applied sciences

MDPI

Review

MALDI-TOF Mass Spectrometry Applications for Food Fraud Detection

Carlo Zambonin

Dipartimento di Chimica, Università degli Studi di Bari "Aldo Moro", Via E. Orabona 4, 70126 Bari, Italy; carlo.zambonin@uniba.it

Abstract: Chemical analysis of food products relating to the detection of the most common frauds is a complex task due to the complexity of the matrices and the unknown nature of most processes. Moreover, frauds are becoming more and more sophisticated, making the development of reliable, rapid, cost-effective new analytical methods for food control even more pressing. Over the years, MALDI-TOF MS has demonstrated the potential to meet this need, also due to a series of undeniable intrinsic advantages including ease of use, fast data collection, and capability to obtain valuable information even from complex samples subjected to simple pre-treatment procedures. These features have been conveniently exploited in the field of food frauds in several matrices, including milk and dairy products, oils, fish and seafood, meat, fruit, vegetables, and a few other categories. The present review provides a comprehensive overview of the existing MALDI-based applications for food quality assessment and detection of adulterations.

Keywords: MALDI-TOF; applications; food; fraud; adulteration; quality

Citation: Zambonin, C. MALDI-TOF Mass Spectrometry Applications for Food Fraud Detection. *Appl. Sci.* **2021**, *11*, 3374. https://doi.org/10.3390/app11083374

Academic Editors: Theodoros Varzakas and Tsarouhas Panagiotis

Received: 16 March 2021
Accepted: 7 April 2021
Published: 9 April 2021

1. Introduction

Defining and identifying the types of food fraud is still an open issue since the relevant literature is characterized by a considerable variability of the related terms [1]. The European Commission defines food frauds as "intentional actions by businesses or individuals for the purpose of deceiving purchasers and gaining undue advantage therefrom, in violation of the rules referred to in Article 1(2) of Regulation (EU) 2017/625 (the agri-food chain legislation)" [2]. The most common foods subjected to illegal manipulations [3] include oil, fish, honey, milk and dairy products, meat, grain-based foods, fruit juices, wine and alcoholic beverages, organic foods, spices, coffee, tea, and many others.

According to the European Commission [2,4], the most common fraud is adulteration, which can occur in food products in different ways: "replacing a nutrient, an ingredient, a food or part of a food with another one with lower value" (substitution), "mixing an ingredient with high value with an ingredient with a lower value" (dilution), "adding unknown and undeclared compounds to food products in order to enhance their quality attributes" (unapproved enhancement), and "hiding the low quality of food ingredients or products" (concealment). Food frauds can also take others forms, including mislabeling, the process of putting false claims on packaging for economic gain, counterfeiting, when intellectual property rights are infringed, and grey market, referring to unauthorized sales channels for products.

Based on the above consideration, a chemical analysis on a given food can be carried out for many reasons, such as individuation of adulteration, authentication and traceability, confirmation of geographical origin assessment of toxicity, and many others. Food sample analysis, then, constitutes a crucial challenge for analytical chemistry and numerous scientists are focused on the development of reliable, fast, cost-effective analytical processes to solve analytical problems related to food frauds. Food-based matrices are complex and characterized by a wide range of chemical composition that influence the performance of chemical analytical measurements, while the nature of the manipulation is often unknown,

making the analysis even more complicated. Moreover, as technologies develop to detect deceptions, they become more sophisticated since fraudulent suppliers also adapt to finding new ways to circumvent the controls.

Targeted and non-targeted analytical approaches are mainly used for food controls [5–7]. A targeted analysis, generally laborious and time-consuming, is based on the knowledge of the contaminants and focused on the detection of one or a few classes of compounds that represent the markers of the fraud. Since in most cases the type of fraud is unknown, a non-targeted analysis is often necessary. This approach relies on the fast instrumental acquisition of the chemical profile of the whole foodstuff sample, usually represented by spectra, which should provide a unique fingerprint as a reference for suspect samples, often with the help of chemometric data handling [8].

Spectroscopic techniques [5,9–16], namely nuclear magnetic resonance (NMR), near- and mid-infrared (NIR, MIR), Raman, ultraviolet–visible (UV-VIS), and X-ray fluorescence spectroscopy (XRF), have been largely used to successfully carry out non-targeted analysis. Different mass spectrometry (MS) techniques and ionization approaches, including matrix-assisted laser desorption ionization time-of-flight (MALDI-TOF), electrospray (ESI), ambient mass spectrometry (AMS), and high-resolution mass spectrometry (HRMS), have been also widely employed for the same purpose [6,17–23], and their constant advances have enabled the development of numerous new methodologies for food quality and safety controls.

Among them, MALDI-TOF represents an ideal option for fast, reliable, and accurate detection of food frauds due to some intrinsic characteristics such as ease of use and speed with which data can be collected even from complex samples. MALDI MS is based on the use of a pulsed laser beam that hits the sample, represented by co-crystals of the so-called "matrix," present in a vast excess, and the analyte. The laser energy is absorbed by the matrix that vaporized carrying intact analyte molecules into the vapor phase. During this process, ions (mainly H^+ and Na^+) are released by the matrix leading to the formation of charged analyte molecules. Moreover, anions can also be generated by abstracting H^+ or Na^+ from the analyte. After being accelerated in an electric field and passing a charged grid, the ions are separated in a TOF mass analyzer based on their m/z ratios (low mass ions arrive at the detector in a shorter time than high mass ions). A "linear" geometry of TOF analyzers is used for the analysis of high molecular weight molecules. Smaller molecules can be analyzed using a "reflectron" configuration able to balance the different initial velocities of the ions during the vaporization process, leading to a consistent improvement of resolution. MALDI mass spectrometers are capable to rapidly generate spectra, profiles, and/or fingerprints from food matrices, often with simple preparation or no sample preparation at all. The potential of the MALDI approach applied to the fight against food fraud, sometimes coupled to multivariate statistical methods to extract information from complex analytical data such as mass spectra, has been clearly understood, as demonstrated by a considerable number of related publications. The purpose of the present review is to provide a comprehensive overview of the relevant literature. Based on the research carried out, most of the existing MALDI applications dedicated to the field of food fraud have concerned the analysis of milk and dairy products, oils, fish and seafood, vegetables, fruit, meat, and, to a minor extent, a few other categories. Most of the works have been focused on the evaluation of food quality and detection of adulterations, while only few applications have been devoted to the investigation of the geographical origin.

2. MALDI Applications

2.1. Milk and Dairy Products

Due to their high nutritional value, milk and derived products are largely consumed all over the world. According to the Food and Agriculture Organization of the United Nations (FAO), worldwide milk production has grown from 522 to 798 million tons in three decades (1986–2016) [24] and was expected to grow in 2020 to 859 million tons [25]. The increase in consumption also increases the number of dishonest producers willing to

commit fraud to increase their earnings, making the safety and authenticity of milk and derived products an area of growing attention and concern, as demonstrated by several regulations and governing bodies [26,27]. Traditionally, milk dilution by water has been the most common illegal practice, together with the selling of skimmed milk and semi-skimmed milk instead of whole milk. As detection methods technologies has improved, fraudulent suppliers evolved [28] towards most sophisticated fraudulent approaches, such as the addition of milk anhydrous products (caseins and caseinate, milk protein concentrate, whey proteins) to liquid milk and the mixing of high-quality milk, such as buffalo, sheep, and goat, with less expensive products, such as cow milk. Many MALDI-based analytical methods have been developed and improved in the last years to assess the authenticity of milk and dairy products.

Buffalo milk has been extensively investigated by different MALDI proteomic approaches searching for possible adulteration. Cozzolino and co-workers have developed two different methods for the identification of adulteration of water buffalo and sheep milk and water buffalo mozzarella, respectively. In the first work [29], the investigation was performed on raw buffalo and sheep milk samples. The determination of the presence of bovine milk or the addition of powdered milk to fresh raw milk was accomplished by evaluating the protein profiles coming from the most abundant whey proteins, lactalbumin, and lactoglobulins. In the second work [30], patterns of the same whey proteins were obtained from the direct analysis of water buffalo mozzarella cheese, which was able to differentiate between mozzarella cheeses made from pure water buffalo milk or from mixtures of bovine-sheep-buffalo milks. Interesting quality information on the partial resistance of the detected proteins to the thermal and enzymatic processes involved in the cheese production was also inferred. In both methods, mixtures with different percentages of less expensive milk added to water buffalo milk were prepared, and detection limits below 5% were always obtained in adulterated milk or cheese, respectively. The strategies were also fast, accurate, and practically did not require sample pre-treatment.

Sassi at al. have successfully optimized an integrated MALDI-TOF platform [31] for obtaining milk peptidomic/proteomic profiles to detect the addition of either nondeclared bovine material to water buffalo, goat, and ovine milks, or of powdered bovine milk to the fresh bovine milk. Milk samples were directly analyzed permitting a fast individuation of illegal adulterations at protein and peptide level and allowing the identification of unique diagnostic ions of thermal treatment in different types of commercial milks.

A further MALDI proteomic study for the detection of ricotta buffalo cheese adulteration with bovine milk by obtaining peptide profiles for both matrices was developed [32], followed by the search for signals that could represent specific markers for each type of dairy product. A peptide marker corresponding to the region 149–162 of β-lactoglobulin was correlated to the univocal presence of bovine milk in ricotta buffalo cheese at a 5% level.

According to the European reference method, the fraudulent addition of bovine milk in water buffalo milk can be individuated by concomitant isoelectric focusing detection of bovine γ_2- and γ_3-casein fragments after plasminolysis. However, this approach can produce false positive results due to a water buffalo β-casein peptide, which is also formed after plasminolysis of water buffalo milk and comigrates in isoelectric focusing with bovine γ_2-casein. Thus, Caira at al. have developed a proteomic approach [33] to obtain the unambiguous detection of bovine milk in water buffalo milk and derived products (LOD of 0.8% *v/v*) based on the MALDI determination of specific bovine and water buffalo β-casein phosphopeptide markers. The procedure was proposed as an integrative/alternative to the reference method.

Other studies were focused on the development of MALDI methods for the detection of the addition of sheep and goat milk with the less expensive bovine milk. Contrary to some of the above-mentioned works, which were focused on the identification of specific signals that can work as adulteration markers, one study, divided into two parts [34,35], proposed a different approach. The authors suggested that, in the analysis of a complex matrix such as milk, the simultaneous use of many variables reveals more information

compared to the use of single or few variables and proposed a method for quantitative and multivariate use of the whole MALDI mass spectra of milk samples to determine adulteration. The first part of the work [34] was focused on the optimization of sample preparation and instrument setup, the second on the quantitative determination of cow, goat, and sheep milk in mixed milk samples [35]. The results obtained seemed to confirm the original hypothesis since, with optimal parameter settings, multivariate regression on whole spectra allowed to determine the concentrations of milk in mixtures with good accuracy. A further study to detect the presence of cow milk in goat and sheep milk using whole MALDI mass spectra in combination with multivariate techniques was reported by Nicolau at al. [36]. Binary and tertiary mixtures of cow, sheep, and goat milk were easily and rapidly analyzed and accurate information on the amount and type of adulteration were obtained, with typical errors in the range 2–10% for cow milk.

The potential of proteomic approaches to fight illegal manipulations of milk was again demonstrated [37] by the detection of cow milk-specific peptide markers in sheep and goat milk and goat milk-specific peptide markers in sheep milk, by analyzing whole milk samples mixtures subjected to in-solution tryptic digestion. Seven peptide markers of cow milk and two peptide markers of goat milk were identified by MALDI-TOF analysis and the approach was able to detect adulteration up to a 5% level. Moreover, the same markers were found in cheese samples, demonstrating the applicability of the procedure even to milk-derived products. The authors stated that the use of the α-cyano-4-chlorocinnamic acid matrix was essential to reach the high sensitivity observed for the marker peptides. Moreover, the results were found in good agreement with those obtained with a traditional approach based on SDS-PAGE/in-gel digestion. The same research group reported another application [38] for the extraction and MALDI determination of phospholipids in milk, using the same matrix. The method was able to provide peculiar milk phospholipid profiles that were used for the detection of cow milk in sheep and goat milk. The abundance ratio of specific ions (m/z 703 and 706) was found to be species-specific and was used for the identification of the adulteration.

Very recently, liquid atmospheric pressure—MALDI mass spectrometry—was used [39] to optimize a very accurate approach to classify goat and sheep milk and sheep milk containing 10% of goat milk, to evaluate colostrum quality and postnatal stages, through the recording of the milk lipid/protein profiles or the detected orthologs of single proteins.

Donkey milk is a safe alternative for individuals which are allergic to cow milk and is often the object of adulteration, the detection of which is of critical importance for the safety of the consumers. The MALDI mass spectra profiles of α-lactalbumin and β-lactoglobulin were used to detect the fraudulent addition of goat or cow milk in donkey milk [40] in a protocol developed for routine analysis and potentially extendable to other milk species. Detection limits for the analysis of defatted milk samples were in the range 0.5–2.0%, comparable to those obtainable with traditional complex approaches. Despite the typical MALDI quantitative issues, the measured values were in good agreement with the actual composition of the analyzed mixtures. Another study [41] investigated donkey and goat milk adulteration by cow and sheep milk using MALDI in combination with unsupervised hierarchical clustering, principal component (PCA), and Pearson's correlation, focusing on the mass spectra profiles in the m/z mass range 2000–25,000 Da. The approach was shown to be rapid, robust, and sensitive, with detection limits of 0.5%.

The adulteration of fresh milk by reconstituted milk and the selling of reconstituted milk as fresh product is economically advantageous when either a surplus of milk powder exists, or when the importation of dried milk powder is subsidized. Moreover, the addition of powdered derivatives is difficult to detect because the adulterant materials have almost the same chemical composition of liquid milk. Specific peptide markers, attributable to modified whey proteins and/or caseins, formed by thermal degradation during milk powder production, were identified and used to detect the presence of powdered milk in liquid milk samples [42]. Whey and casein fractions of milk samples were directly digested in solution and analyzed by MALDI using α-cyano-4-chlorocinnamic acid as a matrix,

which enhanced the detection of more acid peptides. The approach was able to detect the peptides diagnostic for the presence of powder in liquid milk even at a 1% level. The results were in good agreement with those obtained with a reliable but time-consuming 2D gel approach.

On the contrary, milk powder itself could be the object of adulteration when non-milk fat such as vegetable oils and fats are added. Garcia and co-workers [43] successfully developed a MALDI-qTOF method for the fast individuation of non-milk fats and oils in milk powder. Samples were subjected to a simple n-hexane extraction prior to MS analysis, which provided rapid and unambiguous profiles of the triacylglycerols (TAGs) composition capable to characterize the adulterant and estimate the adulteration level.

Other MALDI applications on the detection of frauds were focused on different kind of milks and adulterations, as well as to the analysis of cheese samples. Hinz at al. [44] compared the principal proteins in bovine, caprine, buffalo, equine, and camel milk, finding interesting differences between the species that could be used to identify sources of hypoallergenic alternatives to bovine milk and detect adulteration of milk samples and derived products. A proteomic approach for the MALDI-TOF analysis of commercial bovine milk, based on in-solution digestion of the whole samples, was also suggested [45] for the routine analysis of raw and processed foods and to detect adulterations.

Due to similar properties to bovine milk, soya milk is added to bovine milk for revenue maximization. In a recent work, England and colleagues [46] used MALDI to develop a solventless, sensitive, and cost-effective method for the discrimination of bovine milk from soya and coconut milk as well as for the individuation of milk adulteration. Samples were simply diluted in water, combined with the matrix, and subjected to instrumental analysis, which allowed to obtain unique lipid profiles (mainly phosphatidylcholine and TAGs).

Magenis at al. reported a qualitative method to check the authenticity of a typical Brazilian cheese using β-lactoglobulin as an adulteration marker [47], showing good precision and sensitivity (7 mg/g). The procedure involved SDS–PAGE and in-gel trypsin digestion followed by MALDI analysis. The applicability to real samples was demonstrated by the analysis of 42 commercial samples, 18 of which were found to be adulterated.

Direct Imprinting in Glass Surface Mass Spectrometry (DIGS-MS) for qualitative cheese analysis in a MALDI instrument was also successfully used [48] to identify complex lipids to be used as quality and/or adulteration marker in different cheese samples. The integration of analytical and statistical data could also be employed for the control of productive stages.

In another recent work [49], Rau and co-workers developed an original method to identify the dairy animal species of mozzarella and white brined cheese by MALDI-TOF in combination with direct protein extraction without tryptic digestion and a small in-house reference spectra database.

Some further MALDI works were oriented towards the quality evaluation of milk and dairy products. The selective extraction of phospholipids from dairy products such as milk, chocolate milk, and butter by micro-solid phase extraction (μ-SPE), based on homemade titanium dioxide (TiO_2) microcolumns, followed by MALDI-TOF MS, was developed by Calvano at al. [50]. Since α-lactalbumin and β-lactoglobulin are among the main cow milk allergens, Gasilova at al. [51] developed a sensitive quantitative method for their determination by immunoaffinity capillary electrophoresis, using magnetic beads functionalized with opportune antibodies, coupled to MALDI. A transient isotachophoresis preconcentration step allowed to obtain LOD values of 0.02 and 0.03 μg/mL for β-lactoglobulin and α-lactalbumin, respectively, suitable for allergen detection. The method was then successfully tested on cow milk and fortified soy milk, proving the capability to determine the analytes at both high and low concentration levels.

To identify and characterize oxidized and glycated phospholipids in heat-treated food, namely milk powders, pasteurized milk, ultra-high-temperature milk, and soy flour, an extraction protocol [52] was developed by means of a methanolic solution of 1,8-bis(dimethylamino) naphthalene (DMAN), used as both extraction medium and matrix

for the successive MALDI detection, performed in negative ion mode. Thermally modified lipid products were first characterized by heating representative standards and eventually determined in real samples. MALDI-TOF, combined with C18-stage tip extraction, was also used [53] to rapidly obtain peptide profiles from different commercial milk products in view of the identification of possible changes induced by different heating regimens and storage conditions. Several peptide ions showed relative abundance variations following specific treatments, such as heating or proteolytic activity of enzymes during storage, suggesting their potential use as markers to draw information on milk types and freshness. A similar approach permitted [54] the generation of polypeptide profiles from buffalo milk samples subjected to different freezer storage times, to assess their freshness through the identification of specific markers. The statistical evaluation of data relevant to the analysis of several fresh and frozen samples allowed to identify 28 polypeptide markers of freezing storage originated from the breakdown of buffalo proteins, being α-lactalbumin, β-lactoglobulin, γ2-, γ3-, and γ4-caseins, β-casein-derived phosphopeptides, and GLYCAM1 phosphorylated peptides as the most significant components. Their progressive formation even in freezing conditions was attributed to an unknown protease stable at low temperatures. MALDI profiling of milk proteins, in combination with multivariate data analyses, also proved to be an optimal mean to discriminate between different milk types [55]. Protein fingerprints of mammalian (various species), human (at different lactation stages), and formula (different brands) milks were rapidly obtained, permitting to obtain key information on the matrices under study.

2.2. Oils

Olive oil is one of the main ingredients in the Mediterranean diet [56]. The International Olive Council defines two categories of olive oil [57], the first comprising oils suitable for consumption, such as extra-virgin, virgin, and ordinary olive oil, the second comprising oils that must be further processed prior to ingestion. Extra-virgin olive oil (EVOO) is the most valuable, since it is obtained from olive fruits using mechanical processes or other physical means [58] that lead to a product of unmatched value, characterized by unique features, such as nutritional quality, health benefits, and pleasant flavor. These features make EVOOs expensive products that are continuously counterfeited in many countries [59] with oils produced from cheaper fruits/seeds or with other lower quality olive oils or even mislabeling virgin/refined olive oils. Of course, analytical methods are crucial for detecting EVOO frauds [60] and many scientists are committed to the development of MALDI-TOF MS applications.

A matrix-less laser desorption/ionization (LDI) approach using a stainless-steel target plate was proposed [61] for the fast analysis of diluted soy, sunflower, and extra-virgin olive oil samples. MS spectra characterized by oil-specific profiles and free of MALDI-matrix peaks were obtained, allowing the easy discrimination of the oil under study. Most of the m/z ions present in the spectrum were easily attributed to tri/diacylglycerols compounds, some of which were found to be diagnostic ions for olive (m/z 907.77) and sunflower oil (903.79 and 901.78), thus permitting the detection of adulteration of olive with sunflower oil. All the diagnostic ions were potentially attributable to different compounds, namely OOO, SOL, SLO, LSO (907.77), OLL, LOL, SLLn, LSLn, SLnL, OOLn, OLnO (903.79), LLL, OLLn, OLnL, and LOLn (901.78), with O being oleic acid, S, stearic acid, L, linoleic acid, and Ln, linolenic acid. Over the following years, the same research group published three more papers focused on the development of MALDI methods for the challenging detection of hidden hazelnut oil in extra virgin olive oil, each time using different classes of compounds as markers for the adulteration. In the first work [62], the polar fraction of oils was enriched and characterized using hydrophilic liquid chromatography micro-columns coupled with MALDI. Lysophosphatidylcholine (LPC) (16:0/0:0), LPC (18:1/0:0), and LPC (18:2/0:0) were identified and used as diagnostic compounds for the presence of hazelnut oil in EVOO to a level of 5%. The second application [63] exploited a modified Bligh–Dyer method for the selective extraction of phospholipids, present in seed oils at much higher concentration

levels and then used as markers for hazelnut in olive oil. The solution resulting from the combination of α-Cyano-4-hydroxycinnamic acid (176 mM) and tributylamine (equimolar) was used as both extraction solvent and MALDI matrix. The method was capable to detect adulterations at a 1% contamination level. The last work [64] used cold acetone precipitation followed by in-solution tryptic digestion and final MALDI analysis for the revealing of hazelnut peptide markers arising from the main hazelnut proteins Cor a 9, Cor a 11, and Cor a 1. These markers can potentially be used for the determination of hazelnut traces in oils and processed foods. SDS–PAGE analysis confirmed the presence of hazelnut proteins in hazelnut extracts with molecular masses in the range of 10–60 kDa.

Arlorio and colleagues [65] reported that the adulteration of extra virgin olive oil with solvent-extracted hazelnut oil can be directly traced down to a 1% level by SDS–PAGE analysis of hazelnut proteins, even if a MALDI analysis was indeed necessary to confirm the identity of the alleged allergens, i.e., two oleosin isoforms and Cor a 9. MALDI-TOF, combined with unsupervised hierarchical clustering, principal component analysis, and Pearson's correlation analysis, was also successfully adopted [66] to detect very low amounts (0.5%) of corn oil in EVOO.

As described in the work of Calvano at al. [61], when the fraud to be revealed concerns the presence of seed oils in EVOO, it may be sufficient to target their TAGs profile to characterize the samples and eventually determine the presence of the adulterant product. In fact, two more applications based on MALDI in conjunction with statistical approaches were successfully developed for the detection of sunflower (or refined) [67] and canola [68] oils in EVOO, respectively, using the TAGs profiles present in the relevant mass spectra.

A hardly detectable adulteration is represented by the addition of sunflower oil to poppy seed oil because of the similar fatty acid ratios. In fact, a further application [69] reported the successful MALDI-TOF MS detection of mixtures of sunflower oil with high levels of triolein (high-oleic acid type) down to the 5–10% level, but the same approach failed to discover adulteration of pure poppy seed oil by sunflower oil.

Several works were focused on the quality evaluation of edible oils (mainly EVOO). Taking into account that squalene concentrations in olive oil vary considerably depending on the cultivar, its determination in this matrix should be able to discriminate between varieties. Thus, Zambonin at al. [70] reported on the LDI-TOF MS determination of squalene and derived oxides involved in the biosynthetic pathway of cholesterol in extra virgin olive oil. The same research group used the same matrix-less approach to characterize olive and sunflower oils before and after thermally assisted oxidation [71]. The obtained MS profiles provided information about the identity of thermally induced oxidation products, such as TAGs epoxy/hydroxy, hydroperoxy derivatives, and β-scission products, making the method a tool to rapidly check the quality of cooking oil. TAGs thermal oxidation of sunflower and olive oils was also studied by Picariello at al. two years later [72]. To increase the detection of oxidized components, a chromatographic separation of polar and non-polar compounds was performed on silica gel before MALDI analysis. Tri- and diacylglycerols, TAGs oxidative dimers, oxidized TAGs, and TAGs fragments arising from the β-scission of linoleyl, peroxy, and alkoxy radicals were observed in the relevant spectra.

For authentication and characterization purposes, detailed MALDI TAG profiles of olive oils were also successfully obtained from samples coming from six different cultivars [73] and of two different varieties grown in the same area at different olive ripening stages [74].

Shen and co-workers [75] optimized a matrix solid-phase dispersion (MSPD) procedure to extract several phospholipids from olive fruit and oil samples, exploiting the ability of the sorbent (TiO_2 nanoparticles) to selectively interact with the phosphate group of the analyte by a chelating bidentate bond. After elution, MALDI-TOF analysis in both positive and negative ion modes was performed. The method proved to possess a great potential in lipidomic fingerprinting of olive samples for quality control.

Different analytical instrument, namely MALDI, GC, and LC-MS, were synergically used to perform a study of the lipid composition of commercial extra virgin and virgin

olive oils [76], in an attempt to define specific lipid patterns and/or establish a set of lipid markers representing the identity of a specific oil. Significant differences between EVOOs and VOOs were found, and five classes of phospholipids were identified in the polar lipid fraction, with remarkable variations in phosphatidylcholines.

MALDI-SpiralTOF was employed [77] to obtain TAG fingerprints relevant to sesame, sunflower, and olive oils to draw traceability and authenticity information. The application of PCA allowed the discrimination of Istrian olive oils from those coming from other Croatian coastal regions. Furthermore, high energy collision-induced dissociation (CID) MALDI-TOF/TOF analysis of TAGs was suggested as a mean that could correlate oil TAGs to the geographical origin, analyzing a high number of samples that can provide statistically significant data. A multi-instrumental analysis (MALDI for TAGs, GC-MS for fatty acids, and NIRS for non-selective analysis) coupled to PCA and partial least square-discriminant analysis (PLS-DA) was also used [78] for geographical origin sample grouping evaluation and for testing of predictive capabilities of measured variables on accurate classification of EVOO regional category.

A synergic MALDI-TOF/GC-MS approach was proposed to study the different components of pomegranate oil [79] and of several nut oil varieties [80], respectively. In particular, MALDI confirmed its ability and reliability to profile the TAG component, showing unique fingerprints that allows to differentiate pomegranate from most edible oils and nut oils exhibiting quite similar fatty acid composition (hazelnut, pistachio, and beech oil) between each other.

Unique TAGs profiles were also displayed [81] by different Amazonian oils and fats, characterized by MALDI-TOF without prior separation. The variable combinations of fatty acids provided detailed information that could permit the development of a database from spectra to be used for fast and reliable typification, screening, and quality control. The triacylglycerol content of shea butter fat, palm kernel oil, and peanut oil was also rapidly characterized [82]. The potential of the method as a tool for quality control of the matrices under study was demonstrated by the detection, in addition to intact and specific triacylglycerols, of oxygenated and fragmented TAGs, likely arising from poor handling and production processes.

2.3. Fish and Meat

Fish represents and is perceived by consumers as a healthy and nutritious food resource. However, a common problem in the fish processing industry is adding or replacing cheap fish instead of expensive ones, as an accidental event due to the lack of experience or as a deliberate fraud. An adequate level of protection is then required to ensure seafood quality and safety, making the development of rapid, effective, accurate, and reliable analytical methods the key to effectively supervising the market. This need has prompted the issue of directives and regulations for quality control and encouraged the development of innovative MALDI analytical methodologies, almost always based on proteomic techniques.

Highly specific mass spectrometric profiles from 25 different fish species were obtained using a new MALDI method [83] meant for the fast assessment of authenticity and fraudulent substitutions. Specific protein signals at m/z values around 11 kDa were selected as markers to discriminate the various species, while a structural characterization permitted to identify some major fish allergens arising from parvalbumin.

In a pilot study [84], three freshwater fish species were discriminated based on the cluster analyses of the overall profiles generated by the MALDI analyses of muscle and liver tissues, after a simple single-step extraction procedure. Each tissue provided species-specific profiles, even if muscle is more suitable for routine controls since fillets are more commonly commercialized. The authors pointed out that the clear discrimination of the species was possible even though the settings and statistical algorithms used were originally designed for the analysis and identification of bacteria and fungi. Then, they suggested that performing an optimization of mass spectral analysis and data processing

targeted on fish species could lead to exhaustive evaluation of the potential of MALDI analysis for studies on freshwater fishes.

The analysis of muscles taken from two closely related fish species was undertaken by two-dimensional gel electrophoresis (2-DE) [85] and the interspecies differences between the protein spots, which could be useful for their differentiation, were visually identified. MALDI-TOF MS and/or LC-MS were then necessary to identify 19 proteins, some of which resulted to be specific for each species. Another MALDI method [86] for the profiling of protein extracted from fish muscle was reported in a book chapter by Siciliano at al. for fish authentication purposes and to detect fraudulent substitutions.

Since universal sample preparation protocols prior to MALDI analysis were available to other species but not to fish, Spielmann at al. [87] tested the performances of five preparation protocols to verify the capability to produce reproducible and high-quality spectra dependent on storage conditions and food processing, and eventually differentiate between different fish species. After the optimization of the best protocol, it was concluded that MALDI could be used for the purpose as soon as a valid species database is available. This need was evidently shared by Stahl and co-workers, who almost simultaneously used MALDI to establish a database [88] of protein patterns from 54 fish species susceptible to fraud, in order to detect and prevent substitution, characterized by low intraspecies but high interspecies variability.

MALDI-TOF combined with multivariate analysis was exploited [89] for the development of a method to directly analyze fish skin or muscle tissues surface, for authentication purposes. Samples were quickly discriminated, hinting at potential future developments for the authentication of seafood in general and/or other protein food products.

Another study centered on the comparison of several one-step sample pre-treatment protocols of fish muscle tissues, prior to MALDI determination of the relevant extracts, was recently carried out [90] by Wang and colleagues. The best results in terms of repeatability and spectral resolution were obtained by boiling samples in 0.1 M trifluoroacetic acid (TFA) for 5 min, permitting to discriminate between different fish samples, when combined with similarity coefficient-based analysis for their mass spectra.

MALDI also turned out to be a good system for assessing fish freshness. For instance, the effect of storage time on fish muscle proteins was investigated using 2-DE coupled to MALDI [91], permitting the identification of three altered proteins. More recently [92], the same approach was involved in the analysis of fish samples, both fresh and stored in a refrigerator for different days, looking for protein markers for its freshness. It was found that the comparison of three specific proteins, l-lactate dehydrogenase, adenylate kinase isoenzyme 1, and myosin heavy chain, permitted to trace the freshness of the products. In a different study, the vitreous fluid of the eyes was taken from fishes subjected to different days of post-mortem storage, which was immediately analyzed by MALDI-TOF to evaluate fish spoilage [93]. Software spectra processing allowed the identification of four m/z ions able to differentiate between the tested days of storage, although a limited applicability was shown within the end of the tested period.

A further study [94] of a comparison of different protein extraction protocols from seafood (marine mussel) prior to 2-DE was conducted by Campos and co-workers. Then, MALDI-TOF/TOF analysis of the gels was performed and proteins with several functions, such as energy metabolism, cell signaling and regulation, and stress response, were identified. The method was a precious tool to investigate the protein expression in the species under investigation and potentially in other affiliated species.

Several analytical methods are used in the meat industry for detecting contamination, adulteration, and authenticity, to safeguard safety, and to reassure consumers, who are increasingly aware and attentive to the quality of the food they consume. Two MALDI methods to determine the origin of raw and processed meat (pork, beef, horse, veal, and chicken) and of gelatin (pork or beef), respectively, were developed by Flaudrops and colleagues [95]. In the first method, intact proteins were determined in linear mode prior to cluster analysis, allowing the separation of meat into distinct mass spectra clusters depend-

ing on the origin. In the second method, gelatin was digested with trypsin and analyzed in reflectron mode. The relevant spectra showed specific profiles that permitted to distinguish pork from bovine gelatin (1% of gelatin in spiked candies and 20% of pork gelatin in beef gelatin). Although less sensitive compared to other approaches, these methods are fast and easy to perform and can be conveniently used for fast screening controls.

An approach to reveal the differences in protein expression between young and old buffalo meat looking for biological markers of tenderness was performed by 2-DE coupled to MALDI-TOF/TOF [96]. Structural proteins with expression levels associated with meat tenderness were successfully identified through digestion and MS/MS analysis of selected gel spots. Moreover, the study demonstrated that through the ageing process, it was possible to reduce the variation in tenderness between young and old buffalo meat that, consequently, requires different processing strategies for their effective utilization. The 2-DE-MALDI combination was also exploited [97] to compare meat quality traits and to identify different protein expression between low and high pH pig muscles. Fourteen proteins that differed in spot density between the two groups were identified and nine of them involved in meat quality attributes significantly increased in high-pH muscles. The whole results obtained in the work provided useful information to understand the molecular mechanism at the base of meat quality.

Furthermore, the 2-DE-MALDI-TOF/TOF approach was again used [98] to assess the protein modifications occurring in the duck breast muscle collected form three breeds during the early post-mortem storage period. Evidence of changes in the protein expressions for each breed were found in several spots, some of which (10 for each breed) were subjected to MS/MS analysis, which allowed the identification of at total of 22 proteins.

2.4. Fruits and Vegetables

Intake of fruits and vegetables is highly recommended to promote good health due to their concentrations of bioactive compounds, including vitamins, minerals, antioxidants, and fiber. Indeed, the quality of these precious foods must be safeguarded and monitored using suitable analytical methods. MALDI-TOF was adopted for the development of many related applications. For instance, fruit skins were analyzed in two different works. It was demonstrated [99] that anthocyanins profiles of the berry skins of 23 red grape varieties can be easily and rapidly obtained by MALDI-TOF, enabling the identification of several varietal traits useful for the differentiation of authentic cultivars from hybrid ones on a molecular basis. Very recently, proanthocyanidin profiles of different fruit skins were obtained [100] by MALDI-TOF coupled to multivariate analysis, which proved to be a useful tool to evaluate authenticity in mixtures of different proanthocyanidin.

Three different MALDI studies were focused on the assessment of the authenticity of saffron, an expensive spice made from *Crocus sativus* L. dried stigmas, which is often the object of frauds. MALDI MS imaging (MSI) was successfully applied [101] to the determination of different crocins species in saffron. This original approach was also compared to a traditional one, i.e., MALDI analysis after solvent extraction, and the relevant results were found in good agreement. The other two studies were both performed by Aiello at al., using MS or MS/MS as mass analyzer and curcumin as the non-isotopic isobaric internal standard. In the first one [102], powdered saffron was subjected to a one-step sample pre-treatment and subjected to MALDI analysis. Crocins C-1–C-6, flavonols, unknown highly glycosylated crocins C-7, C-8, and C-9, and carotenoid-derived metabolites were detected. The method was shown to be fast, sensitive, reproducible, and suitable for routine quality controls, including the assessment of adulterations, as ascertained through the analysis of commercial samples. In the second one [103], picrocrocin was used as a saffron authenticity marker. Again, a rapid and simple method was developed, and very good quantitation parameters were obtained, with LOD (47.63 ppm) comparable or even lower than those obtained with other approaches.

The high demand for cereals, a major part of the diet in most countries providing nutrients such as vitamins, minerals, carbohydrates, fats, and proteins, makes relevant

frauds a severe global problem. Sequenom® MassARRAY® (Agena Bioscience, San Diego, CA, USA) MALDI-TOF MS, a reliable platform for detection and validation of single nucleotide polymorphisms (SNPs) for varietal analysis, was used to target specific genes in order to genotype and differentiate 35 barley varieties [104]. Information was drawn from the majority (33) of the tested loci (45), permitting the generation of a unique barcode of SNPs for each barley cultivar. This reliable and fast approach can potentially identify more than 150,000 SNPs per day, making the platform a suitable alternative for cereal varieta identification.

Jin at al. [105] used 2-DE followed by MALDI-TOF to compare the proteome extracted from barley malts of two selected cultivars, to find correlations between the protein content and malt qualities. Almost 700 total spots were detected; most were shared by the two cultivars, 377 of which were attributed to 192 proteins, mainly enzymes and enzyme inhibitors. The same research group performed another comparative study on green malts from two cultivars using two-dimensional fluorescent difference gel electrophoresis (2D-DIGE) [106]. Several metabolic proteins were identified by MS/MS and significant differences between cultivars were detected, suggesting potential applications for malt quality assessment. MALDI-TOF and two-dimensional difference gel electrophoresis (2D-DIGE) were also used by Fernando at al. [107] in a differential proteomic study on wheat grain, grown under normal CO_2 concentration and Free Air CO_2 Enrichment, respectively. It was found that a decrease of 9% in the protein content, in particular glutenin high molecular weight subunits associated with lower flour rheological properties and bread quality, occurred at higher CO_2 concentrations.

Since soybean is a known source of allergens that can also be hidden in other food commodities, a MALDI-TOF/TOF study was developed [108] to identify potential markers of its presence. Soybean protein extracts were digested with trypsin, separated using an LC system and eventually subjected to MS/MS analysis. Peptides arising from G1 glycinin and β-conglycinin were identified and proposed as potential markers for the detection of soybean protein traces in processed foods. Furthermore, these peptides were found to be stable when subjected to simulated food processing reactions, such as denaturation, Maillard reaction, and oxidation.

Rapid, simple, and reliable MALDI-TOF methods has been also proposed for cultivar characterization of hazelnut kernels through proteomic analysis [109], for geographical origin discrimination (coupled to multivariate analysis) of fermented salted vegetables comparing the relevant mass fingerprints [110] and to understand the effect of organic and inorganic crop nourishments on the nutritional quality of yardlong bean through two-dimensional proteome profiling [111]. MALDI-TOF/TOF was used by Pinto at al. [112] for the untargeted analysis of dark chocolate from cocoa beans of different geographical areas to characterize the relevant metabolites (including sucrose, choline, sphingolipids, phospholipids, peptide material, and polyphenols) based on molecular weights and fragmentation patterns.

2.5. Other Matrices

Product quality, authentication, and identification of adulterants are ongoing challenges facing several other food commodities. Hence, other MALDI-based methods have been developed for the detection of different frauds in various matrices. MALDI coupled to capillary zone electrophoresis was successfully exploited [113] to rapidly detect cheap sweeteners (sucrose from cane or beet, starch hydrolysates) in orange juices by monitoring the variation of concentration ratio of low molecular mass saccharides, such as glucose, fructose, and sucrose, and/or the presence of compounds that are absent in the sugar profiles of citrus fruits.

Two other proteomic studies were devoted to the assessment of authenticity and traceability of wine. A fast approach proposed [114] the direct tryptic digestion and subsequent MALDI analysis of extracts of white wine produced from different *V. vinifera* cultivars. The detailed and peculiar peptide profiles present in the relevant mass spectra were converted

into simulated images that represented unique "mass codes" able to display differences between samples, suggesting their potential use for food quality assessment. The comparison of anthocyanin concentration, main organic acids and sugars, and proteomic profiles of berry with different geographical origin, grape variety, and ripening stage was performed by Fraige at al. [115]. In particular, 2-DE combined with MALDI was employed to obtain information about the proteome changes subjecting 128 gel spots to MS analysis, 80 of which were identified as proteins mainly expressed as a response to defense/stress or related to carbohydrate metabolism. A multivariate analysis of protein abundance was able to divide the analyzed samples in different groups according to the considered variables, clearly showing the potential of the approach to provide useful information for wine characterization.

Two strategies for the analysis of honey targeting different compounds were successfully developed to differentiate various types of honey and to detect adulterated samples, respectively. Won and colleagues [116] exploited the molecular weight differences (56 and 59 kDa, respectively) of major proteins of honey produced from different bee species to discriminate between two honey types by 2-DE coupled to MALDI analysis, while Qu at al. [117] targeted oligosaccharide and polysaccharide profiles to reveal adulterations by MALDI MS or MS/MS.

Edible insects are available on the European market in ground form, in which any visual identification is impossible, thus causing concrete risks of adulteration that imposes quality and safety controls of such products. A reliable MALDI method [118] was then developed for the detection of proteins in whole insect powder extracts. Species-specific mass spectra were obtained permitting the easy differentiation of the different species under investigation (buffalo worms, mealworms, crickets, and grasshoppers).

A further common fraud is represented by truffle counterfeiting, since different varieties are almost impossible to recognize visually, and less expensive species absorb the aroma of higher prized ones when closely stored together. MALDI analysis and clustering permitted [119] to distinguish seven *Tuber* species confirming misidentifications in 26% of commercial specimens. To the same purpose, MALDI-TOF was applied [120] for the generation of specific mass spectra from 73 truffle tubers belonging to eight different species. Both studies demonstrated the potential of MALDI-TOF to provide useful information for quality assurance and fraud control in the truffle market in a fast, reliable, and inexpensive way.

The entire food industry, as well as the field of dietary and sport nutritional supplements, suffers the occurrence of several frauds. *Echinacea* species (*E. purpurea* and *E. angustifolia*) are widely used in dietary supplements and their adulteration is a great concern. Greene and colleagues [121] developed a rapid automated sample-preparation system combined with MALDI analysis for the differentiation of *Echinacea* species by the obtained mass fingerprints, which was even able to confirm the published composition of a commercial product and identify signatures suggestive of additional product components. An approach involving in-solution digestion followed by MALDI-TOF was proposed for the fast and simple screening of food supplements declaring high value protein components [122]. In this case, contrary to the products label statements, proteins were absent or present at very low concentrations in most products, clearly indicating the potential of the method for quality control purposes. The results obtained by in solution digestion were validated by a comparison with SDS–PAGE followed by tryptic in-gel digestion.

3. Conclusions

The range of analytes typically targeted in MALDI-TOF MS analyses has expanded over the years from macromolecules, such as peptides and proteins, to smaller molecules, such as lipids, hydrocarbons, sugars, phenols, and many others, widening the possible applications of the technique, which has been projected towards fields not initially contemplated, including food quality evaluation and adulteration detection. Consequently, several MALDI-based applications for the fight against food frauds have been reported in the

literature over the years. The higher number of papers have been focused on milk, oils, fish and seafood, meat, fruits, and vegetables. In the case of milk, the target analytes have been mainly proteins and peptides and, to a minor extent, lipids and phospholipids. Oils were mostly characterized by means of triacylglycerols profiles, even if some studies focused on proteins/peptides and phospholipids were also reported. Again, proteomic studies were the most performed in matrices such as fish and meat as well as in fruit and vegetables samples, where smaller polyphenolic and carotenoid compounds were also determined. The MALDI approach has proved to be an excellent system for the determination of food fraud, allowing in many cases the development of reliable, fast, and cost-effective analytical methods, often requiring very simple sample pre-treatment protocols, and sometimes assisted by chemometrics. On these bases, also considering the noticeable number of recent papers available in the literature, a further increase of these applications is likely to be observed in the next future.

Funding: This research received no external funding.

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Data Availability Statement: Not applicable.

Conflicts of Interest: The authors declare no conflict of interest.

References

1. Robson, K.; Dean, M.; Haughey, S.; Elliott, C. A comprehensive review of food fraud terminologies and food fraud mitigation guides. *Food Control.* **2021**, *120*, 107516. [CrossRef]
2. European Comission. Food Fraud: What Does It Mean? Available online: https://ec.europa.eu/food/safety/food-fraud/what-does-it-mean_en (accessed on 5 April 2021).
3. Hong, E.; Lee, S.Y.; Jeong, J.Y.; Park, J.M.; Kim, B.H.; Kwon, K.; Chun, H.S. Modern analytical methods for the detection of food fraud and adulteration by food category. *J. Sci. Food Agric.* **2017**, *97*, 3877–3896. [CrossRef]
4. Morin, J.F.; Lees, M. *Food Integrity Handbook, A Guide to Food Authenticity Issues and Analytical Solutions*; Eurofins Analytics France: Nantes, France, 2018.
5. McGrath, T.F.; Haughey, S.A.; Patterson, J.; Fauhl-Hassek, C.; Donarski, J.; Alewijn, M.; van Ruth, S.; Elliott, C.T. What are the scientific challenges in moving from targeted to non-targeted methods for food fraud testing and how can they be addressed?—Spectroscopy case study. *Trends Food Sci. Technol.* **2018**, *76*, 38–55. [CrossRef]
6. Cavanna, D.; Righetti, L.; Elliott, C.; Suman, M. The scientific challenges in moving from targeted to non-targeted mass spectrometric methods for food fraud analysis: A proposed validation workflow to bring about a harmonized approach. *Trends Food Sci. Technol.* **2018**, *80*, 223–241. [CrossRef]
7. Gao, B.; Holroyd, S.E.; Moore, J.C.; Laurvick, K.; Gendel, S.M.; Xie, Z. Opportunities and challenges using non-targeted methods for food fraud detection. *J. Agric. Food Chem.* **2019**, *67*, 8425–8430. [CrossRef] [PubMed]
8. Rodionova, O.; Pomerantsev, A. Chemometric tools for food fraud detection: The role of target class in non-targeted analysis. *Food Chem.* **2020**, *317*, 126448. [CrossRef]
9. Rodriguez-Saona, L.; Allendorf, M. Use of FTIR for rapid authentication and detection of adulteration of food. *Annu. Rev. Food Sci. Technol.* **2011**, *2*, 467–483. [CrossRef] [PubMed]
10. Cozzolino, D. The role of vibrational spectroscopy as a tool to assess economically motivated fraud and counterfeit issues in agricultural products and foods. *Anal. Methods* **2015**, *7*, 9390–9400. [CrossRef]
11. Lohumi, S.; Lee, S.; Lee, H.; Cho, B.-K. A review of vibrational spectroscopic techniques for the detection of food authenticity and adulteration. *Trends Food Sci. Technol.* **2015**, *46*, 85–98. [CrossRef]
12. Sørensen, K.M.; Khakimov, B.; Engelsen, S.B. The use of rapid spectroscopic screening methods to detect adulteration of food raw materials and ingredients. *Curr. Opin. Food Sci.* **2016**, *10*, 45–51. [CrossRef]
13. Sobolev, A.P.; Thomas, F.; Donarski, J.; Ingallina, C.; Circi, S.; Marincola, F.C.; Capitani, D.; Mannina, L. Use of NMR applications to tackle future food fraud issues. *Trends Food Sci. Technol.* **2019**, *91*, 347–353. [CrossRef]
14. Power, A.C.; Néill, C.N.; Geoghegan, S.; Currivan, S.; Deasy, M.; Cozzolino, D. A brief history of whiskey adulteration and the role of spectroscopy combined with chemometrics in the detection of modern whiskey fraud. *Beverages* **2020**, *6*, 49. [CrossRef]
15. Hassoun, A.; Måge, I.; Schmidt, W.F.; Temiz, H.T.; Li, L.; Kim, H.-Y.; Nilsen, H.; Biancolillo, A.; Aït-Kaddour, A.; Sikorski, M.; at al. Fraud in animal origin food products: Advances in emerging spectroscopic detection methods over the past five years. *Foods* **2020**, *9*, 1069. [CrossRef]
16. Valand, R.; Tanna, S.; Lawson, G.; Bengtström, L. A review of Fourier Transform Infrared (FTIR) spectroscopy used in food adulteration and authenticity investigations. *Food Addit. Contam. Part A* **2019**, *37*, 19–38. [CrossRef]

17. Cozzolino, R.; De Giulio, B. Application of ESI and MALDI-TOF MS for triacylglycerols analysis in edible oils. *Eur. J. Lipid Sci. Technol.* **2010**, *113*, 160–167. [CrossRef]
18. Kaufmann, A. The current role of high-resolution mass spectrometry in food analysis. *Anal. Bioanal. Chem.* **2012**, *403*, 1233–1249. [CrossRef] [PubMed]
19. Castro-Puyana, M.; Herrero, M. Metabolomics approaches based on mass spectrometry for food safety, quality and traceability. *Trends Anal. Chem.* **2013**, *52*, 74–87. [CrossRef]
20. Black, C.; Chevallier, O.P.; Elliott, C.T. The current and potential applications of Ambient Mass Spectrometry in detecting food fraud. *Trends Anal. Chem.* **2016**, *82*, 268–278. [CrossRef]
21. Morisasa, M.; Sato, T.; Kimura, K.; Mori, T.; Goto-Inoue, N. Application of matrix-assisted laser desorption/ionization mass spectrometry imaging for food analysis. *Foods* **2019**, *8*, 633. [CrossRef]
22. Creydt, M.; Fischer, M. Food phenotyping: Recording and processing of non-targeted liquid chromatography mass spectrometry data for verifying food authenticity. *Molecules* **2020**, *25*, 3972. [CrossRef]
23. Stachniuk, A.; Sumara, A.; Montowska, M.; Fornal, E. 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.* **2021**, *40*, 3–30. [CrossRef]
24. FAO. *Milk Facts*; FAO: Rome, Italy, 2018; Available online: http://www.fao.org/3/I9966EN/i9966en.pdf (accessed on 15 March 2021).
25. FAO. *Food Outlook—Biannual Report on Global Food Markets*; FAO: Rome, Italy, 2020. [CrossRef]
26. Thompson, L.A.; Darwish, W.S. Environmental chemical contaminants in food: Review of a global problem. *J. Toxicol.* **2019**, *2019*, 2345283. [CrossRef]
27. Ulberth, F. Tools to combat food fraud—A gap analysis. *Food Chem.* **2020**, *330*, 127044. [CrossRef]
28. Montgomery, H.; Haughey, S.A.; Elliott, C.T. Recent food safety and fraud issues within the dairy supply chain (2015–2019). *Glob. Food Secur.* **2020**, *26*, 100447. [CrossRef]
29. Cozzolino, R.; Passalacqua, S.; Salemi, S.; Malvagna, P.; Spina, E.; Garozzo, D. Identification of adulteration in milk by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. *J. Mass Spectrom.* **2001**, *36*, 1031–1037. [CrossRef]
30. Cozzolino, R.; Passalacqua, S.; Salemi, S.; Garozzo, D. Identification of adulteration in water buffalo mozzarella and in ewe cheese by using whey proteins as biomarkers and matrix-assisted laser desorption/ionization mass spectrometry. *J. Mass Spectrom.* **2002**, *37*, 985–991. [CrossRef]
31. Sassi, M.; Arena, S.; Scaloni, A. MALDI-TOF-MS platform for integrated proteomic and peptidomic profiling of milk samples allows rapid detection of food adulterations. *J. Agric. Food Chem.* **2015**, *63*, 6157–6171. [CrossRef]
32. Russo, R.; Rega, C.; Chambery, A. Rapid detection of water buffalo ricotta adulteration or contamination by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. *Rapid Commun. Mass Spectrom.* **2016**, *30*, 497–503. [CrossRef]
33. Caira, S.; Nicolai, M.A.; Lilla, S.; Calabrese, M.G.; Pinto, G.; Scaloni, A.; Chianese, L.; Addeo, F. Eventual limits of the current EU official method for evaluating milk adulteration of water buffalo dairy products and potential proteomic solutions. *Food Chem.* **2017**, *230*, 482–490. [CrossRef]
34. Liland, K.H.; Mevik, B.-H.; Rukke, E.-O.; Almøy, T.; Skaugen, M.; Isaksson, T. Quantitative whole spectrum analysis with MALDI-TOF MS, Part I: Measurement optimisation. *Chemom. Intell. Lab. Syst.* **2009**, *96*, 210–218. [CrossRef]
35. Liland, K.H.; Mevik, B.-H.; Rukke, E.-O.; Almøy, T.; Isaksson, T. Quantitative whole spectrum analysis with MALDI-TOF MS, Part II: Determining the concentration of milk in mixtures. *Chemom. Intell. Lab. Syst.* **2009**, *99*, 39–48. [CrossRef]
36. Nicolaou, N.; Xu, Y.; Goodacre, R. MALDI-MS and multivariate analysis for the detection and quantification of different milk species. *Anal. Bioanal. Chem.* **2011**, *399*, 3491–3502. [CrossRef]
37. Calvano, C.D.; De Ceglie, C.; Monopoli, A.; Zambonin, C.G. Detection of sheep and goat milk adulterations by direct MALDI-TOF MS analysis of milk tryptic digests. *J. Mass Spectrom.* **2012**, *47*, 1141–1149. [CrossRef]
38. Calvano, C.D.; De Ceglie, C.; Aresta, A.; Facchini, L.A.; Zambonin, C.G. MALDI-TOF mass spectrometric determination of intact phospholipids as markers of illegal bovine milk adulteration of high-quality milk. *Anal. Bioanal. Chem.* **2012**, *405*, 1641–1649. [CrossRef]
39. Piras, C.; Ceniti, C.; Hartmane, E.; Costanzo, N.; Morittu, V.M.; Roncada, P.; Britti, D.; Cramer, R. Rapid liquid AP-MALDI MS profiling of lipids and proteins from goat and sheep milk for speciation and colostrum analysis. *Proteomes* **2020**, *8*, 20. [CrossRef]
40. Cunsolo, V.; Muccilli, V.; Saletti, R.; Foti, S. MALDI-TOF mass spectrometry for the monitoring of she-donkey's milk contamination or adulteration. *J. Mass Spectrom.* **2013**, *48*, 148–153. [CrossRef]
41. Di Girolamo, F.; Masotti, A.; Salvatori, G.; Scapaticci, M.; Muraca, M.; Putignani, L. A Sensitive and effective proteomic approach to identify she-donkey's and goat's milk adulterations by MALDI-TOF MS fingerprinting. *Int. J. Mol. Sci.* **2014**, *15*, 13697–13719. [CrossRef]
42. Calvano, C.D.; Monopoli, A.; Loizzo, P.; Faccia, M.; Zambonin, C. Proteomic approach based on MALDI-TOF MS to detect powdered milk in fresh cow's milk. *J. Agric. Food Chem.* **2013**, *61*, 1609–1617. [CrossRef] [PubMed]
43. Garcia, J.S.; Sanvido, G.B.; Saraiva, S.A.; Zacca, J.J.; Cosso, R.G.; Eberlin, M.N. Bovine milk powder adulteration with vegetable oils or fats revealed by MALDI-QTOF MS. *Food Chem.* **2012**, *131*, 722–726. [CrossRef]
44. Hinz, K.; O'Connor, P.M.; Huppertz, T.; Ross, R.P.; Kelly, A.L. Comparison of the principal proteins in bovine, caprine, buffalo, equine and camel milk. *J. Dairy Res.* **2012**, *79*, 185–191. [CrossRef] [PubMed]

45. Calvano, C.D.; De Ceglie, C.; Zambonin, C.G. Proteomic analysis of complex protein samples by MALDI–TOF mass spectrometry. *Methods Mol. Biol.* **2014**, *1129*, 365–380.
46. England, P.; Tang, W.; Kostrzewa, M.; Shahrezaei, V.; Larrouy-Maumus, G. Discrimination of bovine milk from non-dairy milk by lipids fingerprinting using routine matrix-assisted laser desorption ionization mass spectrometry. *Sci. Rep.* **2020**, *10*, 5160. [CrossRef]
47. Magenis, R.B.; Prudêncio, E.S.; Molognoni, L.; Daguer, H. A control method to inspect the compositional authenticity of minas frescal cheese by gel electrophoresis. *J. Agric. Food Chem.* **2014**, *62*, 8333–8339. [CrossRef]
48. Damário, N.; Delafiori, J.; Ferreira, M.S.; De Oliveira, D.N.; Catharino, R.R. Cheese lipid profile using direct imprinting in glass surface mass spectrometry. *Anal. Methods* **2015**, *7*, 2877–2880. [CrossRef]
49. Rau, J.; Korte, N.; Dyk, M.; Wenninger, O.; Schreiter, P.; Hiller, E. Rapid animal species identification of feta and mozzarella cheese using MALDI-TOF mass-spectrometry. *Food Control.* **2020**, *117*, 107349. [CrossRef]
50. Calvano, C.D.; Jensen, O.N.; Zambonin, C.G. Selective extraction of phospholipids from dairy products by micro-solid phase extraction based on titanium dioxide microcolumns followed by MALDI-TOF-MS analysis. *Anal. Bioanal. Chem.* **2009**, *394*, 1453–1461. [CrossRef]
51. Gasilova, N.; Gassner, A.-L.; Girault, H.H. Analysis of major milk whey proteins by immunoaffinity capillary electrophoresis coupled with MALDI-MS. *Electrophoresis* **2012**, *33*, 2390–2398. [CrossRef]
52. Calvano, C.D.; De Ceglie, C.; Zambonin, C.G. Development of a novel direct in-matrix extraction (DIME) protocol for MAL-DI-ToF-MS detection of glycated phospholipids in heat treated food samples. *J. Mass Spectrom.* **2014**, *49*, 831–839. [CrossRef]
53. Ebner, J.; Baum, F.; Pischetsrieder, M. Identification of sixteen peptides reflecting heat and/or storage induced processes by profiling of commercial milk samples. *J. Proteom.* **2016**, *147*, 66–75. [CrossRef] [PubMed]
54. Arena, S.; Salzano, A.M.; Scaloni, A. Identification of protein markers for the occurrence of defrosted material in milk through a MALDI-TOF-MS profiling approach. *J. Proteom.* **2016**, *147*, 56–65. [CrossRef]
55. Di Francesco, L.; Di Girolamo, F.; Mennini, M.; Masotti, A.; Salvatori, G.; Rigon, G.; Signore, F.; Pietrantoni, E.; Scapaticci, M.; Lante, I.; at al. A MALDI-TOF MS approach for mammalian, human, and formula milks' profiling. *Nutrients* **2018**, *10*, 1238. [CrossRef]
56. Martinez-Gonzalez, M.A.; Martin-Calvo, N. Mediterranean diet and life expectancy; beyond olive oil, fruits, and vegetables. *Curr. Opin. Clin. Nutr. Metab. Care* **2016**, *19*, 401–407. [CrossRef] [PubMed]
57. International Olive Council. Trade Standard Applying to Olive Oils and Olive-Pomace Oils, (2016) COI/T.15/NC No. 3/Rev. 11. Available online: https://www.internationaloliveoil.org/wp-content/uploads/2019/11/COI-T.15-NC.-No-3-Rev.-13-2019-Eng.pdf (accessed on 15 March 2021).
58. Frankel, E.; Bakhouche, A.; Lozano-Sánchez, J.; Segura-Carretero, A.; Fernández-Gutiérrez, A. Literature review on pro-duction process to obtain extra virgin olive oil enriched in bioactive compounds. Potential use of byproducts as alternative sources of polyphenols. *J. Agric. Food Chem.* **2013**, *61*, 5179–5188. [CrossRef]
59. Casadei, E.; Valli, E.; Panni, F.; Donarski, J.; Farrús Gubern, J.; Lucci, P.; Conte, L.; Lacoste, F.; Maquet, A.; Brereton, P.; at al. Emerging trends in olive oil fraud and possible countermeasures. *Food Control* **2021**, *124*, 107902. [CrossRef]
60. Meenu, M.; Cai, Q.; Xu, B. A critical review on analytical techniques to detect adulteration of extra virgin olive oil. *Trends Food Sci. Technol.* **2019**, *91*, 391–408. [CrossRef]
61. Calvano, C.D.; Palmisano, F.; Zambonin, C.G. Laser desorption/ionization time-of-flight mass spectrometry of triacylglycerols in oils. *Rapid Commun. Mass Spectrom.* **2005**, *19*, 1315–1320. [CrossRef] [PubMed]
62. Calvano, C.D.; Aresta, A.; Zambonin, C.G. Detection of hazelnut oil in extra-virgin olive oil by analysis of polar components by micro-solid phase extraction based on hydrophilic liquid chromatography and MALDI-ToF mass spectrometry. *J. Mass Spectrom.* **2010**, *45*, 981–988. [CrossRef]
63. Calvano, C.D.; De Ceglie, C.; D'Accolti, L.; Zambonin, C.G. MALDI-TOF mass spectrometry detection of extra-virgin olive oil adulteration with hazelnut oil by analysis of phospholipids using an ionic liquid as matrix and extraction solvent. *Food Chem.* **2012**, *134*, 1192–1198. [CrossRef]
64. De Ceglie, C.; Calvano, C.D.; Zambonin, C.G. Determination of hidden hazelnut oil proteins in extra virgin olive oil by cold acetone precipitation followed by in-solution tryptic digestion and MALDI-TOF-MS analysis. *J. Agric. Food Chem.* **2014**, *62*, 9401–9409. [CrossRef]
65. Arlorio, M.; Coisson, J.D.; Bordiga, M.; Travaglia, F.; Garino, C.; Zuidmeer, L.; Van Ree, R.; Giuffrida, M.G.; Conti, A.; Martelli, A. Olive oil adulterated with hazelnut oils: Simulation to identify possible risks to allergic consumers. *Food Addit. Contam. Part A* **2010**, *27*, 11–18. [CrossRef]
66. Di Girolamo, F.; Masotti, A.; Lante, I.; Scapaticci, M.; Calvano, C.D.; Zambonin, C.; Muraca, M.; Putignani, L. A Simple and effective mass spectrometric approach to identify the adulteration of the Mediterranean diet component extra-virgin olive oil with corn oil. *Int. J. Mol. Sci.* **2015**, *16*, 20896–20912. [CrossRef]
67. Jergovic, A.M.; Persuric, Z.; Saftic, L.; Kraljevic, S. Pavelic, evaluation of MALDI-TOF/MS technology in olive oil adulteration. *J. Am. Oil Chem. Soc.* **2017**, *94*, 749–757. [CrossRef]
68. Kuo, T.-H.; Kuei, M.-S.; Hsiao, Y.; Chung, H.-H.; Hsu, C.-C.; Chen, H.-J. Matrix-assisted laser desorption/ionization mass spectrometry typings of edible oils through spectral networking of triacylglycerol fingerprints. *ACS Omega* **2019**, *4*, 15734–15741. [CrossRef]

69. Krist, S.; Stuebiger, G.; Bail, S.; Unterweger, H. Detection of adulteration of poppy seed oil with sunflower oil based on volatiles and triacylglycerol composition. *J. Agric. Food Chem.* **2006**, *54*, 6385–6389. [CrossRef]
70. Zambonin, C.G.; Calvano, C.D.; D'Accolti, L.; Palmisano, F. Laser desorption/ionization time-of-flight mass spectrometry of squalene in oil samples. *Rapid Commun. Mass Spectrom.* **2005**, *20*, 325–327. [CrossRef]
71. Calvano, C.D.; Aresta, A.; Palmisano, F.; Zambonin, C.G.; Laser, A. Desorption ionization time-of-flight mass spectrometry in-vestigation on triacylglycerols degradation during thermal stressing of edible oils. *Anal. Bioanal. Chem.* **2007**, *389*, 2075–2084. [CrossRef]
72. Picariello, G.; Paduano, A.; Sacchi, R.; Addeo, F. MALDI-TOF mass spectrometry profiling of polar and nonpolar fractions in heated vegetable oils. *J. Agric. Food Chem.* **2009**, *57*, 5391–5400. [CrossRef]
73. Chapagain, B.P.; Wiesman, Z. MALDI-TOF/MS Fingerprinting of triacylglycerols (TAGs) in olive oils produced in the Israeli Negev Desert. *J. Agric. Food Chem.* **2009**, *57*, 1135–1142. [CrossRef]
74. Vichi, S.; Lazzez, A.; Grati-Kamoun, N.; Caixach, J. Modifications in virgin olive oil glycerolipid fingerprint during olive ripening by MALDI-TOF MS analysis. *LWT Food Sci. Technol.* **2012**, *48*, 24–29. [CrossRef]
75. Shen, Q.; Dong, W.; Yang, M.; Baibado, J.T.; Wang, Y.; Alqouqa, I.; Cheung, H.-Y. Lipidomic study of olive fruit and oil using TiO_2 nanoparticle based matrix solid-phase dispersion and MALDI-TOF/MS. *Food Res. Int.* **2013**, *54*, 2054–2061. [CrossRef]
76. Alves, E.; Melo, T.; Rey, F.; Moreira, A.S.; Domingues, P.; Domingues, M.R. Polar lipid profiling of olive oils as a useful tool in helping to decipher their unique fingerprint. *LWT Food Sci. Technol.* **2016**, *74*, 371–377. [CrossRef]
77. Persuric, Z.; Osuga, J.; Grbac, T.G.; Katalinic, J.P.; Kraljevic Pavelic, S. MALDI-SpiralTOF technology for assessment of triacylglycerols in Croatian olive oils. *Eur. J. Lipid Sci. Technol.* **2017**, *119*, 1500375. [CrossRef]
78. Peršurić, Ž.; Saftić, L.; Mašek, T.; Pavelić, S.K. Comparison of triacylglycerol analysis by MALDI-TOF/MS, fatty acid analysis by GC-MS and non-selective analysis by NIRS in combination with chemometrics for determination of extra virgin olive oil geographical origin. A case study. *LWT Food Sci. Technol.* **2018**, *95*, 326–332. [CrossRef]
79. Kaufman, M.; Wiesman, Z. Pomegranate Oil Analysis with Emphasis on MALDI-TOF/MS Triacylglycerol Fingerprinting. *J. Agric. Food Chem.* **2007**, *55*, 10405–10413. [CrossRef]
80. Bail, S.; Stuebiger, G.; Unterweger, H.; Buchbauer, G.; Krist, S. Characterization of volatile compounds and triacylglycerol profiles of nut oils using SPME-GC-MS and MALDI-TOF-MS. *Eur. J. Lipid Sci. Technol.* **2009**, *111*, 170–182. [CrossRef]
81. Saraiva, S.A.; Cabral Marcos, E.C.; Eberlin, N.; Catharino, R.R. Amazonian vegetable oils and fats: Fast typification and quality control via triacylglycerol (TAG) profiles from dry matrix-assisted laser desorption/ionization time-of-flight (MALDI−TOF) mass spectrometry fingerprinting. *J. Agric. Food Chem.* **2009**, *57*, 4030–4034. [CrossRef]
82. Badu, M.; Awudza, A.M.J. Determination of the triacylglycerol content for the identification and assessment of purity of shea butter fat, peanut oil, and palm kernel oil using maldi-tof/tof mass spectroscopic technique. *Int. J. Food Prop.* **2016**, *20*, 271–280. [CrossRef]
83. Mazzeo, M.F.; De Giulio, B.; Guerriero, G.; Ciarcia, G.; Malorni, A.; Russo, G.L.; Siciliano, R.A. Fish authentication by MALDI-TOF mass spectrometry. *J. Agric. Food Chem.* **2008**, *56*, 11071–11076. [CrossRef]
84. Volta, P.; Riccardi, N.; Lauceri, R.; Tonolla, M. Discrimination of freshwater fish species by matrix-assisted laser desorption/ionization-time of flight mass spectrometry (MALDI-TOF MS): A pilot study. *J. Limnol.* **2012**, *71*, 164–169. [CrossRef]
85. Barik, S.K.; Banerjee, S.; Bhattacharjee, S.; Das Gupta, S.K.; Mohanty, S.; Mohanty, B.P. Proteomic analysis of sarcoplasmic peptides of two related fish species for food authentication. *Appl. Biochem. Biotechnol.* **2013**, *171*, 1011–1021. [CrossRef]
86. Siciliano, R.A.; D'Esposito, D.; Mazzeo, M.F. Food authentication by MALDI MS: MALDI-TOF MS analysis of fish species. In *Advances in MALDI and Laser-Induced Soft Ionization Mass Spectrometry*; Cramer, R., Ed.; Springer International Publishing: Cham, Switzerland, 2016; pp. 263–277.
87. Spielmann, G.; Huber, I.; Maggipinto, M.; Haszprunar, G.; Busch, U.; Pavlovic, M. Comparison of five preparatory protocols for fish species identification using MALDI-TOF MS. *Eur. Food Res. Technol.* **2017**, *244*, 685–694. [CrossRef]
88. Stahl, A.; Schröder, U. Development of a MALDI–TOF MS-based protein fingerprint database of common food fish allowing fast and reliable identification of fraud and substitution. *J. Agric. Food Chem.* **2017**, *65*, 7519–7527. [CrossRef]
89. Shao, M.; Bi, H. Direct identification of fish species by surface molecular transferring. *Analyst* **2020**, *145*, 4148–4155. [CrossRef]
90. Wang, C.; Bi, H. Super-fast seafood authenticity analysis by one-step pretreatment and comparison of mass spectral patterns. *Food Control* **2021**, *123*, 107751. [CrossRef]
91. Zhao, J.; Li, J.; Wang, J.; Lv, W. Applying different methods to evaluate the freshness of large yellow croacker (*Pseudosciaena crocea*) fillets during chilled storage. *J. Agric. Food Chem.* **2012**, *60*, 11387–11394. [CrossRef]
92. Deng, X.; Lei, Y.; Yu, Y.; Lu, S.; Zhang, J. The discovery of proteins associated with freshness of Coregonus Peled muscle during refrigerated storage. *J. Food Sci.* **2019**, *84*, 1266–1272. [CrossRef] [PubMed]
93. Ulrich, S.; Beindorf, P.; Biermaier, B.; Schwaiger, K.; Gareis, M.; Gottschalk, C. A novel approach for the determination of freshness and identity of trouts by MALDI-TOF mass spectrometry. *Food Control.* **2017**, *80*, 281–289. [CrossRef]
94. Campos, A.; Puerto, M.; Prieto, A.; Cameán, A.; Almeida, A.M.; Coelho, A.V.; Vasconcelos, V. Protein extraction and two-dimensional gel electrophoresis of proteins in the marine mussel *Mytilus galloprovincialis*: An important tool for protein expression studies, food quality and safety assessment. *J. Sci. Food Agric.* **2012**, *93*, 1779–1787. [CrossRef]
95. Flaudrops, C.; Armstrong, N.; Raoult, D.; Chabrie, E. Determination of the animal origin of meat and gelatin by MAL-DI-TOF-MS. *J. Food Compos. Anal.* **2015**, *41*, 104–112. [CrossRef]

96. Kiran, M.; Naveena, B.M.; Reddy, K.S.; Shahikumar, M.; Reddy, V.R.; Kulkarni, V.V.; Rapole, S.; More, T.H. Understanding tenderness variability and ageing changes in buffalo meat: Biochemical, ultrastructural and proteome characterization. *Animal* **2016**, *10*, 1007–1015. [CrossRef]
97. Subramaniyan, S.; Kang, D.R.; Jung, Y.-C.; Choi, Y.-I.; Lee, M.J.; Choe, H.S.; Shim, K.S. Comparative studies of meat quality traits and the proteome profile between low pH and high pH muscles in longissimus dorsi of Berkshire. *Can. J. Anim. Sci.* **2017**, *97*, 640–649. [CrossRef]
98. Zheng, N.; Zhu, Z.; Xin, Q.; Zhang, Z.; Miao, Z.; Li, L.; Zhang, L.; Wang, Z.; Huang, Y. Differential protein profiles in duck meat during the early postmortem storage period. *Anim. Sci. J.* **2019**, *90*, 757–768. [CrossRef]
99. Picariello, G.; Ferranti, P.; Chianese, L.; Addeo, F. Differentiation of Vitis vinifera L. and hybrid red grapes by matrix-assisted laser desorption/ionization mass spectrometry analysis of berry skin anthocyanins. *J. Agric. Food Chem.* **2012**, *60*, 4559–4566. [CrossRef] [PubMed]
100. Esquivel-Alvarado, D.; Alfaro-Viquez, E.; Krueger, C.G.; Vestling, M.M.; Reed, J.D. Classification of proanthocyanidin profiles using matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) spectra data combined with multivariate analysis. *Food Chem.* **2021**, *336*, 127667. [CrossRef]
101. Pittenauer, E.; Rados, E.; Koulakiotis, N.; Tsarbopoulos, A.; Allmaier, G. Processed stigmas of *Crocus sativus* L. imaged by MALDI-based MS. *Proteomics* **2016**, *16*, 1726–1730. [CrossRef]
102. Aiello, D.; Siciliano, C.; Mazzotti, F.; Di Donna, L.; Athanassopoulos, C.M.; Napoli, A. Molecular species fingerprinting and quantitative analysis of saffron (*Crocus sativus* L.) for quality control by MALDI mass spectrometry. *RSC Adv.* **2018**, *8*, 36104–36113. [CrossRef]
103. Aiello, D.; Siciliano, C.; Mazzotti, F.; Di Donna, L.; Athanassopoulos, C.M.; Napoli, A. A rapid MALDI MS/MS based method for assessing saffron (*Crocus sativus* L.) adulteration. *Food Chem.* **2020**, *307*, 125527. [CrossRef]
104. Pattemore, J.A.; Rice, N.; Marshall, D.F.; Waugh, R.; Henry, R.J. Cereal variety identification using MALDI-TOF mass spec-trometry SNP genotyping. *J. Cereal Sci.* **2010**, *52*, 356–361. [CrossRef]
105. Jin, Z.; Mu, Y.-W.; Sun, J.-Y.; Li, X.-M.; Gao, X.-L.; Lu, J. Proteome analysis of metabolic proteins (pI 4–7) in barley (*Hordeum vulgare*) malts and initial application in malt quality discrimination. *J. Agric. Food Chem.* **2012**, *61*, 402–409. [CrossRef]
106. Jin, Z.; Cai, G.-L.; Li, X.-M.; Gao, F.; Yang, J.-J.; Lu, J.; Dong, J.-J. Comparative proteomic analysis of green malts between barley (*Hordeum vulgare*) cultivars. *Food Chem.* **2014**, *151*, 266–270. [CrossRef] [PubMed]
107. Fernando, N.; Panozzo, J.; Tausz, M.; Norton, R.; Fitzgerald, G.; Khan, A.; Seneweera, S. Rising CO_2 concentration altered wheat grain proteome and flour rheological characteristics. *Food Chem.* **2015**, *170*, 448–454. [CrossRef]
108. Cucu, T.; De Meulenaer, B.; Devreese, B. MALDI based identification of soybean protein markers—Possible analytical targets for allergen detection in processed foods. *Peptides* **2012**, *33*, 187–196. [CrossRef] [PubMed]
109. Ciarmiello, L.F.; Mazzeo, M.F.; Minasi, P.; Peluso, A.; De Luca, A.; Piccirillo, P.; Siciliano, R.A.; Carbone, V. Analysis of different European hazelnut (*Corylus avellana* L.) cultivars: Authentication, phenotypic features, and phenolic profiles. *J. Agric. Food Chem.* **2014**, *62*, 6236–6246. [CrossRef] [PubMed]
110. Yoon, S.R.; Kim, S.H.; Lee, H.W.; Ha, J.H. A novel method to rapidly distinguish the geographical origin of traditional fer-mented-salted vegetables by mass fingerprinting. *PLoS ONE* **2017**, *12*, e0188217. [CrossRef] [PubMed]
111. Kumar, D.K.; Mathew, D.; Nazeem, P.A.; Abida, P.S.; Thomas, C.G. A comparative proteome assay on the quality of yardlong bean pods as influenced by the organic and inorganic nourishment systems. *Acta Physiol. Plant.* **2017**, *39*, 265. [CrossRef]
112. Pinto, G.; Aurilia, M.; Illiano, A.; Fontanarosa, C.; Sannia, G.; Trifuoggi, M.; Lettera, V.; Sperandeo, R.; Pucci, A.P. From un-targeted metabolomics to the multiple reaction monitoring-based quantification of polyphenols in chocolates from different geographical areas. *J. Mass Spectrom.* **2021**, *56*, e4651. [CrossRef] [PubMed]
113. Žídková, J.; Chmelík, J. Determination of saccharides in fruit juices by capillary electrophoresis and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. *J. Mass Spectrom.* **2001**, *36*, 417–421. [CrossRef]
114. Chambery, A.; del Monaco, G.; Di Maro, A.; Parente, A. Peptide fingerprint of high quality Campania white wines by MALDI-TOF mass spectrometry. *Food Chem.* **2009**, *113*, 1283–1289. [CrossRef]
115. Fraige, K.; González-Fernández, R.; Carrilho, E.; Jorrín-Novo, J.V. Metabolite and proteome changes during the ripening of Syrah and Cabernet Sauvignon grape varieties cultured in a nontraditional wine region in Brazil. *J. Proteom.* **2015**, *113*, 206–225. [CrossRef]
116. Won, S.-R.; Lee, D.-C.; Ko, S.H.; Kim, J.-W.; Rhee, H.-I. Honey major protein characterization and its application to adulteration detection. *Food Res. Int.* **2008**, *41*, 952–956. [CrossRef]
117. Qu, L.; Jiang, Y.; Huang, X.; Cui, M.; Ning, F.; Liu, T.; Gao, Y.; Wu, D.; Nie, Z.; Luo, L. High-throughput monitoring of multiclass syrup adulterants in honey based on the oligosaccharide and polysaccharide profiles by MALDI mass spectrometry. *J. Agric. Food Chem.* **2019**, *67*, 11256–11261. [CrossRef] [PubMed]
118. Ulrich, S.; Kühn, U.; Biermaier, B.; Piacenza, N.; Schwaiger, K.; Gottschalk, C.; Gareis, M. Direct identification of edible insects by MALDI-TOF mass spectrometry. *Food Control.* **2017**, *76*, 96–101. [CrossRef]
119. El Karkouri, K.; Couderc, C.; Decloquement, P.; Abeille, A.; Raoult, D. Rapid MALDI-TOF MS identification of commercial truffles. *Sci. Rep.* **2019**, *9*, 17686. [CrossRef]
120. Klein, M.; Kielhauser, R.; Dilger, T. Optimized rapid and reliable identification of *Tuber* spp. by matrix-assisted laser de-sorption ionization time-of-flight mass spectrometry. *J. Mass Spectrom.* **2020**, *55*, e4655.

121. Greene, L.A.; Isaac, I.; Gray, D.E.; Schwartz, S.A. Streamlining plant sample preparation: The use of high-throughput robotics to process echinacea samples for biomarker profiling by MALDI-TOF mass spectrometry. *J. Biomol. Tech. JBT* **2007**, *18*, 238–244. [PubMed]
122. De Ceglie, C.; Calvano, C.D.; Zambonin, C.G. MALDI-TOF MS for quality control of high protein content sport supplements. *Food Chem.* **2015**, *176*, 396–402. [CrossRef] [PubMed]