

# We are IntechOpen, the world's leading publisher of Open Access books Built by scientists, for scientists

5,100

Open access books available

127,000

International authors and editors

145M

Downloads

Our authors are among the

154

Countries delivered to

TOP 1%

most cited scientists

12.2%

Contributors from top 500 universities



WEB OF SCIENCE™

Selection of our books indexed in the Book Citation Index  
in Web of Science™ Core Collection (BKCI)

Interested in publishing with us?  
Contact [book.department@intechopen.com](mailto:book.department@intechopen.com)

Numbers displayed above are based on latest data collected.  
For more information visit [www.intechopen.com](http://www.intechopen.com)



---

# Food Metabolomics: A New Frontier in Food Analysis and its Application to Understanding Fermented Foods

---

Oluwafemi Ayodeji Adebo, Patrick Berka Njobeh, Janet Adeyinka Adebiji, Sefater Gbashi and Eugenie Kayitesi

Additional information is available at the end of the chapter

<http://dx.doi.org/10.5772/intechopen.69171>

---

## Abstract

The emergence of food metabolomics, otherwise known as foodomics, has opened new frontiers and possibilities for scientists to characterize and simultaneously determine and obtain the comprehensive profile of the food metabolome. Qualitative and quantitative determinations of this metabolome offer insights into the underlying processes involved and details about the content of the food analytes. This had seemed technically challenging and impossible over time, but can now be done due to the advent of sophisticated analytical equipment and chemometric tools. The application of this technique offers enormous opportunities to obtain detailed information that can be correlated to various properties, functionalities and potentials in fermented foods. This chapter thus evaluated and documented studies presented in the literature on the food metabolomics study of fermented foods, with a view of appraising its prospects, applications and subsequent utilization in the study of fermented foods.

**Keywords:** foodomics, food metabolomics, fermentation, fermented foods, chemometrics

---

## 1. Introduction

Fermentation continues to be a viable food processing technique all over the world. This might be attributed to the ease and simplicity of the process and its numerous other benefits, including providing variety in foods, improving palatability and aesthetic value, detoxification and imparting desirable sensorial properties [1–3]. Furthermore, it plays significant role in conferring health promotion and functional benefits to fermented foods. In line with this are different

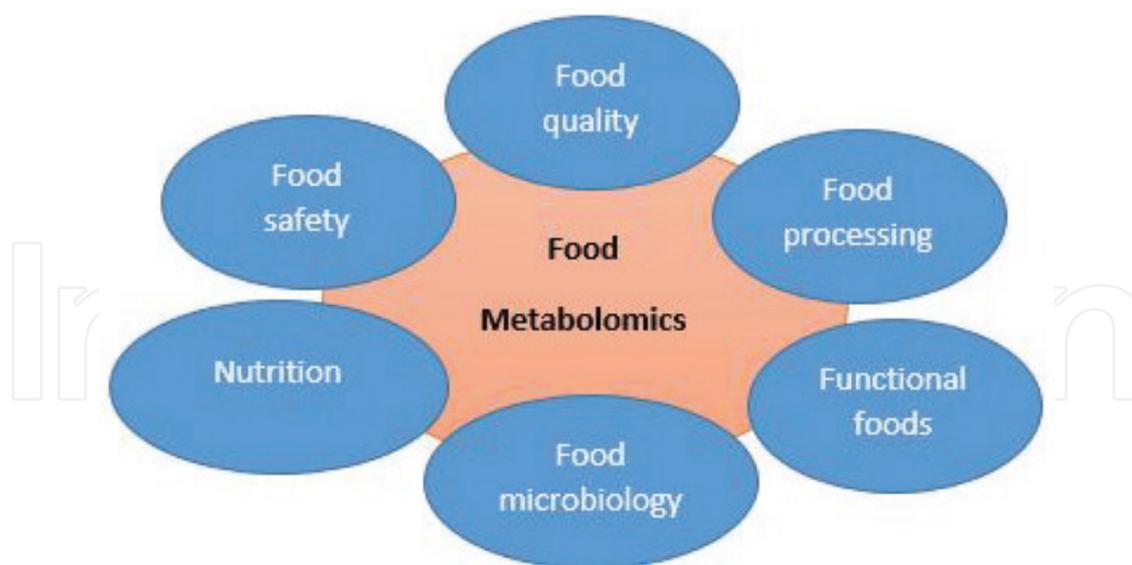
studies on fermented foods reporting their ability to reduce diarrhea, malnutrition, encourage child growth and development, exhibit nutraceutical and functional effects including being antidiabetic, antihypertensive, chemoprotective, reducing oxidative stress, cardiovascular diseases and possessing probiotic properties [1–8]. Sequel to these benefits and the ever growing market for functional foods, fermented food products are positioned as food sources that can improve consumer well-being and reduce the risk of diseases.

Although fermentation like other food processing techniques is needed for the transformation of food prior to consumption, it results in structural changes, formation, modification and/or degradation of compounds and an increase or decrease in these constituents could occur. Characterization and comprehensive monitoring of the metabolic, physicochemical, biochemical and structural changes occurring during the fermentation process have thus been relatively difficult. The advent of food metabolomics, also known as “foodomics” enables scientists to obtain detailed and comprehensive molecular profile of thousands of metabolites in foods, all in a single run [9, 10]. Food metabolomics thus presents a holistic approach of providing insight, resolving and identifying the complexities and multifunctionality of fermentation and its subsequent food products.

According to Cifuentes [9] and Garcia-Canas [11], food metabolomics is a valuable and promising tool for food processors and scientists to understand the metabolome of food, including its biochemistry and composition. Being one of the “omics” technology, it offers enormous opportunities to obtain detailed information that can be correlated to the functional and nutraceutical composition of foods. This chapter thus provides an overview of food metabolomics studies that have applied this to fermented foods in the literature and its prospects for further use.

## 2. Fundamentals of food metabolomics

Metabolomics itself is designated to mean a comprehensive analysis, study, identification and quantification of “as many small metabolites” as possible in a system at a specific time and condition through the use of omics technologies [12–18]. Related to this and taking a cue from earlier authors [9, 11, 19, 20], food metabolomics or foodomics can thus be defined as the study of “as many small metabolites” in food under a specific condition and time through the application of omics technologies. It is a discipline involving the combination of food, nutrition, advanced analytical and data processing techniques and bioinformatics. According to Wishart [21], metabolomics permits the simultaneous characterization of a variety of compounds and metabolites and thus offer food and nutrition scientists the privilege to acquire comprehensive and detailed molecular composition of food. This feature makes metabolomics applicable to different aspects of food science including food safety, food quality, functional foods, food microbiology, food processing and nutrition (**Figure 1**). Sequel to the potential embedded in food metabolomics, scientists are gradually utilizing advanced analytical strategies as opposed to the traditional and classical existing methodologies, which does not provide the much-needed information to understand the complexities in food. Such complexities are however compounded in fermented foods, containing a variety of nutrients, compounds and



**Figure 1.** Different aspects of food metabolomics.

volatiles with diverse concentrations, chemical structures, affinity and polarities. Food metabolomics thus provides the opportunity for understanding this multifaceted analyte.

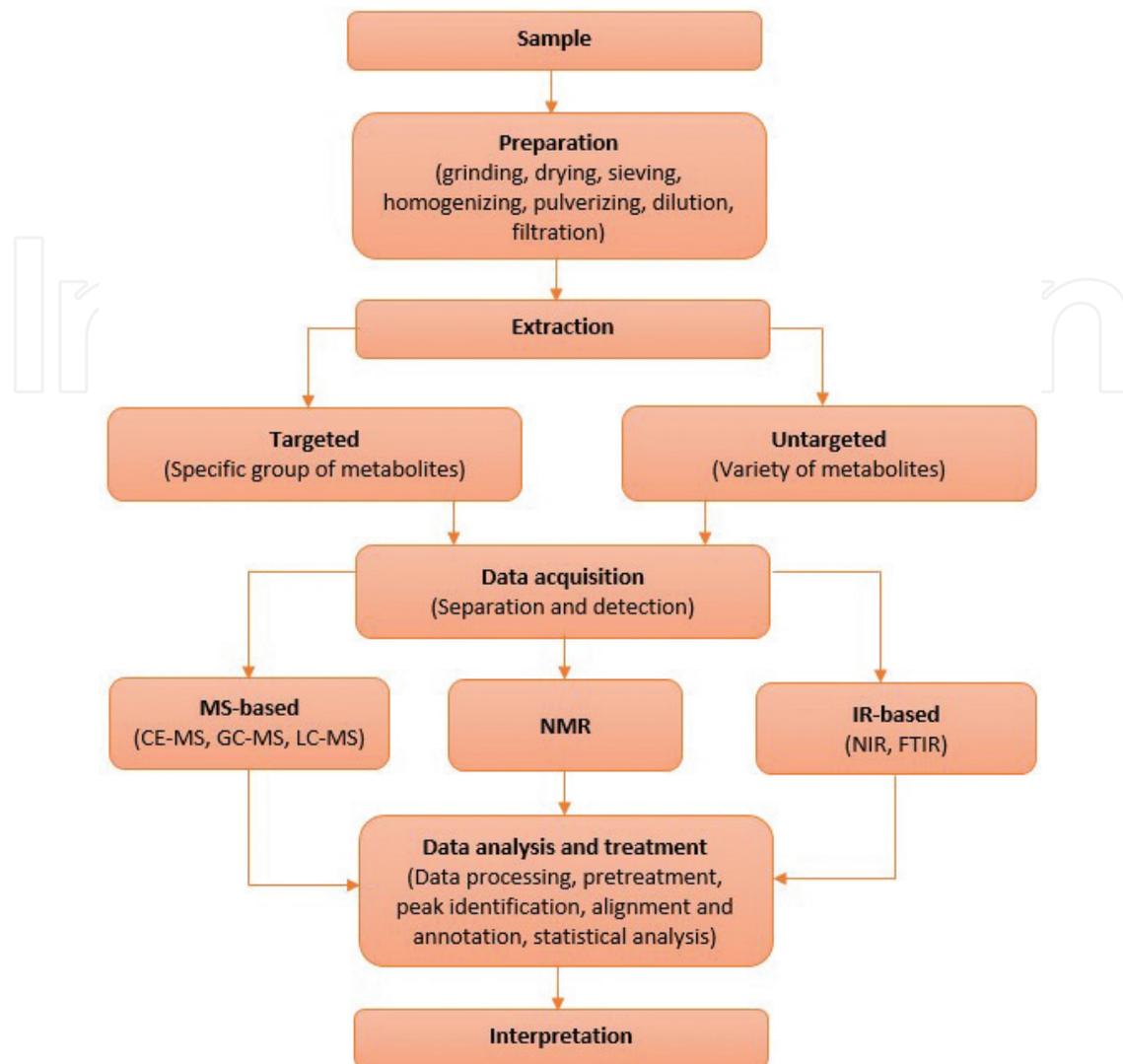
As with another metabolomics study, food metabolomics analyses can generally be classified into either targeted or untargeted. The targeted analysis focuses on a specific group of intended metabolites with such requiring subsequent quantification and identification [18, 22]. They are thus more detailed and require greater levels of extraction and purification prior to analysis. In contrast to targeted analysis, untargeted metabolomics analysis is broader and focused on the detection of a variety of metabolites to obtain fingerprints or patterns without essentially quantifying or identifying specific metabolites [16, 23, 24].

### 3. The process of food metabolomics analysis

Every metabolomics analysis consists of a sequence of steps prior to obtaining the data [16, 19, 24]. Not all the steps, depicted in **Figure 2** are not, however, necessary for food metabolomics or any other metabolomics studies. Major factors that determine the selection of steps include the type of study (targeted or untargeted), sample form (solid, liquid) and the available instrumentation and detection technique [gas chromatography-mass spectrometry (GC-MS), liquid chromatography-mass spectrometry (LC-MS), nuclear magnetic resonance (NMR), etc.] [16]. A description of these steps is nevertheless summarized in the ensuing sections of this chapter.

#### 3.1. Sample preparation

Sample preparation is essential and vital in any analysis. This is needed to prepare the sample into a “ready state” form, release the analyte (metabolites) available, reduce experimental error



**Figure 2.** Schematic presentation of the food metabolomics process.

and ensure the analytical procedure is reproducible. Grinding, size reduction and homogenization are some of the needed steps prior to analysis to ensure proper mixing and present a sample that is a true representative. The concentration of samples is also important with freeze-drying and use of liquid nitrogen commonly used in food metabolomics studies of fermented foods. This not only concentrates the metabolites but also reduces the possibility of losing heat labile components during conventional oven drying techniques. Both freeze drying and liquid nitrogen have been applied in the preparation of fermented foods in food metabolomics studies for *cheonggukjang* [25, 26], *meju* [27], *doenjang* [28] and cocoa beans [29]. Nevertheless, care must be taken to avoid the introduction of any form of unwanted variability throughout this step, which might result in significant experimental discrepancy, that would surpass biological variance. Sampling conditions and time should also be controlled to limit inconsistency in results.

### 3.2. Extraction

Among the many steps for food metabolomics studies, extraction is a vital and important one. Considering the varying and diverse constituents and composition of fermented foods,

including but not limited to amino acids, organic acids, phytochemicals, sugars, minerals, nucleic acids, vitamins and other volatile compounds, extraction may be somewhat tricky. Hence, extraction techniques to be utilized would be largely dependent on the form of study (targeted or untargeted), characteristics, number and quantity of metabolites of interest [15, 30, 31]. Extraction protocol would not thus be an express decision but rather influenced by the focus of analysis (study).

For targeted analysis, a suitable purification scheme and the use of appropriate internal standards is important [15]. This might not be the case for untargeted analysis due to the need to target as many metabolites as possible. Extraction techniques commonly used for fermented foods are solvents (methanol, chloroform, ethanol, acetonitrile) [27, 28, 32], similar to those used in other metabolomics studies [15, 17, 24, 31]. When the focus of the study is on specific non-volatile metabolites, derivatization may be required prior to analysis on GC-MS. This is necessary to make sure the samples are thermostable, increase volatility and improve the detectability of the analyte [16, 18].

### 3.3. Data acquisition

Data acquisition in form of separation and detection of metabolites is a key step in metabolomics studies. It essentially requires advanced analytical techniques, considering the complexity, diversity and number of metabolites to characterize in food [16, 18]. Separation techniques commonly used for food and fermented foods include high-performance liquid chromatography (HPLC), ultra-performance liquid chromatography (UPLC), gas chromatography (GC), capillary electrophoresis (CE) and ion mobility spectrometry (IMS) [16, 18, 21, 33]. Detection techniques include mass spectrometry (MS), NMR, high-resolution magic angle spinning (HRMAS) NMR, Fourier transform (FT) NMR, near infrared spectroscopy (NIR) and Fourier transform infrared spectroscopy (FTIR) [15, 16, 18, 21]. A detailed review and working principle of these separation and detection techniques have been presented in the literature and can be consulted for further reading [15, 18, 21, 24, 30, 31, 34, 35].

In the studies of fermented foods using metabolomics, most separation are either done by GC or LC (for polar compounds), while detection is done majorly by MS with few other studies reporting the use of NMR and FTIR. A major consideration and factor in the use of GC and LC is their higher sensitivity and separation. While GC-MS is usually utilized for the determination of primary metabolites i.e., carbohydrates, amino acids, organic acids, fatty acids and phytochemicals, LC-MS are frequently employed for secondary metabolites including alkaloids, flavonoids, phenolic acids, peptides, polyamines and saponins [31, 36]. As indicated by Tugizimana et al. [24], developments towards the enhancement of chromatographic include the use of multi-dimensional separation systems such as two-dimensional liquid chromatography (LC × LC) and two-dimensional gas chromatography (GC × GC). Furthermore, the use of better MS platforms including time of flight (TOF), Orbitrap, MS × MS/MS<sup>n</sup> provides better resolution, higher scan speeds, detailed fragmentation information, higher resolution, selectivity and better molecular specificity as seen with the Pegasus HRT GC. For separation, MS is most preferred and coupled with either GC or LC, it allows for the comprehensive evaluation and discrimination of compounds [18]. It should, however, be noted that due to the varying behaviors, polarity, volatility, structure, configuration, solubility and molecular weight of different metabolites in fermented

foods, a single data acquisition technique for the detecting and separating all these components is quite impossible. A combination of different techniques would rather provide a better analytical potential for a full metabolomics study.

### 3.4. Data analysis and treatment

Metabolomic studies are quite synonymous with the generation of a large amount of data, that may be somewhat confusing at first. Subsequent analysis of such high-throughput data can be roughly divided into two: pretreatment and analysis [37]. Handling these huge data would require an automated software for quantification and identification [24]. Pretreatment basically involves alignment, normalization, compound identification, centering, transformation, scaling, removing baseline artefacts and peak picking [16, 24, 38, 39], in order to convert the raw data set into a form that can be utilized for subsequent analysis. Succeeding analysis of the cleaned data in food metabolomics studies are majorly done using different chemometric tools, to provide a description and understanding of the variations and/or similarities in the metabolites. Wold [40] has defined chemometrics as a branch of science concerned with the data analysis (extracting information from data), ensuring that the data set contains maximum information using several mathematical multivariate data analysis (MVDA) tools.

Depending on the purpose of the food metabolomics study, there are three major categories of MVDA. These are exploratory/informative, classification/discrimination and regression/prediction [16, 38, 41]. While informative analyses are focused on identification and quantification to obtain sample intrinsic information (such as the development of metabolite databases and the discovery of biomarkers), discriminative analyses are majorly aimed at finding differences between samples/treatments [16, 42]. In contrast, predictive models are focused on quantification and prediction of a variable that may be difficult to quantify [16, 38]. MVDA tools commonly used in food metabolomics studies include artificial neural networks (ANN), principal component analysis (PCA), orthogonal projection to latent structures-discriminant analysis (OPLS-DA), partial least square discriminant analysis (PLS-DA), principal component regression (PCR), hierarchical cluster analysis (HCA), canonical correlation analysis (CCA) and others [16, 38, 43]. Detailed strategies, algorithms and explanation on these MVDA techniques have been described in detail elsewhere [24, 39, 43–46].

## 4. Food metabolomics of fermented foods

Food metabolomics has been applied and adopted in the study of different foods in the literature [11, 16–18, 21, 33, 47, 48]. Specifically, for fermented foods, which is the focus of this chapter, it is conventionally used to observe, monitor metabolite changes occurring during fermentation and to investigate the composition of such fermented food. Such knowledge has assisted in providing a comprehensive understanding of the fermentation process and probably predict sensory, nutritional, functionality and nutraceutical quality of the final fermented product. Few studies presented in the literature on food metabolomics studies of fermented foods are summarized in **Table 1**. This section of this chapter would thus focus on the

documented changes in metabolite groups and the use of metabolomics in understanding the modifications occurring during the fermentation process of these foods.

Metabolites produced during the fermentation of a Korean cuisine called *cheonggukang*, have been investigated by several authors [25, 26, 49–51] (**Table 1**). Using  $^1\text{H}$  NMR, Choi et al. [25] observed a decrease in sugars and citric acid with fermentation time. Acetic acid, phenylalanine and tyrosine however increased with time. Baek et al. [49], reported a total of 5 sugar alcohols, 10 sugars, 7 organic acids and 20 amino acids in the same product after obtaining it using different *Bacillus* sp. with subsequent analysis on gas chromatography-time of flight mass spectrometry (GC-TOF-MS). Most of the amino acids showed increasing amounts with time, sugars and sugar alcohols (arabitol, ribitol, sorbitol, myoinositol and lactitol) showed decreases, whereas there were variations in organic acids. Similar occurrences and variations in amino acids, organic acids and also fatty acids, carbohydrates, soyasaponins, isoflavonoids and nucleosides were observed using different metabolomics techniques [26, 50, 51].

Chen et al. [52] reported the occurrence of 28 metabolites including 13 amino acids, six organic acids, three organic bases and sucrose in fermented crab paste as analyzed on NMR. Using PCA and OPLS-DA the authors were able to observe a decline in taurine, betaine, trigonelline, trimethylamine-N-oxide and inosine with an accumulation of sugars and hypoxanthine. 53 compounds including organic acids, alcohols, sugars, amino acids were identified from the metabolomic profiling of *daju* fermented with *Bacillus licheniformis* [53]. Using NMR and PCA, the authors observed a decomposition of polymers such as protein, starch and cellulose to smaller monomers and accumulation of saccharides. *Doenjang*, a Korean delicacy has been studied using food metabolomics techniques (**Table 1**). Characterization and profiling on  $^1\text{H}$  NMR, GC-MS, GC-TOF-MS and data analysis on PCA, PLS-DA revealed the presence of amino acids, sugars and sugar derivatives and organic acids in *doenjang* [28, 54]. Using PCA, Yang et al. [54] was able to discriminate *doenjang* samples fermented for different days and reported increasing levels of amino acids, with no significant change in sugars and variation in the levels of fatty acids. Likewise, Lee et al. [28] observed an increase in monosaccharides, sugar alcohols and most amino acids during fermentation of *doenjang*. Variations were also observed in the levels of organic acids, fatty acids isoflavones and soyasaponins [28]. Kang et al. [27], reported a decrease in the concentration of citric acid during fermentation, with variations in the quantities of peptides, amino acids, nucleosides, organic acids and urea cycle intermediates were reportedly altered throughout the fermentation process.

Using both GC-MS, high-performance liquid chromatography coupled to a diode array detector (HPLC-DAD) in combination with hierarchical cluster analysis (HCA), a strong correlation was observed between volatiles, flavonoids and polyphenolic compounds of two types of wheat dough [55]. The authors observed a general increase in polyphenol content of the wheat doughs, but a diverse metabolite profile in the two wheat substrates used. Likewise, Mayorga-Gross et al. [29] investigated the metabolites changes occurring during cocoa fermentation on an ultra-high performance liquid chromatography with electrospray ionization quadrupole time of flight mass spectrometry (UPLC-ESI<sup>+</sup>-Q-TOF-MS) system and adopted a PLS-DA model for data processing. The clustering of ions according to retention times and mass spectrum on the PLS-DA model yielded a total of 37 discriminating metabolites. Sugars,

Produce	Raw material	Metabolite group	Metabolite forms	Data acquisition method	Data processing technique	Reference
<i>Cheonggukjang</i>	Soybean	Al <sup>a</sup> ↑↓	1, 2, 3, 4-tetrakis[(trimethylsilyl)oxy]-butane, 2, 3-bis (trimethylsilyl)-butane, δ-tocopherol, γ-tocopherol, D-ribose, tyramine, glycerol, hydroxylamine, phytol	<sup>1</sup> HNMR*,CE-TOF-MS*, GC-FID <sup>b</sup> ,GC-TOF-MS*,LC-MS/MS*	PCA, PLS-DA	[25, 26, 49–51]
		Am <sup>b</sup>	1,3-diamino-propane, phenethylamine, putrescine, tryptamine, serotonin, spermidine			
		AA <sup>c</sup>	α-aminobutyric, β-alanine, γ-aminobutyric (GABA), g-aminobutyric, 2, 6-diaminopimelate, alanine, amino adipate, arginine, asparagine, aspartic, betanine, choline+, citrulline, DL-2-aminobutyric, DL-asparagine, DL-cysteine, DL-glutamine, DL-homoserine, DL-leucine, DL-methionine, DL-N-acetyl-serine, DL-ornithine, DL-phenylalanine, DL-threonine, DL-tryptophan, DL-valine, glutamic, glutamate, glycine, histidine, homotyrosine, homovaline, hydroxyproline, isoleucine, leucine, lysine, L-arginine, L-aspartic, L-cysteine, L-histidine, L-isoleucine, L-lysine, L-serine, L-tyrosine, methionine, N-α-acetylorithine, N-acetyl-glutamic acid, ornithine, phenylalanine, proline, pyroglutamate, pyroglutamic, serine, threonine, tryptophan, tyrosine, valine			
		SUG, SUGDs <sup>d</sup>	δ-trehalose, arabinose, arabinol, D-fructose, D-galactosamine, D-glucosamine, D-lactose, D-maltose, D-pinitol, D-ribose, D-xylobiose, D-xylose, fructose, fructose-6-phosphate, galactose, galactinol, glucose, glucose-6-phosphate, inositol, isomaltose, lactate, lactitol, maltose, mannose, mannotriose, melibiose, myo-ribose, N-acetyl-ribose, raffinose, ribose, sorbitol, sucrose, xylose			
		FA <sup>e</sup>	Arachidic, behenic, linoleic, linolenic, myristic, oleic, palmitic, palmitoleic, stearic			
		IFVN <sup>f</sup>	6''-O-acetyl daidzin, 6''-O-acetylgenistin, 6''-O-malonylglycitin, daidzin, glycitin, genistin, quercetin-tri-O-β-glucopyranoside			
		NTs <sup>g</sup>	Adenine, adenosine, cytidine, cytosine, dihydrouracil, guanine, guanosine, hypoxanthine, thymine, uracil, xanthine			

Produce	Raw material	Metabolite group	Metabolite forms	Data acquisition method	Data processing technique	Reference
Crab paste	Crab	OA <sup>h</sup>	2-hydroxyisobutyric, 2-hydroxy-glutaric, 3-methyl-2-[(trimethylsilyl)oxy]-pentanoic acid, acetic, benzenepropanoic, calcium pantothenate, <i>cis</i> -aconitate, citric, citramalic, D-galacturonic, DL-isocitric, DL-lactic, DL-malic, formic, fumaric, galactaric, gluconic, glutamic, glutaric, glycerate, glycolic, itaconic, lactic, malic, malinic, malonic, <i>n</i> -octadecanoic, oxalic, palmitic, phenylpyruvate, quinate, saccharic, shikimic, succinic, succinate, tartaric, <i>trans</i> -aconitic acid, <i>trans</i> -caffeic, <i>trans</i> -sinapic, trimethylsilyl, 3, 5-bis(trimethylsilyl)-3-methylvalerate	<sup>1</sup> HNMR*	PCA, OPLS-DA	[52]
		SSAPN <sup>i</sup>	A3, Bg, I, II, IV, V			
		V <sup>j</sup>	1, 3-diamino-propane, phenethylamine, putrescine, tryptamine, serotonin, spermidine Choline, nicotinic acid			
		O <sup>k</sup>	3-amino-2-one-piperidin, allantoinate, glycerol-3-phosphate, mevalonolactone, phosphoric acid, R-(-)-1-amino-2-propanol, trigonelline, urea			
		AA <sup>c</sup>	Alanine, arginine, glutamate, glycine, histidine, isoleucine, leucine, methionine, phenylalanine, tryptophan, tyrosine, valine			
		OA <sup>h</sup>	Acetate, formate, fumarate, lactate, succinate, taurine			
		OB <sup>l</sup>	Betaine, trimethylamine (TMA), trimethylamine- <i>N</i> -oxide			
Daqu	Barley and peas	PUR, PYR <sup>m</sup>	2-pyridinemethanol, adenosine diphosphate (ADP), hypoxanthine, inosine, trigonelline	<sup>1</sup> HNMR <sup>δ</sup>	PCA	[53]
		SUG <sup>d</sup>	Sucrose			
		Al <sup>a</sup>	Ethanol, glycerol, isopropanol			
		AA <sup>c</sup>	2-Aminobutyrate, cysteine, glutamate, glycine, glycylproline, homoserine, isoleucine, proline, serine, threonine			

Produce	Raw material	Metabolite group	Metabolite forms	Data acquisition method	Data processing technique	Reference
Doenjang	Soybean	SUG, SUGDs <sup>d</sup>	Arabinitol, fructose, galactitol, galactose, glucose, glucitol, lactose, maltose, mannitol, myo-inositol, ribose, sucrose			
		OA <sup>h</sup>	2-hydroxyisobutyrate, 2-phosphoglycerate, acetate, glycerate, glycolate, isobutyrate, lactate, pyruvate, succinate, taurine			
		OB <sup>l</sup>	Betaine, <i>cis</i> -aconitate			
		O <sup>k</sup>	Acetone, allantoin, ascorbate, choline, ethylene glycol, galactonate, maltate, malonate, <i>N</i> -nitrosodimethylamine, <i>O</i> -phosphocholine, <i>O</i> -phosphoserine, oxypurinol, propionate, propylene glycol, <i>S</i> -sulfo-cysteine, urea			
		AA <sup>c</sup>	$\gamma$ -aminobutyric, alanine, aminoaldiphic, aminobutyric, asparagine, aspartic, glutamine, glutamic, glycine, histidine, isoleucine, leucine, lysine, methionine, ornithine, phenylalanine, proline, pyroglutamic, sarcosine, serine, thioproline, threonine, tryptophan, tyrosine, valine	<sup>1</sup> HNMR <sup><math>\delta</math></sup>	PCA, PLS-DA	[28, 54]
		SUG, SUGDs <sup>d</sup>	$\alpha$ -glucose, $\beta$ -glucose, arabinose, arabitol, erythrose, fructose, galactonic, galactose, glucitol, glucose, glycerol, glucosamine, inositol, mannitol, mannose, maltose, melibiose, <i>myo</i> -inositol, raffinose, ribitol, ribonic acid, sucrose, xylitol	GC-TOF-MS*, UPLC-Q-TOF-MS*		
		FA <sup>e</sup>	Arachidic, behenic, caproc, eicosanic, eicosadienoic, lauric, linoleic, linolenic, magaric, myristic, oleic, palmitic, palmitoleic, pentadecyclic, stearic, tricosanoic			
		IFVN <sup>f</sup>	Acetylaidzin, acetylgenistin, acetylglycitin, daidzin, daidzein, genistin, glycitin, glycitein, malonyldaidzin, malonyglycitin, malonygenistin			
OA <sup>h</sup>	2-ketoglutaric, acetic, carbonic, citric, formic, fumaric, glucaric, glycolic, lactate, lactic, maleic, malic, malonic, malonic, manelic, oxalic, pipecolic, propionic, pyroglutamic, succinic, vanilic					
		SSAPN <sup>i</sup>	$\gamma$ g, $\gamma$ a, Bd, Be, I, II, III, IV, V			

Produce	Raw material	Metabolite group	Metabolite forms	Data acquisition method	Data processing technique	Reference
		O <sup>k</sup>	Choline, phosphocholine			
Fermented cereal	Wheat	Al <sup>a</sup>	1-decanol, 1-dodecanol, 1-octanol, 1, 2-dodecanediol, 7-methyl-4-octanol, dimethyl-1-octanol, ethylalcohol, hexanol, isoamylalcohol, methyl-2-buten-1-ol, methyl-3-heptanol, octadien-2-ol, octen-3-ol, pentanol, phenethylalcohol	SPME-GC-MS*	HCA	[55]
		C <sup>n</sup>	1, 1, 3-trimethyl-3-cyclohexene-5-one, 6-methyl-5-hepten-2-one, acetoin, decadienal, dodecanal heptanal, hexanal, methylpentanal, nonadienal, nonanone, octanone, octenal, pentanal	HPLC-DAD <sup>δ</sup>		
		H <sup>o</sup>	1, 2-dimethyl-benzene, 1, 3-hexadiene, 2-ethyl-furan, 2-pentyl-furan, 2-methyldecane, 3-methyl-dodecane, 4-methyl-dodecane, 5-methyldodecane, 10-methylnonadecane, 10-methyl-eicosane, furanone			
Fermented cocoa beans	Cocoa beans	OA <sup>h</sup>	2-methylbutanoic, 3-methylbutanoic, acetic, dodecanoic, pentanoic, hexanoic, heptanoic			
		O <sup>k</sup>	Ester			
		CTH, CTHd <sup>p</sup>	Epicatechin, <i>O</i> -hexoside-proanthocyanidin A5', <i>O</i> -pentoside-proanthocyanidin A5, procyanidin	UPLC-ESI-QTOF-MS*	PCA, PLS-DA,	[29]
Fermented tea	Green tea, black tea	O <sup>k</sup>	Tripeptide, sucrose			
		AA <sup>c</sup>	Glutamine, glutamic acid, glucoside, histamine, leucine, phenylalanine, proline, theanine, theanine-glucoside, tyrosine, tryptophan, valine	<sup>1</sup> HNMR*, UHPLC-QTOF-MS*	PCA	[56, 57]
		Ak <sup>q</sup>	Caffeine, choline, glycerophosphocholine, theobromine			
		CTH, CTHd <sup>p</sup>	3-galloylprocyanidin B1, Catechin, epiafzelechin, epicatechin-3-gallate, epicatechin, epicatechin gallate, epigallocatechin, epigallocatechin gallate, epigallocatechin methylgallate, theaflavin-3-gallate, theaflavin 3, 3'-digallate, theaflavin-3'-gallate, theasinensin A, theasinensin F, pigallocatechin-3-gallate, procyanidin B1, procyanin B2			

Produce	Raw material	Metabolite group	Metabolite forms	Data acquisition method	Data processing technique	Reference	
		FVNG, VOG <sup>r</sup>	Apigenin-6, 8-C-diglucoside, apigenin 6-C-glucoside 8-C-arabinoside, apigenin-6-C-arabinoside-8-C-glucoside, isoquercitrin, isovitexin, kaempferol 3-O-galactosylrutinoside, kaempferol 3-O-glucosylrutinoside, kaempferol-3-O-galactoside, kaempferol-3-O-glucoside, kaempferol-3-O-rutinoside myricetin 3-galactoside, quercetin-3-O-galactoside, quercetin 3-O-glucosylrutinoside, rutin				
		L <sup>s</sup>	LysoPC, MG				
		NTs <sup>s</sup>	(S)-5'-deoxy-5'(methylthio)adenosine, 5'-deoxy-5'(methylthio)adenosine, adenine, guanosine, inosine				
		OA <sup>h</sup>	3-O- <i>p</i> -coumaroylquinic, 4-O- <i>p</i> -coumaroylquinic, <i>p</i> -coumaric, caffeoylshikimic, theogallin				
		SUG <sup>d</sup>	$\alpha$ -glucose, $\beta$ -glucose, sucrose				
		O <sup>k</sup>	Caffeine, gallic acid, <i>N</i> -(1-deoxy-1-fructosyl)leucine, <i>N</i> -(1-deoxy-1-fructosyl)tyrosine, <i>N</i> -vinyl-2-pyrrolidone, <i>O</i> -demethylfonsecin, theanine, unknown compounds				
Fermented milk	Milk	AA <sup>c</sup> ↓	3-aminobutyric, alanine, arginine, asparagine, aspartic, GABA, glutamine, glycine, isoleucine, methionine, threonine	CE-TOF-MS*		[58]	
		Am <sup>b</sup> ↓	Cyclohexylamine				
		OA <sup>h</sup> ↓↑	2-oxoglutaric, citric, isocitric				
		PUR↓↑	Adenine, guanine, hypoxanthine				
		P <sup>t</sup> ↑	Ala-Pro, Leu-Pro, Pro-Pro, Val-Leu, Val-Pro, Val-Pro-Pro				
		SUG <sup>d</sup> ↓	Fructose 1, 6-diphosphate				
		V <sup>j</sup> ↓	Pyridoxamine				
Fermented soymilk	Soymilk	AA <sup>c</sup> ↓	Phenylalanine, tyrosine	<sup>1</sup> HNMR*	PCA	[59]	

Produce	Raw material	Metabolite group	Metabolite forms	Data acquisition method	Data processing technique	Reference
Fermented soybean	Soybean	OA <sup>h</sup> ↓	Acetic, citric, fumaric, lactate, lactic, malic, oxalacetic, succinic,	GC-TOF-MS <sup>δ</sup> , LC-ESI-MS <sup>δ</sup>	PCA, PLS-DA	[60]
		SUG <sup>d</sup> ↓	Raffinose, stachyose, sucrose			
		O <sup>k</sup>	Choline			
		AA <sup>c</sup> ↑↓	Aspartic, GABA, glutamic, glycine, pyroglutamic, serine, threonine			
		SUG, SUGDs <sup>d</sup> ↑↓	Arabitol, fructose, galactose, maltose, mannitol, myo-inositol, ribose, sorbitol, tagatose			
		FA <sup>e</sup> ↑	Palmitic, pentadecanoic, stearic			
		IFVN <sup>f</sup> ↑↓	8-hydroxydaidzein, acetyldaidzin, acetylglucitin, acetylgenistin, daidzein, aidzin, genistin, glycitein, glycitin, hydroxygenistein, hydroxyglycitein			
		NT <sup>g</sup> ↑	Uracil			
<i>Gochujang</i>	Wheat/rice	OA <sup>h</sup> ↓	Cinnamic, citric, malonic	UPLC-Q-TOF-MS <sup>*</sup> , GC-TOF-MS <sup>*</sup>	PCA, PLS-DA	[61]
		SSAPN <sup>i</sup>	I			
		AA <sup>c</sup>	Alanine, GABA, glycine, glutamic, isoleucine, leucine, phenylalanine, proline, pyroglutamic, serine, threonine, tyrosine, valine			
		Ak <sup>q</sup> , DPH <sup>u</sup>	Alnustone, dihydrocapsaicin, capsaicin			
		IFVN <sup>f</sup> , FLVD <sup>v</sup>	Apigenin-diglucoside, daidzein, glycitein, genistein, hydroxydaidzen, kaempferol, luteolin-diglucoside			
		L <sup>w</sup>	Lyso (PC16:0, PC18:1, PC18:2)			
		SUG <sup>d</sup>	Adonitol, arabinose, erythritol, fructose, fumaric, gentibiose, glucitol, gluconic, glucose, glycerol, glyceryl-glucoside, lactose, inositol, myo-inositol, xylose, xylitol			
		OA <sup>h</sup>	Citric, malic, malonic, phosphoric, propanoic, succinic			
SSAPN <sup>i</sup>	I, III, V					

Produce	Raw material	Metabolite group	Metabolite forms	Data acquisition method	Data processing technique	Reference
Kimchi	Vegetables	O <sup>k</sup>	glyceryl-glucoside, unknown compounds	GC-MS*	PCA, PLS-DA	[62]
		AA <sup>c</sup> ↓	δ-aminobutyric, alanine, asparagine, aspartic, glycine, glutamic, glutamine, leucine, ornithine, proline, threonine, valine			
		SUG, SUGDs <sup>d</sup> ↑↓	D-fructose, galactose, glucose, glycerol, mannitol, myo-inositol, sucrose, xylose			
Koji	Rice	OA <sup>h</sup> ↑↓	1-Propene-1, 2, 3-tricarboxylic acid, 2-keto-L-gluconic acid, 2, 3, 4-trihydroxybutyric acid, citric, fumaric, gluconic, isocitric, lactic, malic, octadecanoic, palmitic, pentanedioic, propanoic, pyrotartaric, ribonic, succinic	GC-TOF-MS*, UHPLC-LTQ-IT-MS/MS*	PCA, PLS-DA	[63]
		O <sup>k</sup> ↑↓	Adenine, Urea			
		AA <sup>c</sup> ↑↓	Alanine, aspartic, GABA, glutamic, glycine, isoleucine, leucine, lysine, methionine, ornithine, phenylalanine, proline, pyroglutamic, serine, threonine, tryptophan, tyrosine, valine			
		FA <sup>e</sup> ↑↓	Hydroxy-oxo-octadecenoic, linoleic, linolenic, oleic, palmitic, pinellic, stearic			
		FLVN <sup>v</sup> ↑↓	Apigenin-C-glucosyl-C-arabinoside, chrysoeriol-hexoside, chrysoeriol-rutinoside, isovitexin-O-glucoside, triclin, triclin-7-O-rutinoside, triclin-O-glucoside			
		LPL <sup>x</sup> ↑↓	Lyso (PE14:0, PC14:0, PC18:3, PC16:1, PE18:2, PC18:2, PE16:0, PC16:0, PC18:1)			
		OA <sup>h</sup> ↑↓	Citric, fumaric, gluconic, glyceric, kojic, lactic, malic, malonic, shikimic, succinic, oxalic,			
		PA <sup>y</sup> ↑↓	4-hydroxybenzoic acid, ferulic acid			
SUG, SUGDs <sup>d</sup> ↑↓	Erythritol, fructose, glucose, glycerol, maltose, myo-inositol, pentitol, sorbitol, xylose, xylitol,					

Produce	Raw material	Metabolite group	Metabolite forms	Data acquisition method	Data processing technique	Reference
V <sup>i</sup> ↑↓	Nicotinic acid					
O <sup>k</sup> ↑↓	Bacillibactin, unknowns					
<i>Makgeolli</i>	Rice	AA <sup>c</sup>	Alanine, asparagine, glutamic, glutamine, glycine, leucine, lysine, ornithine, proline, pyroglutamic, tryptophan, tyrosine	GC-MS*	OPLS-DA	[64]
		Al <sup>g</sup> ↑	4-hydroxyphenylethanol			
		OA <sup>h</sup> ↑	2-hydroxyglutaric, citric, lactic, malic, succinic			
		SUG,↑↓ SUGDs <sup>d</sup>	Erythritol, fructose, glucose, glycerol, <i>myo</i> -inositol, ribose			
		O <sup>k</sup> ↑↓	1, 2-propanediol, phosphoric			
<i>Meju</i>	Soybean	AA <sup>c</sup> ↑↓	γ-aminobutyric, acetylornithine, alanine, arginine, citrulline, glutamic, glutamine, histidine, isoleucine, leucine, lysine, methionine, ornithine, phenylalanine, proline, pyroglutamic, threonine, tryptophane, tyrosine, valine	UPLC-Q-TOF MS*	PLS-DA	[27]
		NTs↑↓	Adenine, hypoxanthine, uracil, xanthine	OPLS-DA		
		OA <sup>h</sup> ↑↓	Citric, pipecolic			
		P <sup>t</sup> ↑↓	Glu-Gln, Glu-Tyr, Leu-Gln, Leu-Glu, Glu-Phe, Leu-Pro, Ser-Pro, Val-Glu, Val-Thr, Val-Leu, Leu-Val-Pro-Pro			
<i>Miso</i>	Soybean	AA <sup>c</sup> ↑↓	Arginine, aspartate, glutamate, glutamine, lysine, phenylalanine, pyroglutamic,	LC-MS <sup>b</sup>	PCA	[65]
		OA <sup>h</sup> ↑	Citric			
		O <sup>k</sup>	Fructosyl-leucine, fructosyl-phenylalanine			
<i>Myeolchi-aekjeot</i>	Fish	AA <sup>c</sup> ↑↓	Alanine, arginine, aspartate, glutamate, glutamic, glutamine, glycine, isoleucine, leucine, serine, threonine  Betanine, choline, creatine, inosine, methyl amines	<sup>1</sup> HNMR*		[66]

Produce	Raw material	Metabolite group	Metabolite forms	Data acquisition method	Data processing technique	Reference
<i>Saeu-jeot</i>	Shrimp	Am <sup>b</sup> , NTs <sup>g</sup> ↑↓		<sup>1</sup> HNMR*	CCA	[67]
		OA <sup>h</sup> ↑↓	Acetate, lactate,			
		SUG,↑↓ SUGDs <sup>d</sup>	Glucose, glycerol			
		AA <sup>c</sup> ↑	Alanine, arginine, asparagine, aspartate, glutamate, glutamine, glycine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, pyroglutamate, serine, threonine, tryptophan, tyrosine, valine			
		Am <sup>b</sup> ↑↓	Dimethylamine, trimethylamine			
		OA <sup>h</sup> ↑	Acetate, butyrate, lactate			
		SUG,↑↓ SUGDs <sup>d</sup>	Glucose, glycerol			

a—alcohols, b—amines, c—amino acids, d—carbohydrates, sugars and sugar derivatives, e—fatty acids, f—isoflavonoids, g—nucleotides, h—organic acids, i—soyasaponins, j—vitamins, k—others (not classified), l—organic bases, m—purines and pyrimidines, n—carbonils, o—hydrocarbons, p—catechin and catechin derivatives, q—alkaloids, r—flavonol glycosides and flavone glycosides, s—lipids, t—peptides, u—diphenylheptanoid, v—flavonoids, w—lipids, x—lysophospholipids, y—phenolic acids, ↑—increase in metabolites, ↓—decrease in metabolites, ↑↓—both increase and decrease in metabolites, \*—non-targeted/profiling metabolomics, <sup>o</sup>—targeted metabolomics, CE-TOF-MS—capillary electrophoresis time of flight mass spectrometry, CCA—canonical correspondence analysis, FTIR—Fourier transform infrared spectroscopy, GC-FID—gas chromatography-flame ionization detector, GC-MS—gas chromatography-mass spectrometry, GC-TOF-MS—gas chromatography-time of flight mass spectrometry, <sup>1</sup>HNMR—proton nuclear magnetic resonance, HPLC-DAD—high performance liquid chromatography-diode array detector, LC-MS/MS—liquid chromatography tandem-mass spectrometry, OPLS-DA—orthogonal partial least square discriminant analysis, PCA—principal component analysis, PLS-DA—partial least square discriminant analysis, SPME-GC-MS—solid phase microextraction-gas chromatography-mass spectrometry, UPLC-ESI-QTOF-MS—ultra high performance liquid chromatography with electrospray ionization quadrupole time of flight mass spectrometry, UHPLC-LTQ-IT-MS/MS—ultra high pressure liquid chromatography linear ion trap-high resolution Orbitrap mass spectrometry, UPLC-Q-TOF MS—ultra performance liquid chromatography quadrupole time of flight mass spectrometry.

**Table 1.** Summary of food metabolomics studies of fermented foods reported in literature.

flavanols, anthocyanins were observed to decreased with fermentation time, while most oligopeptides initially increased, with a later decrease during fermentation [29].

Lee et al. [56] and Tan et al. [57] studied metabolic changes during tea fermentation. Using  $^1\text{H}$  NMR, UPLC-Q-TOF-MS and PCA, these authors were able to differentiate partially and fully fermented tea according to their fermentation patterns. The authors observed a decrease in caffeine epicatechin, epigallocatechin, caffeine, quinate, theanine and sucrose, whereas gallic acid and glucose levels increased [56]. Alanine levels remained constant with caffeine being a major discriminator. A similar decrease in catechin, epigallocatechin in fermented tea was observed in another study, though levels of flavanols rapidly increased but later decreased [57]. Varying increases and decreases in the levels of flavonol and flavone glycosides, phenolic acids, alkaloids and amino acids were also recorded by these authors [57].

Other similar studies on the food metabolomics studies of fermented foods that have been reported in the literature include foods from milk [58, 59] soybean [27, 28, 65] and cereals [61, 63, 64] (Table 1). Others include *kimchi* [62], *myeolchi-aekjeot* [66] and *saeu-jeot* [67]. These fermented food products, their corresponding metabolites and trend in terms of increases or decreases in reported metabolites are summarized in Table 1.

## 5. Role of food metabolomics in the development of functional foods

Sequel to the relevance and importance of consuming functional foods for improved health, concerted efforts by relevant stakeholders in academia and food industry have been geared towards the development and delivery of functional foods to the populace. In this regard, food metabolomics as a technique is vital in the efficient and proper evaluation of such products and subsequent elucidation of the metabolite profile. Through the selection of appropriate techniques in combination with adequate MVDAs, a thorough understanding of the effects of processing parameters and different optimization steps during the development of such functional foods is possible. Successive data generated, could thus be interpreted in terms of the functionality and other health benefits such product would confer to intending consumers.

## 6. Future prospects

Fermented foods have distinct ecological niches that present an opportunity to use new approaches that take advantage of advances in 'omics' to understand and characterized them. Considering the wide range of these fermented foods in the world and the number of yet to be characterized and identified components, subsequent analysis of these components needs to be explored to further advance and contribute to existing knowledge. While the future of food metabolomics will involve the development of better analytical techniques, efforts should also be made at developing standardized databases of data from fermented foods.

Currently, metabolomics studies on fermented foods are still limited compared to plants. If harnessed well, the application of food metabolomics would play an invaluable role in the

development of strategies for improving the safety, quality, shelf life and overall composition of fermented foods. In the nearest future with concerted efforts, food metabolomics could be used as an effective alternative and/or complement traditional sensory evaluation for fermented foods. Since metabolites impact sensory qualities, food metabolomics can clarify the influence of fermentation on biomarkers responsible for sensorial qualities.

## 7. Conclusion

There is a steady growing interest in food metabolomics, due to its application and capability in providing high throughput data and a platform for detailed understanding on the fermentation process. The feasibility of food metabolomics approach also suggests its viability for future progress in food science, nutrition and other related fields. This also coincides with the recent sensitization and encouragement of the consumption of functional and nutraceutical foods that can reduce the risks of degenerative diseases and ensure healthy nutrition. Although considerable progress has been made in the field of food metabolomics and its application in understanding fermented foods as demonstrated in this chapter, challenges of fully interpreting the complex data generated from the sophisticated equipment used still needs to be addressed and simplified. Nonetheless, food metabolomics has provided a medium that will greatly improve our understanding of the diversity of fermented foods and even more potential to explore their functionality. Since the delivery of most functional foods to the populace is through the industry, subsequent adoption of this technology would translate to a better understanding of processes and its influence on product quality. This could thus save costs, time and labor that might have been expended in conventional analytical techniques, that would provide less information.

## Acknowledgements

This work was supported via the Global Excellence and Stature (GES) Fellowship of the University of Johannesburg (UJ) granted to the main author (Adebo, O.A). This work was also partly supported by the National Research Foundation (NRF) Center of Excellence (CoE) in Food Security co-hosted by the University of Pretoria (UP) and the University of Western Cape (UWC), South Africa.

## Author details

Oluwafemi Ayodeji Adebo\*, Patrick Berka Njobeh, Janet Adeyinka Adebiyi, Sefater Gbashi and Eugenie Kayitesi\*

\*Address all correspondence to: [oluwafemiadebo@gmail.com](mailto:oluwafemiadebo@gmail.com) and [eugeniek@uj.ac.za](mailto:eugeniek@uj.ac.za)

Department of Biotechnology and Food Technology, University of Johannesburg,  
Johannesburg, Gauteng, South Africa

## References

- [1] Galati A, Oguntotinbo FA, Moschetti G, Crescimanno M, Settanni L. The cereal market and the role of fermentation in cereal-based food production in Africa. *Food Reviews International*. 2014;**30**:317–337. DOI: 10.1080/87559129.2014.929143
- [2] Adebisi JA, Obadina AO, Adebo OA, Kayitesi E. Fermented and malted millet products in Africa: Expedition from traditional/ethnic foods to industrial value added products. *Critical Reviews in Food Science and Nutrition*. DOI: 10.1080/10408398.2016.1188056
- [3] Adebisi JA, Obadina AO, Mulaba-Bafubandi AF, Adebo OA, Kayitesi E. Effect of fermentation and malting on the physicochemical properties of millet flour and biscuit. *Journal of Cereal Science*. 2016;**70**:132–139. DOI: 10.1016/j.jcs.2016.05.026 DOI:10.1016/j.jcs.2016.05.026#doilink
- [4] Jay JM, Loessner MJ, Golden DA. *Modern Food Microbiology*. 7th ed. India: Springer; 2005. DOI: 10.1007/b100840
- [5] Saavedra JM. Use of probiotics in pediatrics: Rationale, mechanisms of action, and practical aspects. *Nutrition in Clinical Practice*. 2007;**22**:351–365. DOI: 10.177/0115426507022003351
- [6] Anukam KC, Reid G. African traditional fermented foods and probiotics. *Journal of Medicinal Food*. 2009;**12**:1177–1184. DOI: 10.1089/jmf.2008.1063
- [7] Wang CY, Wu SJ, Fang JY, Wang YP, Shyu YT. Cardiovascular and intestinal protection of cereal pastes fermented with lactic acid bacteria in hyperlipidemic hamsters. *Food Research International*. 2012;**48**:428–434. DOI: 10.1016/j.foodres.2012.05.006
- [8] Taylor JRN, Duodu KG. Effects of processing sorghum and millets on their phenolic phytochemicals and the implications of this to the health-enhancing properties of sorghum and millet food and beverage products. *Journal of the Science of Food and Agriculture*. 2015;**95**:225–237. DOI: 10.1002/jsfa.6713
- [9] Cifuentes A. Food analysis and foodomics. *Journal of Chromatography A*. 2009;**1216**:7109. DOI: 10.1016.chroma.2009.09.018
- [10] Hu C, Xu G. Mass-spectrometry-based metabolomics analysis for foodomics. *Trends in Analytical Chemistry*. 2013;**52**:36–46. DOI: 10.1016/j.trac.2013.09.005
- [11] Garcia-Canas V, Simo C, Herrero M, Ibanez E, Cifuentes A. Present and future challenges in food analysis: Foodomics. *Analytical Chemistry*. 2012;**84**:10150–10159. DOI: 10.1021/ac301680q
- [12] Niwa T. Metabolic profiling with gas chromatography–mass spectrometry and its application to clinical medicine. *Journal of Chromatography*. 1986;**379**:313–345
- [13] Nicholson JK, Lindon JC, Holmes E. Metabolomics: Understanding the metabolic responses of living systems to pathophysiological stimuli via multivariate statistical analysis of biological NMR spectroscopic data. *Xenobiotica*. 1999;**29**:1181–1189. DOI: 10.1080/004982599238047

- [14] Fiehn O. Metabolomics—The link between genotypes and phenotypes. *Plant Molecular Biology*. 2002;**48**:155–171. DOI: 10.1023/A:1013713905833
- [15] Fukusaki E, Kobayashi A. Plant metabolomics: Potential for practical operation. *Journal of Bioscience and Bioengineering*. 2005;**100**:347–354. DOI: 10.1263/jbb.100.347
- [16] Cevallos-Cevallos JM, Reyes-De-Corcuera JI, Etxeberria E, Danyluk MD, Rodrick GE. Metabolomic analysis in food science: A review. *Trends in Food Science and Technology*. 2009;**20**:557–566. DOI: 10.1016/j.tifs.2009.07.002
- [17] McGhie TK, Rowan DD. Metabolomics for measuring phytochemicals, and assessing human and animal responses to phytochemicals, in food science. *Molecular and Nutrition Food research*. 2012;**56**:147–158. DOI: 10.1002/mnfr.201100545
- [18] Mozzi F, Ortiz ME, Bleckwedel J, De Vuyst L, Pescuma M. Metabolomics as a tool for the comprehensive understanding of fermented and functional foods with lactic acid bacteria. *Food Research International*. 2013;**54**:1152–1161. DOI: 10.1016/j.foodres.2012.11.010
- [19] Herrero M, Garcia-Canas V, Simo C, Cifuentes A. Recent advances in the application of CE methods for food analysis and foodomics. *Electrophoresis*. 2010;**31**:205–228. DOI: 10.1002/elps.200900365
- [20] Capozzi F, Bordoni A. Foodomics: A new comprehensive approach to food and nutrition. *Genes and Nutrition*. 2013;**8**:1–4. DOI: 10.1007/s12263-012-0310-x
- [21] Wishart DS. Metabolomics: applications to food science and nutrition research. *Trends in Food Science and Technology*, 2008;**19**:482–493. DOI: 10.1016/j.tifs.2008.03.003
- [22] Ramautar R, Demirci A, Jong, GJD. Capillary electrophoresis in metabolomics. *Trends in Analytical Chemistry*. 2006;**25**:455. DOI: 10.1016/j.trac.2006.02.004
- [23] Monton MRN, Soga T. Metabolome analysis by capillary electrophoresis-mass spectrometry. *Journal of Chromatography A*. 2007;**1168**:237–246. DOI: 10.1016/j.chroma.2007.02.065
- [24] Tugizimana F, Paiter L, Dubery I. Plant metabolomics: a new frontier in phytochemical analysis. *South African Journal of Science*. 2013;**109**:1–11. DOI: 10.1590/sajs.2013/20120005
- [25] Choi HK, Yoon JH, Kim YS, Kwon DY. Metabolomic profiling of *Cheonggukjang* during fermentation by <sup>1</sup>H NMR spectrometry and principal components analysis. *Process Biochemistry*. 2007;**42**:263–266. DOI: 10.1016/j.procbio.2006.07.014
- [26] Park MK, Cho IH, Lee S, Choi HK, Kwon DY, Kim YS. Metabolite profiling of *Cheonggukjang*, a fermented soybean paste, during fermentation by gas chromatography-mass spectrometry and principal component analysis. *Food Chemistry*. 2010;**122**:1313–1319. DOI: 10.1016/j.foodchem.2010.03.095
- [27] Kang HJ, Yang HJ, Kim MJ, Han ES, Kim HJ, Kwon DY. Metabolomic analysis of meju during fermentation by ultra performance liquid chromatography-quadrupole-time of flight mass spectrometry (UPLC-Q-TOF MS). *Food Chemistry*. 2011;**127**:1056–1064. DOI: 10.1016/j.foodchem.2011.01.080

- [28] Lee SY, Lee S, Lee S, Oh JY, Jeon EJ, Ryu HS, Lee CH. Primary and secondary metabolite profiling of *doenjang*, a fermented soybean paste during industrial processing. *Food Chemistry*. 2014;**165**:157–166. DOI: 10.106/j.foodchem.2014.05.089
- [29] Mayorga-Gross AL, Quiros-Guerrero LM, Fourny G, Vaillant F. An untargeted metabolomic assessment of cocoa beans during fermentation. *Food Research International*. 2016;**89**:901–909. DOI: 10.1016/j.foodres.2016.04.017
- [30] Villas-Boas SG, Mas S, Akesson M, Smedsgaard J, Nielsen J. Mass Spectrometry in metabolome analysis. *Mass Spectrometry Reviews*. 2005;**24**:613–646. DOI: 10.1002/mas.20032
- [31] t'Kindt R, Morreel K, Deforce D, Boerjan W, Van Bocxlaer J. Joint GC-MS and LC-MS platforms for comprehensive plant metabolomics: Repeatability and sample pre-treatment. *Journal of Chromatography B*. 2009;**1152**:3572–3580. DOI: 10.1016/j.jchromb.2009.08.041
- [32] Namgung HJ, Park HJ, Cho IN, Choi HK, Kwon DY, Shim SM, Kim YS. Metabolite profiling of doenjang, fermented soybean paste, during fermentation. *Journal of the Science of Food and Agriculture*. 2010;**90**:1926–1935. DOI: 10.1002/jsfa.4036
- [33] Cevallos-Cevallos JM, Reyes-De-Corcuera JI. Metabolomics in food science. *Advances in Food and Nutrition Research*. 2012;**67**:1–24. DOI: 10.1016/B978-0-12-394598-3.00001-0
- [34] Chin E, Slupsky CM. Applications of metabolomics in food science: Food composition and quality, sensory and nutritional attributes. In: Weimer BC, Slupsky CM. (Eds), *Metabolomics in Food and Nutrition*. 2013. England: Woodhead Publishing. pp. 217–230. DOI: 10.1533/9780857098818.2.217
- [35] Corsaro C, Cicero N, Mallamace D, Vasi S, Naccari C, Salvo A, Giofre SV, Dugo G. HR-MAS and NMR towards Foodomics. *Food Research International*. 2016;**89**:1085–1094. DOI: 10.1016/j.foodres.2016.09.033
- [36] Singh D, Lee S, Lee Ch. Metabolomics for empirical delineation of the traditional Korean fermented foods and beverages. *Trends in Food Science and Technology*. 2017;**61**:103–115. DOI: 10.1016/j.tifs.2017.01.001
- [37] Katajamaa M, Orešič M. Data processing for mass spectrometry-based metabolomics. *Journal of Chromatography A*. 2007;**1158**: 318–328. DOI: 10.1016/j.chroma.2007.04.021
- [38] Cubero-Leon E, Penalver R, Maquet A. Review on metabolomics for food authentication. *Food Research International*. 2014;**60**:95–107. DOI: 10.1016/j.foodres.2013.11.041
- [39] Tugizimana F, Steenkamp PA, Piater LA, Dubery IA. A conversion on data mining strategies in LC-MS untargeted metabolomics: Pre-processing and pre-treatment steps. *Metabolites*. 2016;**6**:1–18. DOI: 10.3390/metabo6040040
- [40] Wold S. Chemometrics; what do we mean with it, and what do we want from it? *Chemometrics and Intelligent Laboratory Systems*. 1995;**30**:109–115. DOI: 10.1016/0169-7439(95)00042-9 DOI:10.1016/0169-7439(95)00042-9#doilink

- [41] Trygg J, Gullberg J, Johansson AI, Jonsson P, Moritz T. Chemometrics in metabolomics—An introduction. In: Saito K, Dixon R, Willmitzer L. (Eds), Plant metabolomics. 2006. Berlin Heidelberg: Springer. Vol. 57. pp. 117–128. DOI: 10.1007/3-540-29782-0\_9
- [42] Wishart DS, Tzur D, Knox C, Eisner R, Guo AC, Young N, Cheng D, Jewell K, Arndt D, Sawhney S, Fung C, Nikolai L, Lewis M, Coutouly MA, Forsythe I, Tang P, Shrivastava S, Jeroncic K, Stothard P, Amegbey G, Block D, Hau DD, Wagner J, Miniaci J, Clements M, Gebremedhin M, Guo N, Zhang Y, Duggan GE, Macinnis GD, Weljie AM, Dowlatabadi R, Bamforth F, Clive D, Greiner R, Li L, Marie T, Sykes BD, Vogel HJ, Querengesser L. HMDB: The human metabolome database. Nucleic Acids Research. 2007;**35**:521–526. DOI: 10.1093/nar/gkl923
- [43] Berrueta LA, Alonso-Salces RM, Héberger K. Supervised pattern recognition in food analysis. Journal of Chromatography A. 2007;**1158**:196–214. DOI: 10.1016/j.chroma.2007.05.024 DOI:10.1016/j.chroma.2007.05.024#doilink
- [44] van der Werf MJ, Jellema RH, Hankemeier T. Microbial metabolomics: replacing trial-and-error by the unbiased selection and ranking of targets. Journal of Industrial Microbiology and Biotechnology. 2005;**32**:234–252. DOI: 10.1007/s10295-005-0231-4
- [45] Broadhurst D, Kell D. Statistical strategies for avoiding false discoveries in metabolomics and related experiments. Metabolomics. 2006;**2**:171–196. DOI: 10.1007/s11306-006-0037-z
- [46] Kemsley EK, Le Gall G, Dainty JR, Watson AD, Harvey LJ, Tapp HS, Colquhoun IJ. Multivariate techniques and their application in nutrition: A metabolomics case study. British Journal of Nutrition. 2007;**98**:1–14. DOI: 10.1017/S0007114507685365
- [47] Kwon SW. Profiling of soluble proteins in wine by nano-high performance liquid chromatography/tandem mass spectrometry. Journal of Agriculture and Food Chemistry. 2004;**52**:7258–7263. DOI: 10.1021/jf048940g
- [48] Moco S, Bino RJ, Vorst O, Verhoeven HA, de Groot J, van Beek TA., Vervoort J, de Vos CH. A liquid chromatography-mass spectrometry-based metabolome database for tomato. Plant Physiology. 2006;**141**:1205–1218. DOI: 10.1104/pp.106.078428
- [49] Baek JG, Shim SM, Kwon DY, Choi HK, Lee CH, Kim YS. Metabolite profiling of *cheonggukjang*, a fermented soybean paste, inoculated with various *Bacillus* strains during fermentation. Bioscience Biotechnology and Biochemistry. 2010;**74**:1860–1868. DOI: 10.1271/bbb.100269
- [50] Kim J, Choi JN, John KMM, Kang D, Son GH, Kim YS, Choi HK, Kwon DY, Lee CH. Correlation between antioxidative activities and metabolite changes during *cheonggukjang* fermentation. Bioscience, Biotechnology, and Biochemistry. 2011;**75**:732–739. DOI: 10.1271/bbb.100858
- [51] Kim J, Choi JN, John KMM, Kusano M, Oikawa A, Saito K, Lee CH. GC–TOF-MS- and CE–TOF-MS-based metabolic profiling of *cheonggukjang* (fast-fermented bean paste) during fermentation and its correlation with metabolic pathways. Journal of Agricultural and Food Chemistry. 2012;**60**:9746–9753. DOI: 10.1021/jf302833y

- [52] Chen D, Ye Y, Chen J, Yan X. Evolution of metabolomics profile of crab paste during fermentation Food Chemistry. 2016;**192**:886–892. DOI: 10.1016/j.foodchem.2015.07.098
- [53] Yan Z, Zheng XW, Han BZ, Yan YZ, Zhang X, Chen JY. <sup>1</sup>H NMR-based metabolomics approach for understanding the fermentation behaviour of *Bacillus licheniformis*. Journal of the Institute of Brewing. 2015;**121**:425–431. DOI: 10.1002/jib.238
- [54] Yang SO, Kim MS, Liu KH, Auh JH, Kim YS, Kwon DY, Choi HK. Classification of fermented soybean paste during fermentation by <sup>1</sup>H nuclear magnetic resonance spectroscopy and principal component analysis. Bioscience Biotechnology and Biochemistry. 2009;**73**:502–507. DOI: 10.1271/bbb.80467
- [55] Ferri M, Serrazanetti DI, Tassoni A, Baldissarri M, Gianotti A. Improving the functional and sensorial profile of cereal-based fermented foods by selecting *Lactobacillus plantarum* strains via a metabolomics approach. Food Research International. 2016;**89**:1095–1105. DOI: 10.1016/j.foodres.2016.08.044
- [56] Lee JE, Lee BJ, Chung JO, Shin HJ, Lee SJ, Lee CH, Hong YS. <sup>1</sup>H NMR-based metabolomic characterization during green tea (*Camellia sinensis*) fermentation. Food Research International. 2011;**44**:597–604. DOI: 10.1016/j.foodres.2010.12.004
- [57] Tan J, Dai W, Lu M, Lv H, Guo L, Zhang Y, Zhu Y, Peng Q, Lin Z. Study of the dynamic changes in the non-volatile chemical constituents of black tea during fermentation processing by a non-targeted metabolomics approach. Food Research International. 2016;**79**:106–113. DOI: 10.1016/j.foodres.2015.11.018
- [58] Hagi T, Kobayashi M, Nomura M. Metabolome analysis of milk fermented by -aminobutyric acid-producing *Lactococcus lactis*. Journal of Dairy Science. 2016;**99**:994–1001. DOI: 10.3168/jds.2015-9945
- [59] Yang SO, Kim SH, Cho S, Lee JH, Kim YS, Yun SS, Choi HK. Classification of fermented soymilk during fermentation by <sup>1</sup>H NMR coupled with principal component analysis and elucidation of free-radical scavenging activities. Bioscience Biotechnology and Biochemistry. 2009;**73**:1184–1188. DOI: 10.1271/bbb.80743
- [60] Lee S, Seo MH, Oh DK, Lee CH. Targeted metabolomics for *Aspergillus oryzae* mediated biotransformation of soybean isoflavones, showing variations in primary metabolites. Bioscience Biotechnology and Biochemistry. 2014;**78**:167–174. DOI: 10.1080/09168451.2014.877827
- [61] Lee DE, Shin GR, Lee S, Jang ES, Shin HW, Moon BS, Lee CH. Metabolomics reveal that amino acids are the main contributors to antioxidant activity in wheat and rice *gochujangs* (Korean fermented red pepper paste). Food Research International. 2016;**87**:10–17. DOI: 10.1016/j.foodres.2016.06.015
- [62] Park SE, Yoo SA, Seo SH, Lee KI, Na CS, Son HS. GC-MS based metabolomics approach of Kimchi for the understanding of *Lactobacillus plantarum* fermentation characteristics. LWT-Food Science and Technology. 2016;**68**:313–321. DOI: 10.1016/j.lwt.2015.12.046

- [63] Lee DE, Lee S, Jang ES, Shin HW, Moon BS, Lee CH. Metabolomic profiles of *Aspergillus oryzae* and *Bacillus amyloliquefaciens* during rice koji fermentation. *Molecules*. 2016;**21**:1–15. DOI: 10.3390/molecules21060773
- [64] Seo SH, Park SE, Yoo SA, Lee KI, Na CS, Son HS. Metabolite profiling of *Makgeolli* for the understanding of yeast fermentation characteristics during fermentation and aging. *Process Biochemistry*. 2016;**51**:1363–1373. DOI: 10.1016/j.procbio.2016.08.005
- [65] Yoshida H, Yamazaki J, Ozawa S, Mizukoshi T, Miyano H. Advantage of LC-MS metabolomics methodology targeting hydrophilic compounds in the studies of fermented food samples. *Journal of Agricultural and Food Chemistry*. 2009;**57**:1119–1126. DOI: 10.1021/jf803235m
- [66] Jung JY, Lee HJ, Chun BH, Jeon CO. Effects of temperature on bacterial communities and metabolites during fermentation of *myeolchi-aekjeot*, a traditional Korean fermented anchovy sauce. *PLoS One*. 2016;**11**:1–20. DOI: 10.1371/journal.pone.0151351
- [67] Lee SH, Jung JY, Jeon CO. Effects of temperature on microbial succession and metabolite change during *saeu-jeot* fermentation. *Food Microbiology*. 2014;**38**:16–25. DOI: 10.1016/j.fm.2013.08.004