Possibilities of Liquid Chromatography Mass Spectrometry (LC-MS)-Based Metabolomics and Lipidomics in the Authentication of Meat Products: A Mini Review

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Abstract The liquid chromatography mass spectrometry (LC-MS)-based metabolic and lipidomic methodology has great sensitivity and can describe the fingerprint of metabolites and lipids in pork and beef. This approach is commonly used to identify and characterize small molecules such as metabolites and lipids, in meat products with high accuracy. Since the metabolites and lipids can be used as markers for many properties of a food, they can provide further evidence of the foods authenticity claim. Chromatography coupled to mass spectrometry is used to separate lipids and metabolites from meat samples. The research data usually is compared to lipid and metabolite databases and evaluated using multivariate statistics. LC-MS instruments directly connected to the metabolite and lipid databases software can be used to assess the authenticity of meat products. LC-MS has good selectivity and sensitivity for metabolomic and lipidomic analysis. This review highlighted the combination of metabolomics and lipidomics can be used as a reference for analyzing authentication meat products.

Keywords meat products, metabolomics, lipidomics, authentication, liquid chromatography mass spectrometry (LC-MS)

Introduction

Meat and meat products are significant sources of nutrition for humans, including proteins, lipids, minerals, and vitamins. Every year, beef consumption rises, and one consequence of this rise is the mixing of beef with other meats, such as pork, during processing. Furthermore, meat adulteration may violate religious beliefs; for example, Kosher and Halal food laws prohibit the consumption of pig or pork-related items (Alzeer et al., 2018; Lim and Ahmed, 2016). Many strategies have been implemented
to ensure the authenticity of meat and meat products (Abbas et al., 2018; Mahbubi et al., 2019) but still the coverage is insufficient, and certification of all meat products for protection against adulteration is unfeasible. As a result, effective methods are necessary for assuring the meat industry’s proper development, and rapid, comprehensive, accurate, and reliable detection technologies are crucial to achieving this goal. One approach for guaranteeing food authenticity could be metabolomic and lipidomic technology (Ali et al., 2020b; El Sheikh et al., 2017; Islam et al., 2021; Vanany et al., 2020) compared to existing methods such as polymerase chain reaction (PCR), which has the limitation of being easily degraded in processed foods so that it has the potential to cause false negatives (Jannat et al., 2018; Jannat et al., 2020; Lubis et al., 2016). Metabolomic as method with high accuracy, comprehensive analysis of the whole metabolome which refer to the full complement of small molecule, while lipidomic explored area within lipid analytics and more specifically meat adulteration, so this method can used authentication of meat product (Emwas et al., 2019; Trivedi et al., 2016).

Metabolomics is a method of qualitative and quantitative analysis of metabolites in cells, tissues and biological fluids with small molecular weights of 100 to 1,000. Metabolites are the result of gene expression derives from the interaction between the genomic system and the environment (Crestani et al., 2020; Erban et al., 2019). Metabolites consist of an intermediate compound and metabolism product. The fingerprint characteristics of metabolites found in meat, such as amino acids, sugars, organic acids, nucleic acids, and their derivatives, could be provided through metabolomics. With minimal sample preparation, this approach can examine the components globally (De Paepe et al., 2018). The metabolomics approach to pork and beef study could provide a picture of the metabolites present in both foods. The metabolite profile of pork differs greatly from that of beef, hence the latter's metabolite profile could be used as a baseline for determining the meat's authenticity. Metabolomic and lipidomic can also distinguish pork mixture in mutton and chicken by looking at the different metabolites and lipid profiles (Wang et al., 2020). Lipidomics could be another way to look into the existence of pork mixture in meat products (Castro-Puyana et al., 2017; Yang et al., 2019).

Lipidomics is a comparatively new field of study, and it is developing quickly because to recent advancements in data analysis, bioinformatics data processing, and system biology techniques that are connected to other omics systems (Kliman et al., 2011). Various types of lipids, such as fatty acids and triglycerides, are found in the metabolome and the most distinctive biomarkers in which each type of tissue in meat has a different lipid profile, making it possible to identify unwanted species in a food product. For each animal species, there are a number of fatty acids located in specific tissue that can be used to differentiate between the various other animal species found in meat products. However, another significant benefit of lipidomic research is that it enables for the identification of animal species based on their lipid profiles (Ballin, 2010; Dettmer et al., 2007; Domínguez et al., 2019). Pork has a completely different lipid profile compare than beef. To evaluate whether a product contains pork or beef, the lipid profile of pork and beef can be utilized as a guideline. Liquid chromatography mass spectrometry (LC-MS) could be used in metabolomic and lipidomic techniques to investigate the authentication of meat.

The LC-MS method that integrates metabolomic and lipidomic analysis in pork and beef is a new technology with excellent sensitivity and provides the fingerprint of metabolites and lipids in biological samples. Organic chemicals and some inorganic substances can be analyzed using LC-MS (Gorrochategui et al., 2016). Sample preparation, data acquisition, and subsequent processing could be made easier using a mix of chromatographic and mass spectrometry techniques (Moosmang et al., 2019). This approach is frequently used to determine and characterize tiny molecules in meat products with high separation, such as metabolites and lipids. One of the advantages of LC-MS is the simplicity with which samples can be prepared. Mass spectrometry could verify that the types of metabolites and lipids present in the sample. Another benefit of LC-MS in metabolomic and lipidomic research is that it can identify all types of metabolites and lipids in a single sample run.
Based on the preceding description, more investigation is necessary to answer the question of whether metabolite and lipid profiles can be utilized to determine the authentication validity of meat. To answer this question, a systematic review involving a comprehensive metabolomic and lipidomic approach is required, and it may be able to provide a comprehensive reference in the assessment of meat products (Demirhan et al., 2012; Mostafa, 2020; Pranata et al., 2021; Rohman and Che Man, 2011).

**Analytical Methods for Authentication of Meat Products**

Authenticity detection technologies for meat and meat products, such as PCR based on deoxyribonucleic acids (DNAs), protein technologies, and spectroscopic technologies based on specific metabolites, have all been developed in the previous two decades (Li et al., 2020). Presently, PCR (Amaral et al., 2017) and proteomics methods are routinely used for the species authentication (von Bargen et al., 2014). PCR is the most extensively used method for determining of meat products based on the presence of DNA, whereas proteomic is a method for determining of meat products based on their protein profile (Nakyinsige et al., 2012). Furthermore, PCR may detect pork DNA in a product (Izadpanah et al., 2017; Nakyinsige et al., 2012; Yuswan et al., 2018) and can detect a very small number of DNA copies. The hybridization of particular oligonucleotides to the target DNA and the synthesis of millions of copies flanked by these primers are the foundations of PCR amplification. Amplification of DNA fragments followed by agarose gel electrophoresis for fragment size verification is the most basic PCR approach for determining the presence of any species in meat products. Appropriate genetic markers are chosen to create the examination in order to properly detect species by PCR (Izadpanah et al., 2017). Porcine gelatin of pork can also be employed as an indicator of meat products in PCR analysis. The presence of DNA porcine gelatin of pork in the sample can be determined using the PCR technique (Rohman et al., 2020). The proteomic technique is another method for determining the validity of meat products. The goal is to determine the validity of meat products by examining for proteins, biological activity, post-translational modifications, and interactions in cells, as well as identifying the proteome in response to changes in porcine biological circumstances in the samples (Zamaratskaia and Li, 2017). Liquid chromatography quadrupole time of flight mass spectrometry (LC-QTOF-MS) is a method for determining the type of meat using a powerful tool for identifying protein peptides (Sarah et al., 2016; Zamaratskaia and Li, 2017). Protein extraction precedes mass spectrometry (MS) or LC-QTOF-MS analysis in the proteomic analysis method. In proteomics, mass spectrometry is the most typical approach for detecting proteins or peptides. This method has a wide range of applications, including meat science research, but it is hampered by the large biochemical heterogeneity of proteins and the inability to detect low protein levels. The detection of meat products using a proteomic technique has a high selectivity because only certain types of pork peptides can be found (Stachniuk et al., 2019). The PCR and proteomics methods both have their own set of difference when it comes to detecting adulteration in meat and meat products. Therefore, recent advances of the omics technologies (particularly metabolomics and lipidomics) are comprehensively discussed in this review.

**Beef Meat and Its Products**

Meat and its products are consumed widely throughout the world as a source of high-quality protein, essential amino acids, vitamins, and necessary minerals (Demirhan et al., 2012). A suitable analytical technique, such as headspace solid-phase micro extraction/gas chromatography-mass spectrometry, which employs volatile compounds to identify the meat authenticity, is used
to ensure the authentication of beef and its products. The presence of alcohol compounds, 2-butanol and 1-octen-3-ol in a mixture of beef and pork can be used as a reference. These chemicals indicate presence of a pork mixture in meat products (Hossain et al., 2020; Pavlidis et al., 2019). Another method to ensure the meat authenticity is by EvaGreen real-time PCR. This validated method is able to detect pork DNA specifically in meat product samples. This method can detect 0.01%–100% pork contamination in beef meatballs with high accuracy and precision. In addition to the two procedures mentioned above, other methods such as Fourier-transform infrared spectroscopy (FTIR) and LC-MS can be used to determine the authenticity of beef and its products (Lubis et al., 2016; Yuswan et al., 2018). FTIR also can be used to assess the meat authenticity. This approach can identify functional groups in proteins as pig identifiers, allowing pork-containing products to be recognized (Lubis et al., 2016). By looking at the peptide fingerprints found in pork, LC-MS can be utilized to detect the meat authenticity. Moreover, chemometric technique also used to assess the type of peptide present in pork using this peptide fingerprint. Pork marker peptide is the result of this chemometric analysis, and it is utilized to determine the meat authenticity (Yuswan et al., 2018).

**Chicken Meat and Its Products**

Chicken meat is one of the meat products that provide the body with essential amino acids, fatty acids, and vitamins that the body need (Ali et al., 2019). The analytical methods are needed to verify that chicken meat authenticity. The high-sensitivity technology for detecting the presence of a pork mixture in the product is necessary in this case. LC-QTOF-MS/MS is the analytical method for analyzing chicken meat and its products. The protein acquired from the MS spectra is matched to the absolute protein expression database using the proteomic principle. The authenticity of chicken meat products can be determined using a peptide derived from other meat such as pork (Montowska and Fornal, 2017). Another method to examine the authenticity of chicken meat and its products is proteomic analysis using matrix-assisted laser desorption/ionization-time of flight. Determination of halal chicken meat is not only based on the presence of a mixture of pork but also the method of slaughter. In this method, it is possible to detect the proteome of chicken meat slaughtered in a halal and non-halal way. Beta-enolase, pyruvate kinase, and creatine kinase compounds are the ones that could have higher levels when slaughtered in an illegal manner (Salwani et al., 2015).

**Animal Fat Products**

There is a growing need for animal fat nowadays, based on the Statistic Government Bureau in Indonesia, export value of animal and vegetable oil fats has increased from 19,329 million USD in 2018 to 197,095 million USD in 2020 (Qodri, 2018). Animal fat is essential product that has various purposes in the body, including providing energy and forming adipose tissue. Fat is the most energy-dense food, producing 9 kcal per gram, 2.5 times the energy provided by carbohydrates and protein in the same quantity. Fat can produce fatty acids and cholesterol needed to form cell membranes in all organs.

Halal meat products are important since consumption of halal meat might influence one's attitude towards halal slaughter (Jalil et al., 2018). To be declared halal, meat products must meet a number of conditions relating to their preparation, condition for analysis such as towing before analysis, and composition. Consumers may trust halal meat labeling to ensure that the meat is of good quality, high value, safe, animal-friendly, and environmentally friendly (Haleem et al., 2021; Lim et al., 2022). Animal fats such as chicken and beef fat are permissible (Sin and Sin, 2019), however pork fat is prohibited for Moslem according to Shariah (Islamic law; Ahmad et al., 2018).
Beef fat is one type of meat products that is usually consumed nowadays. Beef is abundant in fat and contains important nutrients such as essential fatty acids, in addition to protein. Consumers’ concerns and awareness about the eating of high-fat meat items have an impact on meat consumption patterns (Mahbubi et al., 2019). The following is a representation of beef fat content: Saturated fatty acids, n-6 polyunsaturated fatty acids, n-3 polyunsaturated fatty acids, and trans fatty acids are the different types of fatty acids. Fatty acids in beef vary based on genotype, muscle type, and feeding methods in general. Long-chain n-3 and n-6 polyunsaturated fatty acids found in beef provide extra health benefits, including improved maternal and child health, growth and development, and cognitive function and psychological state in humans (Troy et al., 2016). Animal fat can be investigated from the use of technology including spectroscopy and chromatography (Rohman and Fadzillah, 2021). Raman spectroscopy is one of the spectrophotometric methods that can be used to identify the authenticity of animal fats (Lee et al., 2018). The resulting spectra could be forwarded using various types of databases in this manner, allowing them to determine the types of unsaturated and saturated fatty acids. The types of fat are not only qualitatively but also quantitatively examined in this method. It could be possible to accurately detect the type and amount of pork animal fat.

Another method of authenticity analysis of animal fat by chromatographic method is using high-performance liquid chromatography nuclear magnetic resonance (HPLC-NMR) and gas chromatography–mass spectrometry (GC-MS). HPLC-NMR is able to separate well the lard compounds in the sample which is then followed by reading the structure of the compound. Pork fat has the unique characteristic of containing polyunsaturated fatty acids. This fat could be used as a target to determine the authenticity of animal fat. Determination of the authenticity of animal fats can also be conducted with a targeted metabolomic approach using GC-MS, a simple method with good separation technique (Fadzillah et al., 2017; Heidari et al., 2020). Methyl myristate, methyl palmitate, methyl oleate, and methyl stearate are examples of targeted metabolites of lard that can be analyzed in the samples.

**Authentication of Meat Product Using Metabolomics and Lipidomics Approaches**

It is critical to determine authentication of meat. In order to acquire valid results that may be used to declare authenticity, new methods are still being developed. By examining the metabolite profile, one way for determining the authenticity of meat and its products is metabolomics. Metabolomic studies can use either spectrophotometry or chromatography (Muroya et al., 2020). The spectrophotometry used in metabolomic analysis is Ultraviolet-Visible, Infrared, Raman, and nuclear magnetic resonance (NMR) combined with chemometrics for spectral data. MS (Junot et al., 2014) and non-MS such as NMR are the most widely used methods (Consonni and Cagliani, 2019). In addition, different types of separation techniques are incorporated in most MS-based, depending on the lipophilicity and polarity of the desired metabolite. Combined with statistical analysis, multivariate analysis, and bioinformatics databases, metabolomics provides for finding biomarkers (Sugimoto et al., 2012).

The most widely utilized multivariate analyses in certified meat products are principal component analysis (PCA), partial least squares-discriminant analysis (PLS-DA), and orthogonal projections to latent structures discriminant analysis (OPLS-DA; Dailey, 2017). PCA is used to narrow down the list of metabolites and lipids to only the most important ones (Zhang et al., 2022). Other animal species that are present in meat can be identified by PCA when validating LC-MS data (Kang et al., 2022). Typically, Minitab, Orange, R Studio, and Unscamble are used for PCA analysis. The PLS-DA classification is a good choice for recognizing meat products. This is because the PLS-DA approach, whose implementation is exceedingly user-friendly and is extensively utilized in the most well-known statistical software packages like R Studio, is also quite popular.
Additionally, PLS-capacity DA’s to analyze highly linear and noisy data is one of its advantages (Utpott et al., 2022).

Using R Studio software, OPLS-DA provides a quick, easy, and effective multivariate analysis. In order to find meat-specific quantitative peptides created using liquid chromatography-tandem mass spectrometry (LC-MS/MS), OPLS-DA was applied to halal analysis. To choose species-specific peptides that significantly assist in classification, the OPLS-DA model was developed. Three distinct quantitative peptides were found in products with various beef proportions after the statistical process flow. LC-MS/MS was used to build quantitative methodologies for the specific quantitative peptides selected. Commercial beef products were subjected to quantitative results. The devised method is extremely precise, repeatable, and sensitive. According to Kang et al. (2022), LC-MS/MS integration with OPLS-DA is an efficient method to screen for particular quantitative peptides and certify beef product.

Apart from spectrophotometry, chromatography is also used in metabolic analysis. In metabolomic analysis, the use of LC-MS is critical, and one example is the use of ultra-high performance liquid chromatography quadrupole time-of-flight with rapid evaporative ionization mass spectrometry, which can provide metabolites in meat (Wang et al., 2020). The workflow of metabolomics analysis in meat samples can be seen in Fig. 1. Besides metabolomics, lipidomics is another way for determining the validity of meat products. The result of metabolite analysis can be used for authentication meat products such as myosin-2 (Yuswan et al., 2018), 3-Oxohexane acid glycerides, arabbitol, creatinine, glycine and phosphate (Trivedi et al., 2016). Also the lipid component that can be used for authentication such as sphingomyelins, cerebrosides, globo-sides, gangliosides or sulfatides (Trivedi et al., 2016).

The workflow summarizing the different steps in lipidomics analysis can be seen in Fig. 2. The study of lipid profiles that can be applied to meat products in order to assess authenticity is known as lipidomics. Pork’s lipid profile is undoubtedly different from that of other meats, and this unique lipid profile can be used to confirm the meat authenticity. Lipidomic analysis to determine meat authenticity can use LC-MS, one of which uses liquid chromatography electrospray ionization tandem mass spectrometric. This method is able to interpret the lipid profile combined with MS data. The lipid profile of

![Fig. 1. Workflow for metabolomics analysis in meat samples. LC-MS/MS, liquid chromatography-tandem mass spectrometry.](image-url)
pork-containing meat products can be identified well (Dirong et al., 2021).

The information on the compounds resulting from LC-MS in lipidomic and metabolomic study is enormous, reaching in the thousands. The metabolites that have been detected are then determined for the identified compounds using the databased compound discover, and the profile of lipids and sub-lipids is determined using the databased LipidSearch (Korf et al., 2019; Medema and Fischbach, 2015). Due to the size of the database's results for metabolites and lipids, multivariate analysis is necessary to identify the metabolites and lipids that will serve as meat products' authenticity indicators (Trivedi et al., 2016).

**Metabolomic Studies**

Metabolomics is the study of the profile of low molecular weight metabolites. The metabolomics approach can be applied to determine the authenticity of meat. The metabolite profile in pork could certainly be different from that of beef or other meats. For example, research by Rocchetti et al. (2020) was able to identify metabolites in pigs with ultra-high performance liquid chromatography-quadrupole time-of-flight mass spectrometry (UHPLC-QTOF-MS) which obtained hexanoylcarnitine, 4-hydroxy-2-nonenal, 6-hydroxypentadecanedioic acid, 9S, 11S, 15S, 20-tetrahydroxy-5Z, 13E-prostadienoic acid (20-hydroxy-PGF2a), sativa acid, and glycerophospholipid. Moreover, Ali et al. (2020a) was able to identify glucose, amino acid, inosine, hypoxanthine, and arginine in broiler chickens slaughtered in an illegal manner using UHPLC-QTOF-MS. Furthermore, Jia et al. (2021) mentioned that 103 metabolites could be identified such as L-phenylalanine, L-isoleucine, L-histidine, guanosine, guanine, creatinine, glutathione, and nicotinic acid in goat meat using UHPLC-QTOF-MS. Several studies have reported the use of highly accurate metabolomic technologies to evaluate metabolite profiles, indicating that an approach based on this method could be used to determine qualities in the meat.
Metabolomics is a method for determining the numerous metabolite profile found in pork and beef. The qualities of the metabolite profiles in pork and beef could be distinguished by using these metabolites. Chromatography in mass spectrometry is used to separate metabolites from samples. Ultra performance liquid chromatography (UPLC) is usually being used to separate metabolites because of its ability to separate well. The time of flight-mass spectrometry apparatus could be coupled to the UPLC device, making it easier to get the research data. The ultra performance liquid chromatography-quadrupole time-of-flight mass spectrometry (UPLC-TOF-MS) for metabolomic analysis was also described by Jia et al. (2021) and identified 103 metabolite profiles in goat meat. The UPLC-TOF-MS method is an effective way to figure out the metabolite profiles of meat samples. The data could be compared to the Compound Discovered database, and multivariate statistics could be used to interpret the results. Pork's metabolite profile, which distinguishes it from beef, could be utilized as a standard for determining authenticity in food samples. Metabolites such as decanoylcholine, glycyl-lysine, and oleic acid can be used to authenticate meat products. The resume authentication of meat product using metabolomics can be shown in Table 1. Moreover, the metabolite extraction method was according to Jang et al. (2019), sample was mixed with 150 µL methanol: acetonitrile: water (40: 40: 20, extraction solvent), vortexed, and immediately centrifuged at 16,000×g for 10 min at 4°C. The supernatant was collected for analysis.

Lipidomic Studies

Lipidomics is a novel branch of research that examines the structure and function of lipids produced in plant and animal cells, as well as their interactions with other lipids, metabolites, and proteins (Li et al., 2017) can be regarded as a relatively unexplored area in food analysis (Aiello et al., 2011) and more specifically on adulteration of meat. Using the LC-MS approach, Mi et al. (2019) were able to successfully detect the component of lipids in several species of pork in China. They results showed that 61 types of glycerolipids, 17 glycerol phospholipids, 4 sterol lipids, 2 sphingolipids, 3 polyketides, 7 fatty acids, and 6 phenol lipids. Trivedi et al. (2016) used GC-MS and UHPLC-MS to evaluate lipidomic profiles of beef contaminated with pork. They found lipid components in beef, such as sphingomyelins, cerebrosides, globosides, gangliosides or sulfatides. Furthermore, Artegoitia et al. (2019) investigated the metabolomic and lipidomic profiles of beef fed efficiency feed using the UPLC-QTOF-MS technique, the results showed there were 20 types of phospholipids and cholesterol, such as phosphatidylcholine (PC), phosphatidylethanolamine, lysophosphatidic acid, and lysophosphatidylethanolamine. These studies have proven that the lipidomic method may be used to examine lipids in pork and beef utilizing chromatographic techniques to separate lipids for further examination. The type of chromatography used in previous study was column chromatography. With a single run, column chromatography may separate a large number of organic molecules in a short amount of time. Several scientific publications have reported the use of very accurate lipidomic technologies to examine lipid profiles, indicating that this technology could be used to determine meat authenticity, does not containing other meat such as pork. Glycerolipid and spingolipid are examples of lipids that can be used to authenticate meat.

In addition, the sample pretreatment for lipid and metabolite extractions are using similar methods in a different mixture. The lipid from meat were extracted according to the method of Harlina et al. (2021), whereas, meat sample were homogenizer in a mixture of chloroform: methanol: distilled water (120:120:60, v/v/v) at 11,000 g using a homogenizer for 2 min. Then, the homogenized mixture was treated with ultrasound (20°C, 80% power, 30 min). The mixture was filtered through a Buncher filter funnel. The chloroform phase (bottom phase) was drained off into an Erlenmeyer flask. The lipid in chloroform was decanted into a round-bottom flask through a filter paper. Before it was evaporated at 55°C using rotary
evaporator and the residual solvent were removed by flushing with nitrogen. The lipid was stored at –20°C until was analyzed.

Primary lipids such as cholesterol and its esters, as well as triglycerides, are found in nonpolar lipids, lipids are compounds

Table 1. Metabolomics approaches for authentication of meat products

| No | Title                                                                 | Refs                           | yr | Objectives                          | Equipment                      | Metabolite results                                      |
|----|----------------------------------------------------------------------|--------------------------------|----|-----------------------------------|--------------------------------|---------------------------------------------------------|
| 1  | 1H-NMR-based metabolomic profiling and taste of stewed pork-hock in soy sauce | (Yang et al., 2019)             | 2019 | Steward pork                      | 1H-NMR                        | Amino acids, sucrose, β-glucose, acetate, and creatinin |
| 2  | LC-QTOF-MS identification of porcine-specific peptide in heat treated pork identifies candidate markers for meat species determination | (Sarah et al., 2016)           | 2016 | Meat (pork, beef, chicken, and chevon) | LC-QTOF-MS                    | Seven porcine-specific peptides, two were derived from lactate dehydrogenase, one from creatine kinase, and four from serum albumin protein |
| 3  | A volatilomics approach for off-line discrimination of minced beef and pork meat and their admixture using HS-SPME GC/MS in tandem with multivariate data analysis | (Pavlidis et al., 2019)         | 2019 | Meat (beef and pork)              | GC-MS                         | Alcohols, 2-butanol, and 1-octen-3-ol                   |
| 4  | Chemometrics-assisted shotgun proteomics for establishment of potential peptide markers of non-halal pork (Sus scrofa) among halal beef and chicken | (Yuswan et al., 2018)           | 2018 | Meat (beef, chicken, and pork)    | LC-MS                         | 7 Peptides marker                                      |
| 5  | Discrimination between vegetable oil and animal fat by a metabolomics approach using gas chromatography-mass spectrometry combined with chemometrics | (Heidari et al., 2020)          | 2020 | Animal fats                        | GC-MS                         | Methyl myristate, methyl palmitate, methyl oleate, and methyl stearate |
| 6  | Liquid chromatography quadrupole time-of-flight mass spectrometry and rapid evaporative ionization mass spectrometry were used to develop a lamb authentication method: A preliminary study | (Wang et al., 2020)             | 2020 | Meat                              | UHPLC-QTOF-MS                  | 42 Potential metabolites                               |
| 7  | Impact of a pitanga leaf extract to prevent lipid oxidation processes during shelf life of packaged pork burgers: An untargeted metabolomic approach | (Rocchetti et al., 2020)        | 2020 | Meat                              | UHPLC-QTOF-MS                  | Hexanoylcarnitine, 4-hydroxy-2-nonenal, 6-hydroxypentadecanedioic acid, 9S,11S,15S,20-tetrahydroxy-5Z,13E-prostadienoic acid (20-hydroxy-PGF2α), sativic acid |
| 8  | Effect of different slaughtering method on metabolites of broiler chickens using ultra-high performance liquid chromatography-time of flight-mass spectrometry (UHPLC-TOF-MS) | (Ali et al., 2020a)             | 2019 | Chicken meat                       | UHPLC-QTOF-MS                  | Histidin, inosin, hypoxantine                          |
| 9  | Meat, the metabolites: An integrated metabolite profiling and lipidomics approach for the detection of the adulteration of beef with pork | (Trivedi et al., 2016)          | 2016 | Meat                              | GC-MS and UHPLC-MS             | Arabitol, citric acid, glucose 6-phosphat, glycine, malic acid |

1H-NMR, hydrogen-1 nuclear magnetic resonance; LC-QTOF-MS, liquid chromatography quadrupole time of flight mass spectrometry; HS-SPME, headspace solid-phase micro extraction; GC-MS, gas chromatography-mass spectrometry; LC-MS, liquid chromatography-mass spectrometry; UHPLC-QTOF-MS, ultra-high performance liquid chromatography-quadrupole time-of-flight mass spectrometry; UHPLC-TOF-MS, ultra-high performance liquid chromatography-time-of-flight-mass spectrometry; UHPLC-MS, ultra-high performance liquid chromatography-mass spectrometry.
that are soluble in nonpolar solvent such as chloroform (Han and Gross, 2005; Yu et al., 2020). Phospholipids, sphingolipids, rhamnolipids, and glycolipids are the most common lipid classes found in polar lipids. Furthermore, phospholipids are divided into numerous groups based on the phosphate classes, including such as PC, phosphatidylethanolamine (PE), phosphatidylinositol (PI), phosphatidylglycerol, phosphatidylserine (PS), and phosphatidic acid (Li et al., 2017). Glycerophospholipid categories in the meat can be seen in Fig. 3. PC, PE, PI, and PS are the major glycerophospholipids found in the membrane. They have various functions in the plasma membrane's exoplasmic and cytoplasmic functions, and they provide a semi-permeable barrier to keep the cell intact (Arish et al., 2015).

Lipidomics is a technique for determining the numerous lipid species found in the food samples. According to Harlina et al. (2021), depending on the lipid species and head groups, lipids can be identified using positive or negative ions. The majority of phospholipids are found in both positive and negative ion modes as distinct adducts, including +H\(^+\), +NH\(_4\)\(^+\) in positive mode and −H, +CH\(_3\)COO, or +HCOO\(^−\) in negative mode. Triglycerides and diglycerides are examples of neutral lipids that are all recognized in positive mode as NH\(_4\) adducts. However, only negative ion mode can identify the fatty acid contents of phospholipids, while positive ion mode can declare head group and/or neutral loss. Therefore, lipids are amphiphilic substances that ionize in both positive and negative modes. The MS based shotgun of lipidomics can be seen in Fig. 4.

Resume authentication of meat product using lipidomic can be shown in Table 2. UPLC is currently used to separate lipids since it can separate up to the sub-class of lipids. Q-extractive heated electrospray ionization can be coupled to the UPLC equipment, making it easier to get research data. Narváez-Rivas and Zhang (2016) described the use of the ultra performance liquid chromatography q-extractive heated electrospray ionization (UPLC-QE-HESI) for lipidomic analysis. This method has good selectivity and accuracy for determination lipids in sample (Narváez-Rivas and Zhang, 2016). They used this equipment to detect 430 lipid profiles in plasma. The UPLC-QE-HESI is an excellent tool for determining the lipid profiles of meat samples. The research data can be compared to lipid databases evaluated using multivariate statistics. Pork’s lipid profile, which distinguishes it from beef, could be utilized to determine authenticity in food sample (Holčapek et al., 2018; Narváez-Rivas and Zhang, 2016). The advantages and disadvantages of metabolomic and lipidomic for authentication in meat product can be seen in Table 3.

Fig. 3. Glycerophospholipid categories in the meat.
The techniques of metabolomics and lipidomics can be used to identify meat products. The combination of the two will give a clearer picture of the meat profile (Wang et al., 2021a; Wang et al., 2021b). The complete lipid and metabolite profiles can effectively distinguish between meat varieties (Wang et al., 2021a; Wang et al., 2021b; Wu et al., 2021; Zhang et al., 2021).

**Table 2. Lipidomic approaches for authentication of meat product**

| No | Title                                                                 | Refs                     | yr  | Objectives | Equipment                  | Lipids result                                                                 |
|----|----------------------------------------------------------------------|---------------------------|-----|------------|----------------------------|-------------------------------------------------------------------------------|
| 1  | Authentication of butter from lard adulteration using high-resolution nuclear magnetic resonance spectroscopy and high-performance liquid chromatography | (Fadzillah et al., 2017) | 2017 | Lard       | NMR, HPLC                  | Triacylglycerol and fatty acids                                               |
| 2  | Quantitative analysis of lard in animal fat mixture using visible Raman spectroscopy | (Lee et al., 2018)        | 2018 | Lard       | Raman spectroscopy          | Quantitative fat oil                                                          |
| 3  | Liquid chromatography quadrupole time-of-flight mass spectrometry and rapid evaporative ionization mass spectrometry were used to develop a lamb authentication method: A preliminary study | (Wang et al., 2020)       | 2020 | Meat       | UHPLC-QTOF-MS               | Multiple triglyceride (TG), diacylglycerol (DG), and PL                       |
| 4  | Characterization and discrimination of selected China’s domestic pork using an LC-MS-based lipidomic approach | (Mi et al., 2019)         | 2019 | Raw pork meat | LC-MS                      | 61 glycerolipids, 17 glycerophospholipids, 4 sterol lipids, 2 sphingolipids, 7 fatty acyls and 6 prenol lipids |
| 5  | Meat, the metabolites: An integrated metabolite profiling and lipidomics approach for the detection of the adulteration of beef with pork | (Trivedi et al., 2016)    | 2016 | Meat       | GC-MS and UHPLC-MS         | Fatty acid                                                                    |

NMR, nuclear magnetic resonance; HPLC, high performance liquid chromatography; UHPLC-QTOF-MS, ultra-high performance liquid chromatography-quadrupole time-of-flight mass spectrometry; LC-MS, liquid chromatography-mass spectrometry; GC-MS, gas chromatography-mass spectrometry; UHPLC-MS, ultra-high performance liquid chromatography-mass spectrometry.

**Future Perspective**

The techniques of metabolomics and lipidomics can be used to identify meat products. The combination of the two will give a clearer picture of the meat profile (Wang et al., 2021a; Wang et al., 2021b). The complete lipid and metabolite profiles can effectively distinguish between meat varieties (Wang et al., 2021a; Wang et al., 2021b; Wu et al., 2021; Zhang et al., 2021).
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2021). In the identification of meat products, combining metabolomic and lipidomic approaches could provide a more comprehensive overview (Ellis et al., 2016; Munekata et al., 2021). The combination of these two methods can be used to determine the authentication of meat products, by looking at the metabolites and lipids in meat products whether they contain pork (D’Alessandro and Zolla, 2013). In comparison to the metabolomic or lipidomic method alone, the combination of these two procedures could precisely evaluate the authentication of meat products (Capozzi et al., 2017; Chin et al., 2009; Picó, 2015; Yuliana et al., 2022).

**Conclusion**

Metabolomics is the study of metabolite profiles that can be used to identify the authenticity of meat products by examining metabolite profiles in pork that are not represented by beef. Lipidomics is a lipid profile analysis that may be used to determine the authenticity of meat products by examining the lipid profile of pork, which beef excludes. LC-MS instruments such as the UHPLC-QTOF-MS and UPLC-QE-HESI, which are directly connected to the metabolite and lipid databases software, can be used for metabolomic and lipidomic approaches to assess the authenticity of meat products. Combination metabolomic and lipidomic approaches to assess the authenticity of meat products would be more accurate because it can describe extensive lipid and metabolite profiles in meat.

**Conflicts of Interest**

The authors declare no potential conflicts of interest.

**Acknowledgements**

The first author extends thank to the Universitas Padjadjaran, Indonesia for the funding support. The work was supported by the Internal Funding Batch II of Universitas Padjadjaran (Funding RPLK, No. 4895/UN6.3.1/PT.00/2021).

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| No | Method   | Advantages                                                                 | Disadvantages                                                                 | Refs                                  |
|----|----------|-----------------------------------------------------------------------------|-------------------------------------------------------------------------------|---------------------------------------|
| 1  | Metabolom | Has a high accuracy value, Comprehensive analysis of the entire metabolome   | Requires proper instruments for analytical processes such as LC-MS, Metabolomic analysis equipment is expensive. | (Emwas et al., 2019; Trivedi et al., 2016) |
| 2  | Lipidomic | Areas explored in food analysis and more specifically meat adulteration, can be used detection meat with quickly. | The data obtained are limited to lipid compounds and sub lipids. | (Trivedi et al., 2016) |

LC-MS, liquid chromatography-mass spectrometry.
Muchtaridi M.

**Ethics Approval**

This article does not require IRB/IACUC approval because there are no human and animal participants.

**References**

Abbas O, Zadravec M, Baeten V, Mikš T, Lešić T, Vulić A, Prpić J, Jemeršić L, Pleadin J. 2018. Analytical methods used for the authentication of food of animal origin. Food Chem 246:6-17.

Ahmad AN, Ungku Zainal Abidin UF, Othman M, Abdul Rahman R. 2018. Overview of the halal food control system in Malaysia. Food Control 90:352-363.

Aiello D, De Luca D, Gionfriddo E, Naccarato A, Napoli A, Romano E, Russo A, Sindona G, Tagarelli A. 2011. Multistage mass spectrometry in quality, safety and origin of foods. Eur J Mass Spectrom 17:1-31.

Ali M, Lee SY, Park JY, Jung S, Jo C, Nam KC. 2019. Comparison of functional compounds and micronutrients of chicken breast meat by breeds. Food Sci Anim Resour 39:632-642.

Ali NSM, Zabidi AR, Manap MNA, Zahari SMSNS, Yahaya N. 2020a. Effect of different slaughtering methods on metabolites of broiler chickens using ultra high-performance liquid chromatography-time of flight-mass spectrometry (UHPLC-TOF-MS). Food Res 4:133-138.

Ali NSM, Zabidi AR, Manap MNA, Zahari SMSNS, Yahaya N. 2020b. Identification of metabolite profile in halal and non-halal broiler chickens using Fourier-transform infrared spectroscopy (FTIR) and ultra high performance liquid chromatography-time of flight- mass spectrometry (UHPLC-TOF-MS). Malays Appl Biol 49:87-93.

Alzeer J, Rieder U, Hadeed KA. 2018. Rational and practical aspects of halal and tayyib in the context of food safety. Trends Food Sci Technol 71:264-267.

Amaral JS, Santos G, Oliveira MBPP, Mafra I. 2017. Quantitative detection of pork meat by EvaGreen real-time PCR to assess the authenticity of processed meat products. Food Control 72:53-61.

Arish M, Husein A, Kashif M, Sandhu P, Hasnain SE, Akhter Y, Rub A. 2015. Orchestration of membrane receptor signaling by membrane lipids. Biochimie 113:111-124.

Artegoitia VM, Foote AP, Lewis RM, Freely HC. 2019. Metabolomics profile and targeted lipidomics in multiple tissues associated with feed efficiency in beef steers. ACS Omega 4:3973-3982.

Ballin NZ. 2010. Authentication of meat and meat products. Meat Sci 86:577-587.

Capozzi F, Trimigno A, Ferranti P. 2017. Proteomics and metabolomics in relation to meat quality. In Poultry quality evaluation: Quality attributes and consumer values. Petracci M, Berri C (ed). Woodhead, Sawston, UK. pp 221-245.

Castro-Puyana M, Pérez-Miguez R, Montero L, Herrero M. 2017. Reprint of: Application of mass spectrometry-based metabolomics approaches for food safety, quality and traceability. TrAC Trends Anal Chem 96:62-78.

Chin ST, Che Man YB, Tan CP, Hashim DM. 2009. Rapid profiling of animal-derived fatty acids using fast GC × GC coupled to time-of-flight mass spectrometry. J Am Oil Chem Soc 86:949-958.

Consomni R, Cagliani LR. 2019. The potentiality of NMR-based metabolomics in food science and food authentication assessment. Magn Reson Chem 57:558-578.

Crestani E, Harb H, Charbonnier LM, Leirer J, Motsinger-Reif A, Rachid R, Pipatpanakul W, Kaddurah-Daouk R, Chatila
Metabolomics and Lipidomics in Authentication of Meat Product

TA. 2020. Untargeted metabolomic profiling identifies disease-specific signatures in food allergy and asthma. J Allergy Clin Immunol 145:897-906.

Dailey AL. 2017. Metabolomic bioinformatic analysis. In Molecular profiling: Methods and protocols. Espina V (ed). Springer, New York, NY, USA.

D’Alessandro A, Zolla L. 2013. Foodomics to investigate meat tenderness. TrAC Trends Anal Chem 52:47-53.

Demirhan Y, Ulca P, Senyuva HZ. 2012. Detection of porcine DNA in gelatine and gelatine-containing processed food products: Halal/Kosher authentication. Meat Sci 90:686-689.

De Paepe E, Van Meulebroek L, Rombouts C, Huysman S, Verplanken K, Lapauw B, Wauters J, Hemeryck LY, Vanhaecke L. 2018. A validated multi-matrix platform for metabolomic fingerprinting of human urine, feces and plasma using ultra-high performance liquid-chromatography coupled to hybrid orbitrap high-resolution mass spectrometry. Anal Chim Acta 1033:108-118.

Dettmer K, Aronov PA, Hammock BD. 2007. Mass spectrometry-based metabolomics. Mass Spectrom Rev 26:51-78.

Dirong G, Nematbakhsh S, Selamat J, Chong PP, Idris LH, Nordin N, Fatchiyah F, Abdull Razis AF. 2021. Omics-based analytical approaches for assessing chicken species and breeds in food authentication. Molecules 26:6502.

Domínguez R, Pateiro M, Gagaoua M, Barba FJ, Zhang W, Lorenzo JM. 2019. A comprehensive review on lipid oxidation in meat and meat products. Antioxidants 8:429.

El Sheikha AF, Mokhtar NFK, Amie C, Lamasudin DU, Isa NM, Mustafa S. 2017. Authentication technologies using DNA-based approaches for meats and halal meats determination. Food Biotechnol 31:281-315.

Ellis DI, Muhamadali H, Allen DP, Elliott CT, Goodacre R. 2016. A flavour of omics approaches for the detection of food fraud. Curr Opinion Food Sci 10:7-15.

Emwas AH, Roy R, McKay RT, Tenori L, Saccenti E, Gowda GAN, Rafikry D, Alahmari F, Jaremko L, Jaremko M, Wishart DS. 2019. NMR spectroscopy for metabolomics research. Metabolites 9:123.

Erban A, Fehrle I, Martinez-Seidel F, Brigante F, Más AL, Baroni V, Wunderlin D, Kopka J. 2019. Discovery of food identity markers by metabolomics and machine learning technology. Sci Rep 9:1-19.

Fadzillah NA, Rohman A, Salleh RA, Amin I, Shuhaimi M, Farihawhida MY, Rashidi O, Aizat JM, Khatib A. 2017. Authentication of butter from lard adulteration using high-resolution of nuclear magnetic resonance spectroscopy and high-performance liquid chromatography. Int J Food Prop 20:2147-2156.

Gorrochategui E, Jaumot J, Lacorte S, Tauler R. 2016. Data analysis strategies for targeted and untargeted LC-MS metabolomic studies: Overview and workflow. TrAC Trends Anal Chem 82:425-442.

Haleem A, Khan MI, Khan S. 2021. Conceptualising a framework linking halal supply chain management with sustainability: An India centric study. J Islam Mark 12:1535-1552.

Han X, Gross RW. 2005. Shotgun lipidomics: Electrospray ionization mass spectrometric analysis and quantitation of cellular lipids directly from crude extracts of biological samples. Mass Spectrom Rev 24:367-412.

Harлина PW, Ma M, Shahzad R. 2021. Quantification of lipidomics profiling using UPLC-QE-HESI-lipid analysis on the salted duck egg incorporated with clove extract. Eur J Lipid Sci Technol 123:2000284.

Heidari M, Talebpour Z, Abdollahpour Z, Adib N, Ghanavi Z, Aboul-Enein HY. 2020. Discrimination between vegetable oil and animal fat by a metabolomics approach using gas chromatography–mass spectrometry combined with chemometrics. J Food Sci Technol 57:3415-3425.

Holkápek M, Liebisch G, Ekoos K. 2018. Lipidomic analysis. Anal Chem 90:4249-4257.
Hossain MAM, Uddin SMK, Sultana S, Wahab YA, Sagadevan S, Johan MR, Ali ME. 2020. Authentication of Halal and Kosher meat and meat products: Analytical approaches, current progresses and future prospects. Crit Rev Food Sci Nutr 62:285-310.

Islam KZ, Ahasan MAA, Hossain MS, Rahman MH, Mousumi US, Asaduzzaman M. 2021. A smart fluorescent light spectrocope to identify the pork adulteration for halal authentication. Food Nutr Sci 12:73-89.

Izadpanah M, Mohedani N, Elyasi Gorji Z, Farzaneh P, Vakhshiteh F, Shahzadeh Fazeli SA. 2017. Simple and fast multiplex PCR method for detection of species origin in meat products. J Food Sci Technol 55:698-703.

Jalil NSA, Tawde AV, Zito S, Sinclair M, Fryer C, Idrus Z, Phillips CJC. 2018. Attitudes of the public towards halal food and associated animal welfare issues in two countries with predominantly Muslim and non-Muslim populations. PLOS ONE 13:e0204094.

Jang C, Hui S, Zeng X, Cowan AJ, Wang L, Chen L, Morscher RJ, Reyes J, Frezza C, Hwang HY, Imai A, Saito Y, Okamoto K, Vaspoli C, Kasprenski L, Zsido GA 2nd, Gorman JH 3rd, Gorman RC, Rabinowitz JD. 2019. Metabolite exchange between mammalian organs quantified in pigs. Cell Metab 30:594-606.

Jannat B, Ghorbani K, Kouchaki S, Sadeghi N, Eslamifarsani E, Rabban F, Beyramysoltan S. 2020. Distinguishing tissue origin of bovine gelatin in processed products using LC/MS technique in combination with chemometrics tools. Food Chem 319:126302.

Jannat B, Ghorbani K, Shafieyan H, Kouchaki S, Behfar A, Sadeghi N, Beyramysoltan S, Rabban F, Dashtifard S, Sadeghi M. 2018. Gelatin speciation using real-time PCR and analysis of mass spectrometry-based proteomics datasets. Food Control 87:79-87.

Jia W, Fan Z, Shi Q, Zhang R, Wang X, Shi L. 2021. LC-MS-based metabolomics reveals metabolite dynamic changes during irradiation of goat meat. Food Res Int 150:110721.

Junot C, Fenaille F, Colsch B, Bécher F. 2014. High resolution mass spectrometry based techniques at the crossroads of metabolic pathways. Mass Spectrom Rev 33:471-500.

Kang C, Zhang Y, Zhang M, Qi J, Zhao W, Gu J, Guo W, Li Y. 2022. Screening of specific quantitative peptides of beef by LC–MS/MS coupled with OPLS-DAA. Food Chem 387:132932.

Kliman M, May JC, McLean JA. 2011. Lipid analysis and lipidomics by structurally selective ion mobility-mass spectrometry. Biochim Biophys Acta Mol Cell Biol Lipids 1811:935-945.

Korf A, Jeck V, Schmid R, Helmer PO, Hayen H. 2019. Lipid species annotation at double bond position level with custom databases by extension of the mzmine 2 open-source software package. Anal Chem 91:5098-5105.

Lee JY, Park JH, Mun H, Shim WB, Lim SH, Kim MG. 2018. Quantitative analysis of lard in animal fat mixture using visible raman spectroscopy. Food Chem 254:109-114.

Li J, Vosegaard T, Guo Z. 2017. Applications of nuclear magnetic resonance in lipid analyses: An emerging powerful tool for lipidomics studies. Prog Lipid Res 68:37-56.

Li YC, Liu SY, Meng FB, Liu DY, Zhang Y, Wang W, Zhang JM. 2020. Comparative review and the recent progress in detection technologies of meat product adulteration. Compr Rev Food Sci Food Saf 19:2256-2296.

Lim SA, Ahmed MU. 2016. A label free electrochemical immunosensor for sensitive detection of porcine serum albumin as a marker for pork adulteration in raw meat. Food Chem 206:197-203.

Lim YH, Lada S, Ullah R, Abdul Adis AA. 2022. Non-Muslim consumers’ intention to purchase halal food products in Malaysia. J Islam Mark 13:586-607.
Metabolomics and Lipidomics in Authentication of Meat Product

Lubis HN, Mohd-Naim NF, Alizul NN, Ahmed MU. 2016. From market to food plate: Current trusted technology and innovations in halal food analysis. Trends Food Sci Technol 58:55-68.

Mahbubi A, Uchiyama T, Hatanaka K. 2019. Capturing consumer value and clustering customer preferences in the Indonesian halal beef market. Meat Sci 156:23-32.

Medema MH, Fischbach MA. 2015. Computational approaches to natural product discovery. Nat Chem Biol 11:639-648.

Mi S, Shang K, Li X, Zhang CH, Liu JQ, Huang DQ. 2019. Characterization and discrimination of selected China’s domestic pork using an LC-MS-based lipidomics approach. Food Control 100:305-314.

Montowska M, Fornal E. 2017. Label-free quantification of meat proteins for evaluation of species composition of processed meat products. Food Chem 237:1092-1100.

Moosmang S, Pitzscheider M, Sturm S, Seger C, Tilg H, Halabalaki M, Stuppner H. 2019. Metabolomic analysis: Addressing NMR and LC-MS related problems in human feces sample preparation. Clin Chim Acta 489:169-176.

Mostafa MM. 2020. Information diffusion in halal food social media: A social network approach. J Int Consum Mark 33:471-491.

Munekata PES, Pateiro M, López-Pedrous M, Gagaoua M, Lorenzo JM. 2021. Foodomics in meat quality. Curr Opin Food Sci 38:79-85.

Muroya S, Ueda S, Komatsu T, Miyakawa T, Erbbjerg P. 2020. MEATABolomics: Muscle and meat metabolomics in domestic animals. Metabolites 10:188.

Nakyinsige K, Man YBC, Sazili AQ. 2012. Halal authenticity issues in meat and meat products. Meat Sci 91:207-214.

Narváez-Rivas M, Zhang Q. 2016. Comprehensive untargeted lipidomic analysis using core–shell C30 particle column and high field orbitrap mass spectrometer. J Chromatogr A 1440:123-134.

Neef SK, Winter S, Hofmann U, Mürdter TE, Schaeffeler E, Horn H, Buck A, Waleh A, Hennenlotter J, Ott G, Fend F, Bedke J, Schwab M, Haag M. 2020. Optimized protocol for metabolomic and lipidomic profiling in formalin-fixed paraffin-embedded kidney tissue by LC-MS. Anal Chim Acta 1134:125-135.

Pavlidis DE, Mallouchos A, Ercolini D, Panagou EZ, Nychas GJE. 2019. A volatilomics approach for off-line discrimination of minced beef and pork meat and their admixture using HS-SPME GC/MS in tandem with multivariate data analysis. Meat Sci 151:43-53.

Picó Y. 2015. Mass spectrometry in food quality and safety: An overview of the current status. Compr Anal Chem 68:3-76.

Pranata AW, Yuliana ND, Amalia L, Darmawan N. 2021. Volatilomics for halal and non-halal meatball authentication using solid-phase microextraction–gas chromatography–mass spectrometry. Arab J Chem 14:103146.

Qodri M. 2018. Pengharaman lemak hewani bagi bani israil sebagai hukuman (kajian surat al-an’am ayat 146 dalam perspektif sains modern). J Ilmiah Univ Batanghari Jambi 18:647.

Rocchetti G, Bernardo L, Pateiro M, Barba FJ, Munekata PES, Trevisan M, Lorenzo JM. 2020. Impact of a pitanga leaf extract to prevent lipid oxidation processes during shelf life of packaged pork burgers: An untargeted metabolomic approach. Foods 9:1668.

Rohman A, Che Man YB. 2011. Analysis of pig derivatives for halal authentication studies. Food Rev Int 28:97-112.

Rohman A, Fadzillah NA. 2021. Application of spectroscopic and chromatographic methods for the analysis of non-halal meats in food products. In Multifaceted protocols in biotechnology. Amid A (ed). Springer, Cham, Switzerland. pp 75-92.

Rohman A, Windarsih A, Erwanto Y, Zakaria Z. 2020. Review on analytical methods for analysis of porcine gelatine in food and pharmaceutical products for halal authentication. Trends Food Sci Technol 101:122-132.
Salwani MS, Adeyemi KD, Sarah SA, Vejayan J, Zulkifli I, Sazili AQ. 2015. Skeletal muscle proteome and meat quality of broiler chickens subjected to gas stunning prior slaughter or slaughtered without stunning. CyTA J Food 14:375-381.
Sarah SA, Faradali WN, Salwani MS, Amin I, Karsani SA, Sazili AQ. 2016. LC–QTOF-MS identification of porcine-specific peptide in heat treated pork identifies candidate markers for meat species determination. Food Chem 199:157-164.

Sin KY, Sin MC. 2019. Distinguished identification of halal and non-halal animal-fat gelatin by using microwave dielectric sensing system. Cogent Eng 6:1599149.

Stachniuk A, Sumara A, Montowska M, Fornal E. 2019. Liquid chromatography–mass spectrometry bottom-up proteomic methods in animal species analysis of processed meat for food authentication and the detection of adulterations. Mass Spectrom Rev 40:3-30.

Sugimoto M, Kawakami M, Robert M, Soga T, Tomita M. 2012. Bioinformatics tools for mass spectroscopy-based metabolomic data processing and analysis. Curr Bioinform 7:96-108.

Trivedi DK, Hollywood KA, Rattray NJW, Ward H, Trivedi DK, Greenwood J, Ellis DI, Goodacre R. 2016. Meat, the metabolites: An integrated metabolite profiling and lipidomics approach for the detection of the adulteration of beef with pork. Analyst 141:2155-2164.

Troy DJ, Tiwari BK, Joo ST. 2016. Health implications of beef intramuscular fat consumption. Korean J Food Sci Anim Resour 36:577-582.

Utpott M, Rodrigues E, Rios AO, Mercali GD, Flôres SH. 2022. Metabolomics: An analytical technique for food processing evaluation. Food Chem 366:130685.

Vanany I, Soon JM, Maryani A, Wibawa BM. 2020. Determinants of halal-food consumption in Indonesia. J Islam Mark 11:507-521.

von Bargen C, Brockmeyer J, Humpf HU. 2014. Meat authentication: A new HPLC–MS/MS based method for the fast and sensitive detection of horse and pork in highly processed food. J Agric Food Chem 62:9428-9435.

Wang J, Xu L, Xu Z, Wang Y, Niu C, Yang S. 2020. Liquid chromatography quadrupole time-of-flight mass spectrometry and rapid evaporative ionization mass spectrometry were used to develop a lamb authentication method: A preliminary study. Foods 9:1723.

Wang J, Xu Z, Zhang H, Wang Y, Liu X, Wang Q, Xue J, Zhao Y, Yang S. 2021a. Meat differentiation between pasture-fed and concentrate-fed sheep/goats by liquid chromatography quadrupole time-of-flight mass spectrometry combined with metabolomic and lipidomic profiling. Meat Sci 173:108374.

Wang K, Xu L, Wang X, Chen A, Xu Z. 2021b. Discrimination of beef from different origins based on lipidomics: A comparison study of DART-QTOF and LC-ESI-QTOF. LWT-Food Sci Technol 149:111838.

Wu B, Wei F, Xu S, Xie Y, Lv X, Chen H, Huang F. 2021. Mass spectrometry-based lipidomics as a powerful platform in foodomics research. Trends Food Sci Technol 107:358-376.

Yang Y, Pan D, Sun Y, Wang Y, Xu F, Cao J. 2019. 1H NMR-based metabolomics profiling and taste of stewed pork-hock in soy sauce. Food Res Int 121:658-665.

Yu Z, Wang N, Geng F, Ma M. 2020. High-density lipoproteins from egg yolk’s effect on hyperlipidemia in a high-fat-diet obese mouse using lipidomic analysis. Food Biosci 33:100492.

Yuliana ND, Hunaefi D, Goto M, Ishikawa YT, Verpoorte R. 2022. Measuring the health effects of food by metabolomics. Crit Rev Food Sci Nutr 62:6359-6373.
Yuswan MH, Aizat WM, Lokman AA, Desa MNM, Mustafa S, Junoh NM, Yusof ZNB, Mohamed R, Mohmad Z, Lamasudin DU. 2018. Chemometrics-assisted shotgun proteomics for establishment of potential peptide markers of non-halal pork (*Sus scrofa*) among halal beef and chicken. Food Anal Methods 11:3505-3515.

Zamaratskaia G, Li S. 2017. Proteomics in meat science: Current status and future perspective. Theory Pract Meat Process 2:18-26.

Zhang M, Li Y, Zhang Y, Kang C, Zhao W, Ren N, Guo W, Wang S. 2022. Rapid LC-MS/MS method for the detection of seven animal species in meat products. Food Chem 371:131075.

Zhang T, Chen C, Xie K, Wang J, Pan Z. 2021. Current state of metabolomics research in meat quality analysis and authentication. Foods 10:2388.