify the food quality and safety attributes. One such technique is '–omics' based research, which is gaining its own importance for understanding the basic phenomenon in food science, called Foodomics (Cifuentes, 2009; Herrero et al., 2012). Foodomics defined as studies on food through the application of advanced omics approaches. Foodomics includes genomics, transcriptomics, epigenetics, proteomics, peptidomics, and/or metabolomics to investigate food safety, food quality, food traceability and finding new bioactive components in food. The word "Proteomics" was coined by Marc Wilkins at Siena conference in 1994 and the term proteome was abbreviated from "PROTEin complement of the genOME" meaning the complete set of the proteins expressed by the cell (Wilkins et al., 1996). Proteomics, could be described as "the large-scale analysis of proteins" (Pandey and Mann, 2000). "Proteomics includes not only the identification and quantification of proteins, but also the determination of their localization, modifications, interactions, activities, and, ultimately, their function" (Fields, 2001).

The work flow of proteomics methodology (http: / /proteome.co.uk/proteomics)

1. Sample collection, handling and storage.
2. Protein separation (Ingel or OFFGEL).
3. Protein identification (peptide mass fingerprinting)
4. Protein characterisation (amino acid sequencing).
5. Bioinformatics (cross reference of protein)

Proteomic approaches are classified into six groups: expression proteomics, protein–protein interactions, functional proteomics, structural proteomics, proteome mining and post-translational modifications (Carbonaro, 2004). Proteomics is a new promising approach to identify protein in food matrix and to study protein–protein interactions in both raw and processed foods, as well as interactions between proteins and other food components (Kvasnicka, 2003). It provides a sensitive information on changes in protein structure occurring at specific amino acid residues during processing events and helps to predict the quality and stability of food product. In proteomics, analysis of proteins and peptides is major constituent and the most challenging aspects separation of them from the complexity and dynamic concentration range in food.

The main application of proteomic technique is useful in studies on changes in food quality (Werf et al., 2001), identifying bioactive compounds, identifying ingredients in functional foods and neutraceuticals (Galvani et al., 2001), characterization of rice proteins (Koller et al., 2002), molecular marker for physiology and pathobiology (Bouley et al., 2005), integrated foodomics (Ibá˜nez et al., 2013), in-vivo protein digestion trail (Carbonaro, 2003), identification of allergic proteins (Beyer et al., 2002), diagnosis, targeted treatment and vaccine/ drug development (Plowman et al., 2000). In this comprehensive overview, important aspects of animal and animal products, marine products and agro-animal food products are been reviewed.

Meat And Meat Products

Proteomic technologies for understanding muscle biology have been successfully used for mapping of muscle proteins (Bouley et al., 2004); muscle disorders (Ge et al., 2003); muscle physiology (Isfort et al., 2002); meat colour (Naveena et al., 2010) and meat texture research (Kiran et al., 2015). The research priorities mainly focused to characterize the quality (texture, flavour and odour) and processing conditions of meat, in-order to predict the quality of the end-product. Study on biology of muscle differentiation and growth, carcass composition, and fat deposition patterns have been characterized in detail at the proteome level (Liu et al., 2009) and factors involved in interaction of muscle proteins with lipids, carbohydrates, and other meat components. The changes in muscle growth in chicken (Doherty et al., 2004). The proteomic study links the expression of genotype by analysing the proteome and correlating it to the phenotypic expression which documented the bovine hypertrophy due to 11-basepair deletion in the myostatin gene (Bouley et al., 2005). This mutation results in expression of normal levels of inactive myostatin protein. The extensive review on understanding of regulation in skeletal muscle growth, and meat quality models by Bendixen, 2005.

The development of novel methods for identification for meat speciation gaining importance (Sentandreu et al., 2010). The proteomic based tools are efficient in identifying the species-specific peptide biomarkers even after subjecting to harsh meat processing condition (cooking). Which is due to stable primary structure of protein and not been degraded easily. The reports on meat substitution was up to 0.5% w/v of chicken in pork/beef meat mixes using OFFGEL electrophoresis and AQUA labelled tags (Sentandreu et al., 2010). Similarly, in India substitution level up to 0.5% was differentiated between sheep and buffalo meat mixes using OFFGEL electrophoresis and MALDI-TOF/TOF mass spectrometry analysis (Deepak, 2015). The recent trend in identification of meat species using high end mass spectrometry such as Rapid Evaporative Ionization Mass Spectrometry and rapid ambient mass spectrometry (LESA) on identifying the myofibrillar and sarcoplasmic meat proteins and peptidomics (Montowska et al., 2015). Recently, Prandi et al. (2017) differentiated and quantified bovine and pork using mass spectrometry in highly processed Bolognese sauce.

The conversion of "muscle to meat" is normal biochemical process occurring inside the muscle after slaughter/death which mainly depend on both intrinsic and extrinsic factors surrounding the carcass. The meat quality directly proportional to the effect observed in terms of taste, healthy and keeping quality. Proteomics helps to understand the various process occurring in meat. The Water holding capacity (WHC) is factor depends the efficiency of conversion of muscle and final meat pH attained. Any alteration in WHC leads to to development of PSE (Pale, Soft and Exudative) or DFD (Dark Firm and Dry) meat. The post mortem changes been extensively studied and reviewed by Paredi et al. (2012) with the use and application of various proteomic tools and studied different proteins (troponin T, myosin light chain and α-crystallin, and the total absence of heat shock protein) and their proteolysis rate. The water holding capacity (WHC) by identifying peptides and proteins markers (creatine phospho kinase M-type (CPK), desmin, and a transcription activator (SWI/SNF related matrix-associated actin dependent regulator of chromatin subfamily A member1, SNF2L1) for the assessment of meat quality of pork (Dick et al., 2007).

The acceptance of fresh meat for consumption mainly depend appearance parameters such as colour, odour and texture. The colour and odour mainly depend on myoglobin content which is affected by redox potential and microbial load. Based on this parameters Joseph et al. (2015) has reviewed on application of proteomics in characterization of muscle food on colour and oxidative stability of different species of meats on different conditions. Meat colour depends on rate of phosphorylation of muscle proteins, intramuscular fat content and meat tenderness. Protein

markers that can assess development of tenderness during post-mortem storage of the carcass (Jia et al., 2009). The tenderization of meat happens after rigor-mortis (conversion of muscle to meat) later due to dissolution of actin-myosin bonds makes meat better tastier and healthy. The various proteins are involved in this process are broken into smaller fragments (Lana and Zolla, 2016). The meat tenderness depends on post-mortem changes of myofibrillar proteins (Melody et al., 2004). Bendixen (2005) has reviewed the role of Calpains role in meat tenderness, post-mortem metabolism, Growth and development, water holding capacity, markers for technological processing and advanced proteomic tools for improvement of meat quality and safety. Hollung et al. (2007) explained the molecular relations and mechanism behind the meat quality parameters.

The whole muscle proteome mapped by Bouley et al. (2004) where he studied *semitendinosus* (ST) muscle from a bovine origin. His mapping was based on separation of proteins on 2-DE and characterization using mass spectrometry and efficient in reproducing 500 protein spots. Similarly, Hamelin et al. (2006) studied the proteome expression of sarcoplasmic proteins of ovine. In which he characterized proteins of 4 different such as *longissimus dorsi* (LD), *vastus medialis* (VM), *semi membranosus* (SM), and *tensor fasciae latae* (TL). The proteome analysis of SM muscle from normal hams and from PSE-zones of defective hams demonstrated a reduced proteolysis of troponin T, MLC 1, and -crystallin in the defect muscles (Laville et al., 2005).

The proteomic approaches on meat myoglobin characteristics and molecular mechanisms on redox chemistry, Lipid oxidation-induced oxidation, Fresh meat color and/or color stability specificity for individual muscle, Animal variation, of intramuscular variations, Oxidative stability were well discussed in his review. Naveena et al. (2009) reported that ESI–MS/MS fragmentation pattern of turkey and chicken Myoglobin is similar on their primary structure. The redox potential and characterization of myoglobin in turkey and chicken by induced unsaturated aldehydes, where determined that HNE adducts to amino acids residues (HIS 64 and HIS 93) that are critical in maintaining the redox stability in chicken myoglobin and myoglobin oxidation was correlated with number of histidine residues in myoglobin; greater oxidation rate was observed in Mbs containing greater number of histidine residues (Naveena et al., 2009; Naveena et al., 2010) and other various meat-producing livestock and poultry myoglobin oxidation are documented by Yin et al. (2011). Suman et al. (2013) investigated proteomes basis for intramuscular variations in beef muscles and colour stability using semimembranosus muscle. Canto et al. (2015) investigated the animal factor in beef color stability through proteome profiling and selected color-labile and color-stable muscle for retail display colour stability attributes. Sayd et al. (2012) investigated the sarcoplasmic proteome expression of porcine LL muscle in relation to lipid oxidation during storage and cooking. The authors utilized 2-DE and tandem MS (LC–MS/MS) for proteome characterization, while lipid oxidationwas determined by the thiobarbituric acid reactive substances method.

Meat quality Variations attributed to the meat quality characteristics, like tenderness, juiciness, flavour and odour, are closely related to the biological traits and genetic variations of the live animals (Boleman et al. 1997). The alterations in metabolic pathways, post-mortem proteolysis, and other environmental and processing conditions will directly alter the meat tenderness and quality. The effect of pre-slaughter transport stress on proteome changes of some proteins (troponin T, nebulin, cypher protein) in pigs was analysed by Morzel et al. (2004). The low molecular weight peptides or degreaded proteins of bovine on post-mortem storage and cooking were analysed directly by MS (Bauchart et al. 2006). The down and upregulations of proteins in muscle affecting meat tenderness during post-mortem storage (Lametsch and Bendixen, 2001). The enzymatic action of calpins of degradation of myofibrillar proteins for optimum tenderness was studied by Lametsch et al. (2004). The negative effects on meat tenderization by increase in stress proteins and decrease in glycolytic proteins were studied by Hwang et al. (2005), Lametsch et al. (2006). The post-mortem proteolysis in muscle has been closely described in beef (Laville et al. 2009) and in pork (Bjarnadottir et al., 2010).

The differential analysis of muscle between meishan and large weight Yorkshire (Xu et al., 2009) and correlation of between meat quality defect proteins and genotype in pork (Laville et al., 2009). The proteome changes in longissimus thoracis muscle during the early post-mortem storage period and Peroxiredoxin-6 as protein marker for meat tenderness (Jia et al., 2007; 2009). Postmortem proteome changes of porcine muscle related to tenderness (Lametsch et al., 2003), Proteome changes in bovine shifts on different energy status and myofibrillar stability (Bjarnadottir et al., 2010). The post-mortem proteolysis in muscle, muscle toughness, apoptosis in muscle, meat ageing and tenderization proteins of beef (Laville et al., 2009). Protein mapping of liver, kidney, muscle, plasma and red blood cells (Talamo et al., 2003). The prot eomic study of changes of muscle development and myogenesis (Chaze et al., 2008). The study of skeletal muscle and its importance in livestock production (Picard et al., 2010).

Milk And Milk Products

The milk is considered as complete diet, composed of proteins, sugars and fat which blended to form a perfect

emulsion. Hence the study of milk from proteomic aspect is tricky and yet the application in field of milk proteins characterization (D'Alessandro et al., 2011); sugars and their proteins interactions (Picariello et al., 2008); changes in milk proteins upon processing (Arena et al., 2010) detection of milk adulteration (El-Salam, 2014) and milk speciation (Mayer, 2005). The characterization of human milk protein along with composition and identification of bioactive compounds from fat globules using proteomics tools Quaranta et al. (2001). Similarly, characterization of dairy products and proteins involved in maillard reaction was studied by Arena et al. (2017). Manso et al. (2005) reviewed on application of proteomics on study of milk and dairy products. Galvani et al. (2000) described the proteins in commercial milk powders containing lactose-conjugates of beta-lactoglobulin, alpha-lactalbumin and caseins. The bovine milk proteome characterization with the molecular complexity was extensively reviewed by D'Alessandro et al. (2011). The composition of milk protein, coluistrum and phosphoproteins in milk affecting quality was extensively reviewed by Casado et al. (2009). The infant food of milk origin involved in lactosylation profile of milk proteins was studied by Marvin et al. (2002) and Renzone et al. (2015) on characterization of intermediate and glycated proteins from commercial milk samples.

The adulteration of milk was observed frequently across the globe, where milk is diluted with water, fat is removed centrifugation, synthetic milk is synthesised by various compounds. The preservatives and added adulterants pose serious health effects. El-Salam (2014) has extensively reviewed the use of various proteomics analytical techniques (HPLC-coupled MS and MALDI-TOF) for evaluation of various milk contamination, preservatives and adulterants. It was also helpful in identifying the changes in milk protein during different stages of lactation or from mastitis and identification of milk allergen. The detection of milk adulteration and monitoring milk powder derivatives in bovine milk in pasteurised and UHT processed milk was studied by Calvano et al. (2013). Sassi et al. (2015) has integrated proteomic and peptidomic profiling of milk samples for rapid detection of food adulterations.

The complexity in milk proteins arises from the extensive variation in post-translational modifications which includes glycosylation (Picariello et al., 2008; Wilson et al., 2008), phosphorylation (Holland et al., 2004; Kjeldsen et al., 2007) and proteolysis. In a review by Le et al. (2017) on bovine milk proteins which covers identification, characterisation and quantification of milk proteins. Application of proteomics from basic composition to post-translational modifications (PTMs) either in naturally stored and processed milk along with quantitative proteomics and bioinformatics are well discussed. Other review by Caroli et al. (2009) discussed complication of milk proteins due to variation in genetic composition in different breeds, post-translational modifications (PTMs), proteolysis and different processing and preferences. Various other review on milk proteomics discussed on milk protein changes during lactation and during milk processing and storage (Cunsolo et al., 2011; El-Salam 2014; O'Donnell et al., 2004). The whole milk or purified casein on in-vivo digestion trial for identification of bioactive peptides arising from casein digestion provided confirmation for their resistance to proteolytic degradation in the small intestine (Carbonaro et al., 2003).

The speciation of milk and milk products using proteomics and proteins IEF of γ2- and γ3-caseins of cattle and sheep/goat milk (European Commission, 2008; Mayer, 2005; Špoljarić et al., 2013). Boggs et al. (2016; 2015) explained the proteomics quantification of bovine milk proteins of skim milk, processed milk and liquid milk during mammary gland involution over period of storage time. D'Ambrosio et al. (2008) has characterized the various proteome fractions of water buffalo milk on Post translational modification and identified few components involved in nutrient delivery and defense against pathogens and detection of milk adulteration based on 1D SDS-PAGE and 2-DE. Baeker et al. (2002) studied the 2DE pattern of mastitic and healthy milk from bovines in way to find the biomarker for their identification at proteomics level and as a advanced molecular diagnosis. Roncada et al. (2012) has reviewed on various farm animal milk proteomics. Arena et al. (2010; 2011) on changes in milk proteins during various processing techniques. Pinto et al. (2012) described casein lactosylation as its function on heating and can be used as indicator for heated milk. Holland et al. (2011) demonstrated proteomic profile on temperature dependent changes in milk proteins (non-disulfide cross-linking, deamidation and lactosylation) during storage of UHT-treated milk using 2-DE coupled to MALDI-TOF MS.

The application proteomics on quality analysis of milk (Guy et al., 2006) in quantification of milk proteins in host response to mastitis (Danielsen et al., 2010) difference in glycoproteins between human and bovine milk (Wilson et al., 2008).

Animal Health Research

The study of proteomics is an essential component of systems biology, which integrates the growing data of various investigations in a single process by acting as bridge between genome and transcriptomic studies. Therefore proteomic study should be integral in analysis of biological processes, which helps in animal growth, development, production and in related infectious diseases (D'Alessandro and Zolla, 2013). Proteomics tools have been applied in bovine research both as areas of dairy cattle milk (Picariello et al., 2012; Lemay et al., 2009), metabolism (Timperio et al., 2009),

nutrition (Drackley et al., 2006), fertility (Gaviraghi et al., 2010), health (Tollboll et al., 2012) and beef cattle (Bjarnadóttir et al., 2011; Zapata et al., 2009; D'Alessandro et al., 2012). The use of proteomics in pig research is extensively reviewed on various factors such as growth performances, prolificacy, backfat thickness, meat leanness, feed conversion rate, muscle growth development and size, adaptation to harsh rearing environments and stress, flavor and taste-affecting traits, like boar taint and the suitability for biomedical research by de Almeida et al., (2012). A review of farm animal proteomics of various factor such as soil condition its body vital parameter constituents, embryo development, health indicators, production parameters indicators, meat authentication, meat quality, post-mortem changes such as proteolysis, by Bendixen et al. (2011). Bendixen et al. (2010) has reviewed on advancement in porcine genomics and proteomics for developing as a model for molecular biomedical research.

The use of farm animals as a new generation of model for understanding human diseases (Perez et al., 2004) and pigs are monogastric omnivores, with a gastrointestinal anatomy that is very like that of humans (Patterson et al., 2008).

The monitoring health and disease in farm animals based on proteomic studies on body fluids like serum, plasma and milk are important diagnostic samples, since their compositions reflect the overall health status of the individual animal (Eckersall et al., 1997; Eckersall, 2006). Bovine serum pattern changes in animals with acute udder inflammation (Wait et al., 2002) and during pregnancy with or without complications (Cairoli et al., 2006). Identification and verification of new diagnostic markers, therapeutic drugs and vaccine targets is taking more and more advantage of proteomics (Plowman et al., 2000). Proteomic approaches to microbial pathogens include characterization of sub microbial proteomes (example: secreted proteins, surface proteins and immunogenic proteins), comparative analysis of different strains, comparative analysis of different physiological states, identification of proteins related to pathogenicity, identification of proteins involved in host–pathogen interactions and evaluation of mechanisms of action of antimicrobials.

The Holstein Friesian known for its milk production and Chianina cattle breeds for meat traits were studied for changes in liver to know the metabolism, protein expression and identified thirty nine differentially expressed proteins were characterized between Chianina and Holstein Friesian, and allowed to pinpoint proteins whose expression might render the latter capable of greater milk production, anabolic pathways, altered thermoregulatory ability or hormone production which study provides molecular evidences to support the physiological differences between Holstein and Chianina cattle breeds (Timperioa et al., 2009).

Sea Food Research

The substitution of fishes is terms of intentional or unintentional mislabelling, new variety of unknown, inferior/ low values fishes is common in fish industry which jeopardises the safety and quality attributes. There are been many research in this aspect of detection of various tools and techniques using proteins and DNA. The proteins been used since late 1970's for fish speciation mainly, SDS-PAGE, iso-electric focussing, 2 DE and now latest development is by characterization of proteins using tandem mass spectrometry. Proteomics is high-throughput approaches for identification of novel peptide biomarkers of authenticity and large number of samples are screened with minimal time consumption and been discussed by Mazzeo and Siciliano (2016), Salla et al. (2013), Siciliano et al. (2016). Mazzeo has reviewed various techniques and methods used on fish speciation or authentication. López et al. (2002) distinguished the primary structure of paralbumins and other class of proteins for fish authentication. Carrera et al. (2009) discriminated Merluccius spp by de-novo sequencing of specific tryptic peptides of nucleoside-diphosphate kinase B and using these peptides to design ad hoc selective ion reaction monitoring (SIRM) experiments using aldolase A protein with LC/MS-MS analysis. Barik et al. (2013) discriminated the closely related sperata spp into respective species using analysis of MALDI-TOF fingerprints of triosephosphate isomerase isoforms. There are few review on sea and marine food authenticity using proteomics tools by Pineiro et al. (2003) and Martinez and Jakobsen (2004).

Rodrigues et al. (2012) has reviewed the application and novel trends on application of proteomics in aquaculture. Rasinger et al. (2016) has briefed on proteomic tools for species and tissues specific differentiation of processed animal proteins in aquafeeds. Carrera et al. (2013) has reviewed the application of proteomics for the assessment of quality and safety in fishery products. He discussed on fish authentication, allergen detection, detection and identification of spoilage and/or pathogenic microorganisms and quality changes during storage and processing of sea/ marine food products. The low molecular weight proteins of intact bacterial cells on MALDI-TOFMS analysis identified some of the seafood spoilage and pathogenic; Gram-negative bacteria, including Aeromones hydrophila, Acinetobacter baumanii, Pseudomonas spp., and Enterobacter spp. (Böhme et al., 2011; 2010) and Gram-positive bacteria, includes Bacillus spp., Listeria spp., Clostridium spp., and Staphylococcus spp. (Böhme et al., 2011). Biogenic amines such as histamine which is a potential food intoxicant from scombrid fishes (Fernández-No et al., 2011) and the isolation and identification by MALDI-TOF MS of S. parauberis in vacuum-packed seafood

products (Fernández-No et al., 2012). The meat quality of fish on post-mortem changes will affect the fish quality and freshness, tenderization on proteomics analysis was studied by Verrez-Bagnis et al. (2001) and on concentration and some of proteins such as myosin and α-actinin, as well as some glycolytic proteins are studied by Terova et al. (2011). The effects of stress such as overcrowding on muscle and blood proteomes of Atlantic salmon were studied by Veiseth-Kent et al. (2010). Desai et al. (2014) to investigate the quality attributes and muscle proteome (sarcoplasmic and myofibrillar) of normal and discolored (reddish) catfish fillets. Picard et al., 2012 reviewed proteomics on fish and sea food, focussing on nutrition/supplementation, species identification, muscle food safety and quality considerations, as well as toxicity and allergen characterization.

Novel Food Research

Application of proteomic techniques to the study of food quality in respect to nutrition is done by analysing the complete proteome or metabolome of foods or food ingredients is gaining the importance. The farm to fork concept led authentication of food products by identifying the specific markers from specific geographical area. Proteomics approach in the post-marketing surveillance of foods derived from genetically modified crops (Kuiper et al., 2001).

Quality of 'Functional food' depend on the presence of bioactive compounds, which comprise of many peptides that are produced during processing and exert beneficial effect on health. The proteomics based mapping of peptide-based food bioactive is a novel apparatus for peptide separation and identification (Righetti et al., 1997; Galvani et al., 2001). Bioactive proteins and peptides are a large and significant class of nutraceuticals that can be isolated, purified, and characterized by several proteomic tools. A nutraceutical is a bioactive food component that can add value to a food and cause the prevention or treatment of diseases (Lunney, 2007). The beneficial attributes of bioactive range from antioxidant, anti-microbial, and anti-hypertensive agents to modifiers and regulators, in intracellular and extracellular signalling pathways.

Food Borne Pathogen And Allergy

The allergy in general term referred to untoward body response to external or sometimes internal metabolites/compounds/factor. The allergen is the candidate which elucidates the body responses. The allergy in body is generally due to increased immunoglobulin- IgE, increased histamines, cytokines and other body responses particular to antigen or allergen. The food allergic diseases are mainly due to IgE-mediated related conditions. There been an increase in need of molecular techniques to diagnose, prognosis the allergen and body responses related to food based allergy. Sommergruber (2016) reviewed extensive in identification of food allergen from plant origin and animal origin. He has stated that various major food borne allergens such as parvalbumin in fishes, caseins in mammalian milk, Tropomyosins from crustaceae and molluscs and Bet v 1 related proteins in both monocot and dicot plants.

The translation of proteomic research in the field of food allergens is quite extensive (Panchaud et al., 2005) because development of sensitive detection/quantification methods is crucial for allergen diagnosis, therapy, and risk assessment and for reinforcing current legislation on the subject. Identification of either genes for allergic diseases or allergenic proteins (Beyer et al., 2002; Toda and Ono, 2002; Yu et al., 2003). Food quality and safety, and their influence on the health of end consumers have increasingly become a founding principle in the international agenda of health organizations (Thomsen et al., 2006). The food is often prone to spoilage either due to microbial or enzymatic spoilage. spoilage of food not only affects health of individual but also interfere with the social, economic and public health importance. Use of proteomics for analysing nutritional quality of food depends on the identification of molecular markers for specific food spoilage or pathogenic micro-organisms. The fermented food containing different microorganisms and complex substrates, the quality of the proteome or metabolome of the starter culture can be used to predict the final quality of the fermented end-product (Champomier et al., 2002).

The microbes (mostly, bacteria or fungi, sometimes viruses, prions, parasites and protozoa) affect the human by altering the normal homeostasis and can lead to disease, abnormal conditions or even death. These microbes enter the food either preharvest, processing or post harvesting periods. They even enter by contamination by faulty storage or infected food handlers before consumption. The food borne infections are of 3 types namely, food intoxication, food infection and toxico-infection. The toxins from bacterial or fungal origin are liberated preformed or inside the body and are resistant to various processing techniques followed in food preparation (Akhtar et al., 2012). In order to encounter such determinants in food the application of proteomics is reviewed by Martinović et al. (2016). He focussed on variables in food pathogen and toxin detection using different proteomic tools. The shiga toxin producing *E. coli* O104:H4 causing major food borne poisoning was encountered in Germany and France was identified using proteomics and other techniques King et al. (2012). Aberg et al. (2013) discussed mass spectrometric based methods for detection of toxins in different sources including food borne protein-based toxins. Piras et al. (2015) identified the immunoreactive proteins of Mycobacterium avium subsp. Paratuberculosis using proteomic based study. Böhme et al. (2012) established the spectrabank consisting of peptide mass fingerprinting of various bacterial species

which may help in future research pertaining proteomics for pathogen detection.

The microbes interact with host cell and cell organelles and produce the alternations in them which is known as pathogenesis. In this process the proteins are secreted, which are peculiar or up/down regulated which is identified on proteomic analysis and is gaining importance in early diagnosis of diseases in food animals and adds up as interesting application in field of food technology and biotechnology. Some of the important protein secretomes of mycotosin and marine toxins are reviewed by Giacometti et al. (2013). In his review explained the different metabolic pathways of microbial pathogenesis and strategy for identification of biomarker and resistances developed to biotoxin are been explained.

The application of proteomics in understanding of interactions between the host and pathogen will be helpful in development of new targets to ensure food safety. By development of newer methods for identification, monitoring and assessing of foodborne hazards during production, processing and storage and thus important for upliftment of human health and development in fields of animal production, agriculture, food processing and storage.

Miscellaneous

The use of proteomics in drug development, by identifying new targets and facilitating assessment of drug action, cellular targets and toxicity both in the preclinical and clinical phases. The development of protein microarray strategies to address different features of proteins in therapeutic and neutraceuticals is still in infancy. The need for compelling protein chips has led to devise new strategies for producing chips that have utility for biomedical investigations.

Bassols et al. (2014) has reviewed the proteomics Perspective for animal welfare to food safety thru the discovery of biomarkers to identify adaptation to a syndromes and oxidative stress. The in-vivo short protein digestion experimentation in rats and conformation using proteomic based analysis using 2DE followed by MALDI-TOF MS, where whey proteins and caseins are completely observed in gut and detected in analysis (Carbonaro, 2003).

The addition or subtraction of valuable component in food with low value/alternative/alien products in known as adultration (Example: adultration of milk with water and starch/ preparation of synthetic milk). The substitution is known as selling of low value product in place of high value products (Example: Selling of beef/carabeef as mutton). The increased incidence of food adulteration or substitution are frequently reported in various food grains, Pulses, milk, meat and various other food commodities. Hence to tackle them we need improvised tools in applied aspects. The molecular technique are commonly used methods in detection of adulteration but latest developments in proteomics as alternative tool can do so.

The adulteration of whey protein with plant based protein sources such as soybean, wheat and rice, where been reported and identified using shotgun proteomics analyses by MSE multiplexed, low and high-collision energy, data-independent acquisition) by Garrido et al. (2016). A proteomics characterization of rice (Oryza sativa) leaf, root, and seed tissue identified over 2500 proteins, which is most comprehensive proteome exploration (Koller et al., 2002). This type of adulteration is mainly due to decrease in cost of production. The bovine origin whey protein has high bioavailability and high cost, whereas the plant origin products are usual by-products after harvest of crop. Which affects the health of human and as well cheated for hard earned money from his pockets.

Pineiro et al. (2010) has extensively reviewed and discussed on influence of climate change on seafood products and its identification by proteomics. The climate change alters the physico-chemical parameters of water which intern affects fish physiology and is well studied on proteome expression. The stress leads to altered cell expression and some molecular changes in expression of proteins and their modifications. This can help in finding new novel biomarkers for fish on stress due to environmental changes. Ortea et al. (2016) has discussed on proteins role as marker in discussing properties of food, assessing technique used for processing, support food labelling and authentication issues of food. There are some of the extensive review on application of proteomics in food science and technology namely Han and Wang (2008) in milk and milk products Le et al. (2017), D'Alessandro et al. (2012) on Proteomics in food safety and quality; Tedesco et al. (2014) on quality and safety in fishery products; Piras et al. (2016) on quality, safety, microbes, and allergens in food.

CONCLUSION

To unveil the mystery of composition and quality of animal based food products, there been a changeover or upgradation of older technologies to novel, robust and faster techniques. In this aspect, the foodomics plays an important role to match the pace of ongoing biotechnological improvements. Proteomics is study of proteins but proteins are integral part in system biology. In the present review, there been an overview of various proteomics techniques and its application on various fields of animal based food products. The future research aspects need in simplification of sample preparation, improve the reproducibility and authentication.

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CONFLICT OF INTEREST

The authors declare no conflict of interest.

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