fermentation

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Review

Fermentation of Cereals and Legumes: Impact on Nutritional Constituents and Nutrient Bioavailability

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Abstract: Fermented food products, especially those derived from cereals and legumes are important contributors to diet diversity globally. These food items are vital to food security and significantly contribute to nutrition. Fermentation is a process that desirably modifies food constituents by increasing the palatability, organoleptic properties, bioavailability and alters nutritional constituents. This review focuses on deciphering possible mechanisms involved in the modification of nutritional constituents as well as nutrient bioavailability during the fermentation of cereals and legumes, especially those commonly consumed in developing countries. Although modifications in these constituents are dependent on inherent and available nutrients in the starting raw material, it was generally observed that fermentation increased these nutritive qualities (protein, amino acids, vitamins, fats, fatty acids, etc.) in cereals and legumes, while in a few instances, a reduction in these constituents was noted. A general reduction trend in antinutritional factors was also observed with a corresponding increase in the nutrient bioavailability and bioaccessibility. Notable mechanisms of modification include transamination or the synthesis of new compounds during the fermentation process, use of nutrients as energy sources, as well as the metabolic activity of microorganisms leading to a degradation or increase in the level of some constituents. A number of fermented products are yet to be studied and fully understood. Further research into these food products using both conventional and modern techniques are still required to provide insights into these important food groups, as well as for an overall improved food quality, enhanced nutrition and health, as well as other associated socioeconomic benefits.

Keywords: fermented foods; cereal and legume-based product; antinutrients; nutrient bioavailability; socioeconomic benefits

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1. Introduction

Fermented food products are notable all around the world and are sometimes categorized as "functional foods" due to their purported health benefits. These food products have been in existence since the arrival of the human civilization and are likely to be with us far into the future. Fermentation is, thus, an age-long food processing technique used to transform food products [1,2], with different food crops (cereals, legumes, as well as fruits and vegetables) used as starting raw materials. Cereals and legumes are notable and major staple crops around the globe and are frequently fermented to obtain a number of food products [3–5]. The fermentation of cereals and legumes, as with other food crops, can be classified into three categories, viz., natural (also referred to as spontaneous), back slopping and controlled fermentation. Natural or spontaneous fermentation occurs through the sequential and competitive action of a plethora of microorganisms, with the best-adapted

strain(s) having a better growth rate, eventually dominating the microbiota [2,6]. Back slopping fermentation is similar to natural or spontaneous fermentation and a common traditional practice in low-income households and small-scale commercial industries. This process involves the introduction of a small portion of an earlier successful fermentation batch into a new process, to serve as a source of "starter cultures" and guarantees an effective transfer of microorganisms responsible for fermentation [1,2,6]. Controlled fermentation, on the other hand, involves the use of specific strains (starter cultures). Such strains have been isolated earlier and identified and their subsequent use in a controlled fermentation process leads to shorter lag phases, among other benefits [7,8]. Natural fermentation is, however, non-predictable and less effective, although it is the most common form of fermentation in developing countries, especially in Africa and Asia [1,2]. Because of these limitations, starter cultures such as LAB, yeasts, fungi, *Bacillus* species and other microorganisms have been isolated from fermented products and adopted to make the fermentation process more reliable, controlled and reproducible [1,9,10].

Additionally, fermentation could also be classified as either a solid-state fermentation (SSF) or submerged/liquid (SmF) fermentation. The SSF process involves the growth of microorganisms on moist substrates in the absence of free-flowing water, while SmF occurs in the presence of free-flowing liquid medium/water (i.e., SmF has more fluids compared to SSF) [11,12]. Irrespective of these classifications, the primary purpose of food fermentation is to preserve perishable produce; however, recently, with the advent of numerous technologies, different types of fermented foods are being manufactured to meet consumer needs [2,13]. This food processing technique is also well-known to improve the sensory properties of food through imparting unique flavours, textures and aromas. It is also used to improve the bioavailability and bioaccessibility of nutrients, reduce antinutritional factors (such as lectins, phytic acid, proteinase inhibitors, oxalic and tannins acids) and pathogenic microorganisms, preserve food products as well as to enhance the economic value [14,15].

Most well-known fermented foods in Africa and Asia are produced from cereals and legumes to create a variety of diets for households. The fermentation of cereals and legumes into subsequent products involves the interaction of plant tissues with available fermenting microorganisms. These fermented foods mostly contain a complex mixture of proteins, carbohydrates, fats, etc., undergoing a simultaneous modification or in some sequence under the action of a variety of microorganisms and enzymes [16]. Subsequent changes of these nutritional constituents would, thus, be dependent on available nutrients and precursors in the raw material, metabolic capabilities of the raw material and fermentation microorganisms, fermentation conditions as well as interactions among all these suggested elements [1,2,17]. Furthermore, it depends on the particle size distribution of raw materials, water availability, diffusion rates of nutrients and oxygen during fermentation, available microorganisms during fermentation as well as the form of fermentation process (spontaneous/natural, controlled (using starter cultures) or back-slopping) [12,18]. This review, thus, attempts to systematize the knowledge concerning the fermentation process of various nutrients in fermented cereal and legume-based products.

2. Effect of Fermentation on the Nutritional Constituents and Bioavailability of Cereals and Legumes

A number of available studies in the literature have identified different fermented cereal and legume-based products, including condiments, gruels, soups, beverages and porridges (Tables 1 and 2). These products were obtained through natural, back slopping and controlled fermentation. From the literature reviewed, most of the nutritional components investigated and reported included a proximate composition (carbohydrates, fat, protein, ash and crude fibre), energy, starch and fibre fractions, amino acids, minerals and fatty acids. While other constituents not usually investigated were vitamins and fatty acids. Additionally, associated with these nutritional constituents are antinutritional factors, including trypsin inhibitors, tannins, etc., which limit the nutrient bioavailability. These

constituents, conditions under which the fermentation process was performed, the fermented products as well as the percentage differences after fermentation were summarized in Tables 3 and 4, with reported mechanisms of modification described (Figures 1 and 2) in the ensuing sections.

2.1. Protein and Amino Acids

According to Kumitch [11] and Adhikari et al. [127], fermentation is one of the best food processing techniques that can improve protein levels of cereals and legumes. However, different study durations, experimental designs and raw materials do not entirely agree to this assertion (Tables 3 and 4), as most studies reported increases, but some others reported decrease in protein levels.

During the fermentation of pearl millet to fermented pearl millet flour, Adebiyi et al. [128] reported a 6% and 78% increase in protein and AAs, respectively, with the authors attributing this to the increase activities of hydrolytic enzymes, the degradation of complex proteins to AAs through proteolysis as well as the production of additional AAs during fermentation. Similarly, a 4% increase in the protein content of fermented instant *fura* (from pearl millet) was observed and reportedly caused by the production of some AAs more than the requirement during protein synthesis, and these tended to accumulate into an AA pool [129]. The authors also suggested that the degradation of storage protein and synthesis of new protein could have caused this increase. An increase in protein levels and AA compositions was reported in oats (*Avena sativa*) fermented with the oyster mushroom *Pleurotus ostreatus* CS155 strain for 336 h (two weeks) at room temperature [130]. The increase in AA synthesis was as a result of the fermentation with *Pleurotus ostreatus* [130]. Pearl millet fermented at 24 h also had an increased protein content due to the loss of carbohydrates, while the same study reported a decrease in arginine, lysine and glycine [131]. In total, 4.2–16.3% and 13% increased protein levels in fermented sorghum flour [132] and fermented rice flour [133], respectively, were attributed to the accumulation of microbial cells of the fermenting organisms which both studies suggested could have contributed to the increase in protein. Although Suarti et al. [134] reported a 3–20% increase in proteins of fermented rice, ascribing this to the metabolic capacity of the fungi during the fermentation process, a 0.3% decrease was equally reported in some rice varieties, with this decrease attributed to the degradation of protein molecules into AAs by *Rhizopus oligosporus* at the end of the 72 h fermentation, to support their growth. Other authors reporting an increase in proteins during the fermentation of cereals have ascribed this to activities of proteolytic enzymes produced by the fermenting organisms and protein synthesis during fermentation [135,136]. Though seldom so, decreases in protein levels have also been reported in fermented rice (8–19%) [137], fermented maize (9%) [138], fermented sorghum (13%) [139] and a study on *ogi* from two maize varieties (15–24%), attributing this to the leaching of protein into fermenting water and/or the action of degrading enzymes (e.g., proteolytic enzymes), which could have broken down the protein to its lower fractions [140]. While these studies did not investigate AAs, it could possibly be speculated that such degradations might have led to increased AA levels.

Table 1. Some cereal fermented products and associated microorganisms responsible for fermentation.

Product	Raw Materials	Product Form	Microorganisms Involved	Country/Region	Reference
Cereal-Based					
Abreh	Sorghum	Beverage	*Lactiplantibacillus plantarum*	Sudan	Odunfa and Oyewole [19]
Aceda	Sorghum	Thick porridge	Unknown	Sudan	Eggum et al. [20]
Aliha	Maize/sorghum	Beverage	Lactic acid bacteria (LAB)	Benin, Ghana, Togo	Odunfa and Oyewole [19]
Amazake	Rice	Beverage	*Aspergillus* spp.	Japan	Marsh et al. [21]
Ang kak	Rice	Colorant	*Monascus purpureus*	China, Philippines, Taiwan, Thailand	Steinkraus [22]
Apem	Rice	Bread	*Leuconostoc mesenteroides* and *Saccharomyces* spp.	Bali, Indonesia	Wang and Hesseltine [23]
Atole agrio	Maize	Beverage	*Enterococcus asini*, *Enterococcus casseliflavus*, *Enterococcus faecium*, *Enterococcus hirae*, *Enterococcus mundtii*, *Lactococcus lactis*, *Lactococcus piscium*, *Agrilactobacillus composti*, *Lacticaseibacillus casei*, *Lacticaseibacillus paracasei*, *Lacticaseibacillus rhamnosus*, *Lactiplantibacillus fabifermentans*, *Lactiplantibacillus paraplantarum*, *Lactiplantibacillus pentosus*, *Lactiplantibacillus plantarum*, *Latilactobacillus curvatus*, *Lactobacillus dixtrinicus*, *Levilactobacillus brevis*, *Ligilactobacillus araffinosus*, *Liquorilactobacillus mali*, *Loigolactobacillus coryniformis*, *Leuconostoc garlicum*, *Leuconostoc mesenteroides*, *Leuconostoc pseudomesenteroides*, *Pediococcus pentosaceus*, *Pediococcus stilesii*, *Streptococcus equines*, *Weissella cibaria*, *Weissella confusa*, *Weissella hellenica*, *Weissella oryzae* and *Weissella paramesenteroides*	Mexico	Pérez-Cataluña et al. [24]; Väkeväinen et al. [25]
Bagni	Millet	Alcoholic beverage	LAB and yeasts	Russia	Tamang et al. [4]
Banku	Maize and cassava	Dough as staple	*Lactobacillus* spp., yeasts and moulds	Ghana	Blandino et al. [3]; Campbell-Platt [26]
Ben-saalga	Pearl millet	Gruel	*Lactobacillus* spp., *Leuconostoc* spp., *Pediococcus* spp., *Weissela* spp. and yeasts	Burkina Faso, Ghana	Tou et al. [27]
Bouza	Wheat	Alcoholic beverage	LAB	Egypt	Steinkraus [22]
Burukutu	Sorghum	Alcoholic beverage	*Acetobacter* spp., *Candida* spp., *Enterobacter* spp., *Lactobacillus* spp., *Leuconostoc mesenteroides*, *Saccharomyces cerevisiae* and *Saccharomyces chavelieri*	Benin, Ghana, Nigeria	Kolawole et al. [28]; Eze et al. [29]; Alo et al. [30]
Busa	Millet, maize or sorghum	Beverage	*Lactobacillus* spp., *Leuconostoc mesenteroides*, *Pediococcus damnosus* and *Saccharomyces* spp.	East Africa, Kenya	Odunfa and Oyewole [19]

Table 1. *Cont.*

Product	Raw Materials	Product Form	Microorganisms Involved	Country/Region	Reference
Cereal-Based					
Bushera	Sorghum	Beverage	*Enterococcus* spp., *Lacticaseibacillus paracasei*, *Lactobacillus delbrueckii*, *Lactiplantibacillus plantarum*, *Levilactobacillus brevis*, and *Streptococcus thermophilus*	Uganda	Marsh et al. [21]; Mwale [31]
Cheka	Sorghum/maize	Beverage	Unknown	Ethiopia	Worku et al. [32]
Chibuku	Sorghum	Alcoholic beverage	*Lactobacillus* spp.	Botswana, Zimbabwe	Gadaga et al. [33]; Togo et al. [34]
Chicha	Maize	Beverage	Acetobacter *and* LAB	Peru	Bassi et al. [35]
Dalaki	Millet	Thick porridge	Unknown	Nigeria	Blandino et al. [3]
Darassum	Millet	Beverage	Unknown	Mongolia	Blandino et al. [3]
Dégué	Millet	Condiment	*Lacticaseibacillus casei*, *Lactobacillus gasseri*, *Levilactobacillus brevis*, *Limosilactobacillus fermentum and Enterococcus* spp.	Burkina Faso	Abriouel et al. [36]
Doklu	Maize	Dough	*Enterococcus* spp., *Lactiplantibacillus plantarum*, *Limosilactobacillus fermentum*, *Pediococcus acidilactici*, *Pediococcus pentosaceus*, *Streptococcus* spp., *Weissella cibaria*	Côte d'Ivoire	Assohoun-Djeni et al. [37]
Dolo	Sorghum	Alcoholic beverage	*Lactobacillus delbrueckii*, *Limosilactobacillus fermentum*, *Lactococcus lactis*, *Pediococcus acidilactici and Saccharomyces cerevisae*	Burkina Faso, Togo	Van der Aa Kühle et al. [38]; Sawadogo-Lingani et al. [39]
Doro	Millet/sorghum	Alcoholic beverage	Bacteria and yeast	Zimbabwe	Blandino et al. [3]
Enturire	Sorghum	Alcoholic beverage	*Lactiplantibacillus plantarum*, *Saccharomyces cerevisae*, *Weissela confusa*	Uganda	Mukisa et al. [40]
Gowe	Sorghum	Porridge	*Candida krusei*, *Candida tropicalis*, *Kluyveromyces marxianus*, *Limosilactobacillus fermentum* and *Limosilactobacillus mucosae*	Benin	Greppi et al. [41]; Adinsi et al. [42]
Hussuwa	Sorghum	Cooked dough	*Acetobacter xylinum*, *Gluconobacter oxydans*, *Lactobacillus saccharolyticum*, *Limosilactobacillus fermentum*, *Pediococcus acidilactici*, *Pediococcus pentosaceus*, *Saccharomyces cerevisiae* and yeasts	Sudan	Mwale [31]; Yousif et al. [43]
Injera	Tef flour/wheat	Flatbread	*Candida glabrata*, *Lactiplantibacillus plantarum*, *Leuconostoc mesenteroides*, *Limosilactobacillus pontis*, *Pediococcus cerevisiae* and *Saccharomyces cerevisiae*	Ethiopia	Olasupo et al. [44]
Jalebies	Wheat flour	Snack	*Saccharomyces bayanus*	India, Nepal, Pakistan	Blandino et al. [3]

Table 1. *Cont.*

Product	Raw Materials	Product Form	Microorganisms Involved	Country/Region	Reference
Cereal-Based					
Jhan chang	Barley flour	Snack	Unknown	India	Kanwar et al. [45]
Kenkey	Maize	Dough	*Candida kefir*, *Candida krusei*, *Candida mycoderma*, *Candida tropicalis*, *Limosilactobacillus fermentum*, *Limosilactobacillus reuteri* and *Saccharomyces cerevisiae*	Ghana	Odunfa and Oyewole [19]
Keribo	Barley	Beverage	LAB	Ethiopia	Tafere [46]
Kishk	Wheat, oat	Soup	*Bacillus subtilis*, *Lacticaseibacillus casei*, *Lacticaseibacillus rhamnosus*, *Lactiplantibacillus plantarum*, *Latilactobacillus sakei*, *Levilactobacillus brevis* and yeasts	Arabic countries, Egypt, Syria	Kohajdová [47]
Kisra	Sorghum	Flat bread, pancake and sourdough	*Candida intermedia*, *Candida krusei*, *Debrayomyces hansenii*, *Enterococcus faecium*, *Lactobacillus amylovorus*, *Lactobacillus confusus*, *Levilactobacillus brevis*, *Limosilactobacillus fermentum* and *Pichia kudriavzevii*	Sudan	Mohammed et al. [48]; Hamad et al. [49]
Khanom-jeen	Rice	Noodle	*Lactobacillus* spp., *Streptococcus* spp.	Thailand	Blandino et al. [3]
Koko	Maize	Porridge	*Lactiplantibacillus plantarum*, *Levilactobacillus brevis* and *Saccharomyces cerevisiae*	Ghana	Von Mollendor et al. [50]
Kunu-zaki	Maize/sorghum/millet		*Aerobacter* spp., *Aspergillus* spp., *Candida mycoderma*, *Cephalosporium* spp., *Corynebacterium* spp., *Fusarium* spp., *Lacticaseibacillus pantheris*, *Lactiplantibacillus plantarum*, *Paucilactobacillus vaccinostercus*, *Penicillium* spp., *Rhodotorula* spp. and *Saccharomyces cerevisiae*	Nigeria	Franz and Holzapfel [51]
Kutukutu	Maize	Dough	*Lactobacillus* spp., *Lactococcus* spp., *Streptococcus* spp. and *Leuconostoc* spp.	Cameroon	Tchikoua et al. [52]
Kvass	Rye	Beverage	*Lacticaseibacillus casei*, *Lactobacillus mesenteroides* and *Saccharomyces cerevisiae*	Central Europe	Blandino et al. [3]; Kohajdová [47]
Mahewu	Maize	Beverage	*Lactobacillus delbrueckii*, *Lactococcus lactis*, *Leuconostoc* spp. and *Streptococcus lactis*	Arabian gulf countries, South Africa	Prado et al. [53]; Franz et al. [54]
Mantou	Wheat flour	Steamed cake	*Saccharomyces* spp.	China	Blandino et al. [3]
Mawè	Maize	Dough	LAB and yeast	Benin, Nigeria, Togo	Greppi et al. [41]; Hounhouigan et al. [55]; Agati et al. [56]
Mbege	Maize, millet or sorghum	Beverage	*Lactiplantibacillus plantarum*, *Leuconostoc mesenteroides*, *Saccharomyces* cerevisiae and *Schizosaccharomyces pombe*	Tanzania	Odunfa and Oyewole [19]
Merissa	Sorghum and millet	Alcoholic beverage	*Saccharomyces* spp.	Sudan	Blandino et al. [3]

Table 1. *Cont.*

Product	Raw Materials	Product Form	Microorganisms Involved	Country/Region	Reference
Cereal-Based					
Munkoyo	Maize	Beverage	*Lactobacillus* spp. *and Weisella* spp.	Southern Africa	Schoustra et al. [57]
Mutwiwa	Maize	Porridge	*Pediococcus pentosaceus*	Zimbabwe	Gadaga et al. [33]
Ogi	Maize, millet or sorghum	Gruel	*Acetobacter* spp.; *Candida krusei*; *Corynebacterium* spp.; *Lactiplantibacillus plantarum, Lactobacillus acidophilus, Lactobacillus cellobiosus, Lactobacillus confusus, Ligilactobacillus agilis, Ligilactobacillus murinus, Limosilactobacillus fermentum* and *Saccharomyces cerevisiae*	West Africa	Kuye and Sanni [58]; Omemu and Bankole [59]
Otika	Sorghum	Alcoholic beverage	*Bacillus cereus*, *Bacillus subtilis*, *Candida krusei*, *Candida tropicalis*, *Enterobacter clocae*, *Lactiplantibacillus plantarum*, *Levilactobacillus brevis, Limosilactobacillus fermentum*, *Leuconostoc mesenteroides* and *Saccharomyces cerevisae*	Nigeria	Oriola et al. [60]
Pito	Sorghum	Alcoholic beverage	*Bacillus subtillis*, *Candida* spp., *Geotrichum candidum and Lactobacillus* spp.	Ghana, Nigeria	Blandino et al. [3]; Sawadogo-Lingani et al. [39]
Poto poto	Maize	Dough	*Enterococcus* spp., *Escherichia coli*, *Lactiplantibacillus plantarum*, *Lactobacillus acidophilus*, *Lactobacillus casei*, *Lactobacillus delbrueckii*, *Lactobacillus gasseri*, and *Limosilactobacillus reuteri*	Congo	Abriouel et al. [36]
Pozol	Maize	Beverage	*Bifidobacterium* spp., *Enterococcus* spp., *Lactococcus lactis*, *Lacticaseibacillus casei*, *Lactiplantibacillus plantarum, Lactobacillus alimentarium, Lactobacillus delbruekii*, and *Streptococcus suis*	Mexico	Marsh et al. [21]
Saké	Rice	Alcoholic beverage	*Aspergillus oryzae*, *Latilactobacillus sakei*, *Leuconostoc mesenteroides*, *Saccharomyces cerevisiae* and *Saccharomyces sake*	Japan	Blandino et al. [3]; Kotaka et al. [61]
Shaosinghjiu	Rice	Beverage	*Saccharomyces cerevisiae*	China	Blandino et al. [3]
Takju	Rice/wheat	Beverage	LAB and *Saccharomyces cerevisiae*	Korea	Blandino et al. [3]
Tapuy	Rice	Alcoholic beverage	*Aspergillus* spp., *Lactiplantibacillus plantarum*, *Leuconostoc* spp., *Mucor* spp., *Rhizopus* spp. *and Saccharomyces* spp.	Philippines	Ray et al. [62]
Tchapalo	Sorghum	Alcoholic beverage	*Lactiplantibacillus plantarum*, *Lactobacillus cellobiosus*, *Lactobacillus coprophilus, Lentilactobacillus hilgardii, Levilactobacillus brevis* and *Limosilactobacillus fermentum*	Côte d'Ivoire	Djè et al. [63]; N'guessan et al. [64]

Table 1. *Cont.*

Product	Raw Materials	Product Form	Microorganisms Involved	Country/Region	Reference
Cereal-Based					
Tchoukoutou	Sorghum	Alcoholic beverage	*Candida albicans*, *Clavispora lusitaniae*, *Hanseniaspora guillermondii*, *Hanseniaspora uvarum*, *Kluyveromyces marxianus*, *Saccharomyces cerevisiae* and *Torulaspora delbrueckii*	Benin	Greppi et al. [41]; Kayode et al. [65]; Greppi et al. [66]
Ting	Sorghum	Porridge	*Lacticaseibacillus casei*, *Lacticaseibacillus rhamnosus*, *Lactiplantibacillus plantarum*, *Latilactobacillus curvatus*, *Lentilactobacillus parabuchneri*, *Limosilactobacillus fermentum*, *Limosilactobacillus reuteri*, *Loigolactobacillus coryniformis* and *Schleiferilactobacillus harbinensis*	Botswana, South Africa	Madoroba et al. [67]; Madoroba et al. [68]; Sekwati-Monang and Gänzle [69]; Adebo et al. [70]
Tobwa	Maize	Beverage	LAB	Zimbabwe	Blandino et al. [3]
Togwa	Maize flour or finger millet malt		*Lactobacillus* spp., *Candida* spp. and *Saccharomyces cerevisiae*	Tanzania	Marsh et al. [21]
Uji	Sorghum	Porridge	*Lactiplantibacillus plantarum*, *Lactobacillus cellobiosus*, *Limosilactobacillus fermentum*, *Pediococcus acidilactici* and *Pediococcus pentosaceus*	East Africa	Blandino et al. [3]; Nout [71]
Umqombothi	Sorghum/maize	Beverage	*Lactobacillus* spp. and *Saccharomyces cerevisiae*	Southern Africa	Katongole [72]; Van Der Walt [73]

Table 2. Some legume fermented products and associated microorganisms responsible for fermentation.

Product	Raw Materials	Product Form	Microorganisms Involved *	Country/Region	Reference
Legume-Based					
Aakhone/Axone	Soybean	Condiment	*Bacillus subtilis* and *Proteus mirabilis*	India	Singh et al. [74]
Amriti	Black lentils	Snack	LAB and yeasts	India	Steinkraus [22]; Hossain and Kabir [75]
Bedvin roti	Black gram, opium seeds or walnut	Snack	Not reported	India	Rawat et al. [76]
Bekang	Soybean	Paste	*Bacillus amyloliquefaciens*, *Bacillus brevis*, *Bacillus circulans*, *Bacillus coagulans*, *Bacillus licheniformis*, *Bacillus pumilus*, *Bacillus sphaericus*, *Bacillus subtilis*, *Debaryomyces hansenii*, *Enterococcus cecorum*, *Enterococcus durans*, *Enterococcus faecium*, *Enterococcus hirae*, *Enterococcus raffinossus*, *Pichia burtonii*, *Proteus mirabilis*, *Saccharomyces cerevisiae*	India	Singh et al. [74]; Chettri [77]

Table 2. *Cont.*

Product	Raw Materials	Product Form	Microorganisms Involved *	Country/Region	Reference
Legume-Based					
Bhallae	Black gram	Side dish	*Bacillus subtilis*, *Candida curvata*, *Candida famata*, *Candida membraneafaciens*, *Candida variovaarai*, *Cryptococcus humicoius*, *Debaryomyces hansenii*, *Enterococcus faecalis*, *Geotrichum candidum*, *Hansenula anomala*, *Hansenula polymorpha*, *Kluyveromyces marxianus*, *Leuconostoc mesenteroides*, *Limosilactobacillus fermentum*, *Pediococcus membranaefaciens*, *Rhizopus marina*, *Saccharomyces cerevisiae*, *Trichosporon beigelii*, *Trichosporon pullulans* and *Wingea robertsii*	India	Rani and Soni [78]
Chee-fan	Soybean wheat curd	Cheese-like	*Aspergillus glaucus* and *Mucor* spp.	China	Blandino et al. [3]
Cheonggukjang	Soybean	Meal, dish	*Bacillus amyloliquefaciens*, *Bacillus cereus*, *Bacillus subtilis*, *Pantoea agglomerans*, *Pantoega ananatis*, *Enterococcus* spp., *Pseudomonas* spp. and *Rhodococcus* spp.	Korea	Shin et al. [79]
Dalbari (Urad dalbari)	Lentil	Snack	Not reported	India	Sha et al. [80]
Dawadawa	Bambara groundnut and locust bean	Condiment	*Bacillus licheniformis*, *Bacillus pumilus* and *Bacillus subtilis*	Central and West Africa	Amadi et al. [81]; Frias et al. [82]; Akanni et al. [83]
Dhokla	Chickpeas, green gram and rice	Snack	*Enterococcus faecalis*, *Leuconostoc mesenteroides*, *Limosilactobacillus fermentum*, *Streptococcus faecalis*, *Torulaspora candida* and *Torulaspora pullulans*	India	Blandino et al. [3]; Frias et al. [82]
Doenjang	Soybean	Soup	*Aspergillus oryzae*, *Bacillus licheniformis*, *Bacillus subtilis*, *Debaryomyces hansenii*, *Enterococcus faecium*, *Lactobacillus* spp., *Leuconostoc mesenteroides*, *Mucor plumbeus* and *Tetragenococcus halophilus*	Korea	Shin et al. [79]; Frias et al. [82]
Dosa	Black gram dhal (*Phaselus mango*) and rice	Pancake, snack	*Bacillus amyloliquefaciens*, *Enterococcus faecalis*, *Candida boidini*, *Candida glabrata*, *Candida sake*, *Debaryomyces hansenii*, *Hansenula polymorpha*, *Issatchenkia terricola*, *Lactobacillus delbrueckii*, *Lactobacillus fermenti*, *Leuconostoc mesenteroides*, *Streptococcus faecalis* and *Rhizopus graminis*	India, Sri Lanka	Soni et al. [84]
Douchi	Soybean	Condiment	*Aspergillus oryzae*, *Bacillus amyloliquefaciens*, *Bacillus subtilis*, *Enterobacter* spp., *Pichia farinose*, *Pseudomonas* spp., *Saccharomyces cerevisiae*, *Staphylococcus saprophyticus* and *Staphylococcus sciuri*	China, Taiwan	Zhang et al. [85]; Chen et al. [86]
Furu	Soybean curd	Condiment	*Bacillus firmus*, *Bacillus megaterium*, *Bacillus pumilus*, *Bacillus stearothermophilus* and *Staphylococcus hominis*	China	Sumino et al. [87]

Table 2. *Cont.*

Product	Raw Materials	Product Form	Microorganisms Involved *	Country/Region	Reference
Legume-Based					
Gochujang	Soybean and red pepper	Seasoning	*Aspergillus* spp., *Bacillus amyloliquefacious*, *Bacillus liqueformis*, *Bacillus subtilis*, *Bacillus velegensis*, *Candida lactis*, *Penicillium* spp., *Rhizopus* spp., spcecis of *Oceanobacillus*, *Zygorouxii* spp. and *Zygosaccharomyses* spp.	Korea	Kim et al. [88]; Nam et al. [89]
Hawaijar	Soybean	Meal, dish	*Alkaligenes* spp., *Bacillus amyloliquefaciens*, *Bacillus cereus*, *Bacillus licheniformis*, *Bacillus subtilis*, *Proteus mirabilis*, *Providencia rettgers*, *Staphylococcus aureus* and *Staphylococcus sciuri*	India	Singh et al. [74]; Jeyaram et al. [90]
Idli	Black gram and rice	Meal, dish	*Bacillus amyloliquefaciens*, *Candida versatilis*, *Enterococcus faecium*, *Limosilactobacillus fermentum*, *Lactobacillus delbrueckii*, *Lactococcus lactis*, *Loigolactobacillus coryniformis*, *Leuconostoc mesenteroides*, *Pediococcus acidilactis*, *Pediococcus cerevisiae*, *Torulopsis* spp.	India, Malaysia, Singapore, Sri Lanka	Frias et al. [82]; Sridevi et al. [91]
Iru	Locust bean	Condiment	*Tricholsporon pullulans*, *Streptococcus lactis*, *Streptococcus faecalis* and yeast *Bacillus amyloliquefaciens*, *Bacillus atrophaeus*, *Bacillus fumus*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus mojavensis*, *Bacillus pumilus*, *Bacillus subtilis*, *Lysininbacillus sphaericus* and *Staphylococcus saprophyticus*	West Africa	Odunfa and Oyewole [19]; Meerak et al. [92]
Kanjang	Soybean, *meju*, salt and water	Sauce	*Aspergillus oryzae*, *Bacillus citreus*, *Bacillus pumillus*, *Bacillus subtilis*, *Saccharomyces rouxii* and *Sarcina mazima*	Korea	Shin et al. [79]
Kawal	Leaves of legume (*Cassia* spp.)	Meat substitute	*Bacillus subilis*, *Lactiplantibacillus plantarum*, *Propionibacterium* spp. and *Staphylococcus sciuri*, Yeasts	Sudan	Dirar et al. [93]
Kecap	Soybean and wheat	Sauce	*Aspergillus oryzae*, *Candida* spp., *Debaromyces* spp., *Pediococcus halophilus*, *Rhizopus oligosporus*, *Rhizopus oryzae*, *Staphylococcus* spp. and *Sterigmatomyces* spp.	Indonesia	Alexandraki et al. [94]
Ketjap	Black soybean	Syrup	*Aspergillus flavus*, *Aspergillus oryzae*, *Rhizopus arrhizus*, *Rhizopus oligosporus*	Indonesia	Alexandraki et al. [94]
Kinda	Locust bean	Condiment	*Bacillus amyloliquefaciens*, *Bacillus atrophaeus*, *Bacillus licheniformis*, *Bacillus mojavensis*, *Bacillus pumilus*, *Bacillus subtilis* and *Lysininbacillus sphaericus*	Sierra Leone	Meerak et al. [92]
Kinema	Soybean	Meal, dish	*Bacillus cereus*, *Bacillus circulans*, *Bacillus licheniformis*, *Bacillus pumilus*, *Bacillus subtilis*, *Bacillus thuringiensis*, *Bacillus sphaericus*, *Candida parapsilosis*, *Corynebacterium glutamicum*, *Enterococcus faecium*, *Geotrichum candidum* and *Lactococcus lactis*	Bhutan, India, Nepal	Tamang [95]; Kumar et al. [96]

Table 2. *Cont.*

Product	Raw Materials	Product Form	Microorganisms Involved *	Country/Region	Reference
Legume-Based					
Khaman	Bengal gram and chickpeas	Snack	*Bacillus* spp., *Lactobacillus fermentum*, *Lactobacillus lactis*, *Leuconostoc mesenteroides* and *Pediococcus acidilactici*	India	Ramakrishnan [97]
Koikuchi Shoyu	Defatted soybean flake, wheat, brine and *tane-koji*	Soy sauce	*Aspergillus oryzae*, *Aspergillus sojae*, *Bacillus* spp., *Enterococcus faecalis*, *Pediococcus halophilus*, *Torulopsis echellsii*, *Torulopsis versatilis*, *Saccharomyces halomembransis* and *Saccharomyces rouxii*	Japan	Sugawara [98]
Maseura	Black gram	Dry, ball-like, brittle, condiment	*Bacillus laterosporus*, *Bacillus mycoides*, *Bacillus pumilus*, *Bacillus subtilis*, *Candida castellii*, *Enterococcus durans*, *Ligilactobacillus salivarius*, *Limosilactobacillus fermentum*, *Pediococcus acidilactici*, *Pediococcus pentosaceous*, *Pichia burtonii* and *Saccharomyces cerevisiae*	India, Nepal	Chettri and Tamang [99]
Mashbari	Black gram and spices	Meal, dish	*Bacillus* spp. A_{94}, *Lactobacillus* spp. and *Saccharomyces cerevisiae*	India	Sharma et al. [100]
Masyaura	Black gram or green gram	Side dish	*Aspergillus niger*, *Candida versatilis*, *Cladosporium* spp., *Lactobacillus* spp., *Pediococcus acidilactici*, *Pediococcus pentosaceus*, *Penicillium* spp. and *Saccharomyces cerevisiae*	India, Nepal	Dahal et al. [101]; Dahal et al. [102]
Meitauza	Soybean	Meal, dish	*Actinomucor elegans*, *Aspergillus oryzae*, *Bacillus subtilis*, *Mucor meitauza* and *Rhizopus oligosporus*	China, Taiwan	Zhu et al. [103]
Meju	Soybean	Condiment	*Aspergillus flavus*, *Aspergillus fumigatus*, *Aspergillus niger*, *Aspergillus oryzae*, *Aspergillus retricus*, *Aspergillus spinosa*, *Aspergillus terreus*, *Aspergillus wentii*, *Bacillus citreus*, *Bacillus circulans*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus mesentricus*, *Bacillus subtilis*, *Bacillus pumilis*, *Botrytis cineara*, *Candida edax*, *Candida incommenis*, *Candida utilis*, *Hansenula anomala*, *Hansenula capsulata*, *Hansenula holstii*, *Lactobacillus* spp., *Mucor adundans*, *Mucor circinelloides*, *Mucor griseocyanus*, *Mucor hiemalis*, *Mucor jasseni*, *Mucor racemosus*, *Pediococcus* acidilactici, *Penicillium citrinum*, *Penicillium griseopurpureum*, *Penicillium griesotula*, *Penicillium kaupscinskii*, *Penicillium lanosum*, *Penicillium thomii*, *Penicillium turalense*, *Rhizopus chinensis*, *Rhizopus nigricans*, *Rhizopus oryzae*, *Rhizopus sotronifer*, *Rhodotorula flaca*, *Rhodotorula glutinis*, *Saccharomyces exiguus*, *Saccharomyces cerevisiae*, *Saccharomyces kluyveri*, *Zygosaccharomyces japonicus* and *Zygosaccharomyces rouxii*	Korea	Choi et al. [104]
Miso	Soybean	Seasoning	*Aspergillus oryzae*, *Leuconostoc paramesenteroides*, *Micrococcus halobius*, *Pediococcus acidilactici* and *Zygosaccharomyces rouxii*	Japan	Asahara et al. [105]

Table 2. *Cont.*

Product	Raw Materials	Product Form	Microorganisms Involved *	Country/Region	Reference
Legume-Based					
Moromi	Soybean	Seasoning	*Aspergillus oryzae*, *Candida etchellsii*, *Candida versatilis*, *Tetragenococcus halophilus* and *Zygosaccharomyces rouxii*	Japan	Khairil et al. [106]
Natto	Soybean	Meal, dish	*Bacillus subtilis* (*natto*)	Japan	Nagai and Tamang [107]
Ogiri	Castor oil seed, melon seed, groundnut and fluted pumpkin seed	Condiment	*Bacillus licheniformis*, *Bacillus pumilus*, *Bacillus megaterium*, *Bacillus rimus*, *Bacillus subtilis*, *Lactiplantibacillus plantarum*, *Pediococcus* spp. and *Salmonella shigella dysenteria Staphylococcus saprophyticus*	Central, East and West Africa	Odunfa and Oyewole [19]; Okoronkwo et al. [108]
Okpehe	*Prosopis africana* seeds	Condiment	*Bacillus amyloliquefaciens*, *Bacillus cereus*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus subtilis*, *Escherichia coli*, *Saccharomyces cerevisiae* and *Staphylococcus aureus*	Nigeria	Balogun and Oyeyiola [109]
Ontjom/Oncom (Hitam/Merah)	Soybean	Snack	*Neurospora crassa*, *Neurospora intermedia*, *Neurospora sitophila* (from red oncom) and *Rhizopus oligosporus* (from black oncom)	Indonesia	Ho [110]
Owoh	Cotton seed	Condiment	*Bacillus licheniformis*, *Bacillus pumilus*, *Bacillus subtilis* and *Staphylococcus saprophyticus*	Nigeria	Ezekiel et al. [111]
Papad	Black gram, Bengal gram, lentil and red or green gram	Condiment or savoury food	*Candida krusei*, *Debaryomyces hansenii*, *Enterococcus faecalis*, *Leuconostoc mesenteroides*, *Limosilactobacillus fermentum*, *Pediococcus membranaefaciens*, *Saccharomyces cerevisiae* and *Trichosporon beigelii*	India, Nepal	Rani and Soni [78]
Pepok	Soybean	Condiment	*Bacillus* spp.	Myanmar	Nagai and Tamang [107]
Peruyyan	Soybean	Side dish	*Bacillus amyloliquefaciens*, *Bacillus subtilis*, *Enterococcus faecalis*, *Pediococcus acidilactici* and *Vagococcus lutrae*	India	Singh et al. [74]
Sepubari	Black gram, Dangal, spices	Meal, dish	*Bacillus* spp. A_{31}., *Lactobacillus* spp. and *Saccharomyces cerevisiae*	India	Sharma et al. [100]
Sieng	Soybean	Condiment	*Bacillus* spp.	Cambodia, Laos	Nagai and Tamang [107]
Shoyu	Soybean	Seasoning	*Aspergillus oryzae*, *Clavaria versatilis*, *Pediococcus halophilus*, *Saccharomyces rouxii*, *Torulopsis versatilis* and *Zygosaccharomyces rouxii*	China, Japan, Korea	Noda et al. [112]; Inamori et al. [113]
Soumbala	Locust bean	Condiment	*Bacillus amyloliquefaciens*, *Bacillus atrophaeus*, *Bacillus badius*, *Bacillus cereus*, *Bacillus firmus*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus mojavensis*, *Bacillus mycoides*, *Bacillus pumilus*, *Bacillus sphaericus*, *Bacillus subtilis*, *Bacillus thuringiensis*, *Brevibacillus laterosporus*, *Lysininbacillus sphaericus*, *Peanibacillus alvei* and *Peanibacillus larvae*	Burkina Faso	Ouoba et al. [114]; Ouoba et al. [115]

Table 2. *Cont.*

Product	Raw Materials	Product Form	Microorganisms Involved *	Country/Region	Reference
Legume-Based					
Sufu	Soybean curd	Side dish	*Actinomucor elenans*, *Mucor corticolus*, *Mucor hiemalis*, *Mucor praini*, *Monascus purpureus*, *Mucor racemosus*, *Mucor silvatixus*, *Mucor subtilissimus* and *Rhizopus chinensis*	China, Taiwan	Han et al. [116]; Kanlayakrit and Phromsak [117]
Tauco	Soybean	Paste	*Aspergillus oryzae*, *Hansenula* spp., *Lactobacillus delbrueckii*, *Rhizopus ologosporus*, *Rhizopus* oryzae and *Zygosaccharomyces soyae*	Indonesia	Winarno et al. [118]
Teliye mah	Black gram	Semi solid	Not reported	India	Thakur et al. [119]
Tempe/Tempeh	Soybean	Side dish	*Aspergillus niger*, *Aspergillus oryzae*, *Citrobacter freundii*, *Enterobacter cloacae*, *Klebsiella pneumoniae*, *Klebsiella pneumoniae* subspp. *ozaenae*, *Lactiplantibacillus plantarum*, *Lactobacillus lactis*, *Limosilactobacillus fermentum*, *Limosilactobacillus reuteri*, *Pseudomas fluorescens* as vitamin B12-producing bacteria, *Rhizopus arrhizus*, *Rhizopus oligosporus*, *Rhizopus oryzae* and *Rhizopus stolonifer*	Indonesia, Japan, Korea, the Netherlands, New Guinea, Surinam	Frias et al. [82]; Nout and Kiers [120]; Jennessen et al. [121]
Tianmianjiang	Soybean	Sauce	Not reported	China, Korea	Kwon et al. [122]
Thu nao	Soybean	Condiment, side dish	*Bacillus pumilus*, *Bacillus subtilis* and *Lactobacillus* spp.	Thailand	Chunhachart et al. [123]
Tofu (stinky tofu)	Soybean		*Bacillus* spp., *Enterococcus hermanniensis*, *Lactobacillus agilis*, *Lactobacillus brevis*, *Lactobacillus buchneri*, *Lactobacillus crispatus*, *Lactobacillus curvatus*, *Lactobacillus* delbrueckii, *Lactobacillus farciminis*, *Lactobacillus fermentum*, *Lactobacillus pantheris*, *Lactobacillus salivarius*, *Lactobacillus vaccinostercus*, *Lactococcus* lactis, *Lactococcus* spp., *Leuconostoc camosum*, *Leuconostoc citreum*, *Leuconostoc fallax*, *Leuconostoc lactis*, *Leuconostoc mesenteroides*, *Leuconostoc pseudomesenteroides*, *Pediococcus acidilactici*, *Streptococcus bovis*, *Streptococcus macedonicus*, *Weissella cibaria*, *Weissella confusa*, *Weissella paramesenteroides* and *Weissella soli*	China, Japan	Chao et al. [124]
Toyo	Soybean, salt, brown sugar and wheat starter	Cowpea sauce	*Aspergillus oryzae*, *Lactobacillus delbrueckii Hansenula anomala* and *Hansenula subpelliculosa*	Philippines	Alexandraki et al. [94]
Tungrymbai	Soybean	Side dish	*Bacillus amyloliquefaciens*, *Bacillus licheniformis*, *Bacillus pumilus*, *Bacillus subtilis*, *Enterococcus cecorum*, *Enterococcus durans*, *Enterococcus faecium*, *Enterococcus hirae*, *Enterococcus raffinossus*, *Levilactobacillus brevis*, *Debaryomyces hansenii*, *Pichia burtonii*, *Saccharomyces cerevisiae* and *Vagococcus carniphilus*	India	Singh et al. [74]; Chettri [77]
Ugba	African oil bean	Condiment	*Bacillus* spp., *Micrococcus* spp., *Proteus* spp., *Pseudomonas* spp. and *Staphylococcus* spp.	Nigeria	Okorie and Olasupo [125]

Table 2. *Cont.*

Product	Raw Materials	Product Form	Microorganisms Involved *	Country/Region	Reference
Legume-Based					
Uri	Locust bean	Condiment	*Bacillus* spp.	West Africa	Alexandraki et al. [94]
Vadai	Black gram	Snack	*Leuconostoc* spp., *Pediococcus* spp. and *Streptococcus* spp.	India	Blandino et al. [3]
Wari	Black gram or Bengal gram	Snack	*Bacillus subtilis*, *Candida curvata*, *Candida famata*, *Candida krusei*, *Candida parapsilosis*, *Candida vartiovaarai*, *Cryptococcus humicolus*, *Debaromyces hansenii*, *Debaromyces tamarii*, *Enterococcus faecalis*, *Geotrichum candidum*, *Hansenula anomala*, *Kluyveromyces marxianus*, *Rhizopus lactosa*, *Saccharomyces. cerevisiae*, *Trichosporon beigelii* and *Wingea robetsii*	India, Pakistan	Rani and Soni [78]

* Name of all *Lactobacillus* species have been modified according to novel classification of Zheng et al. [126].

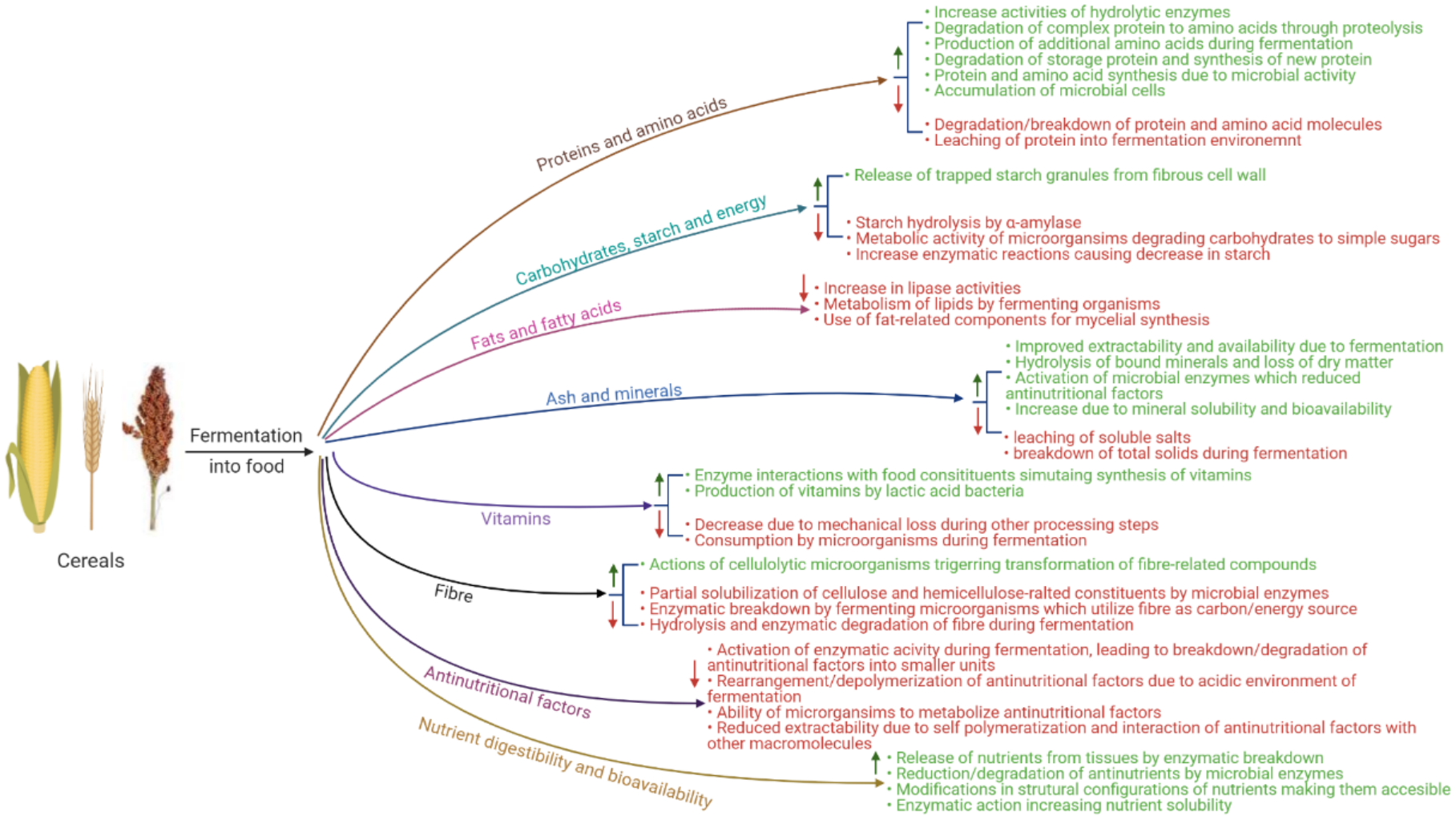

Figure 1. A summarized mechanisms of nutrient modifications in fermented cereals.

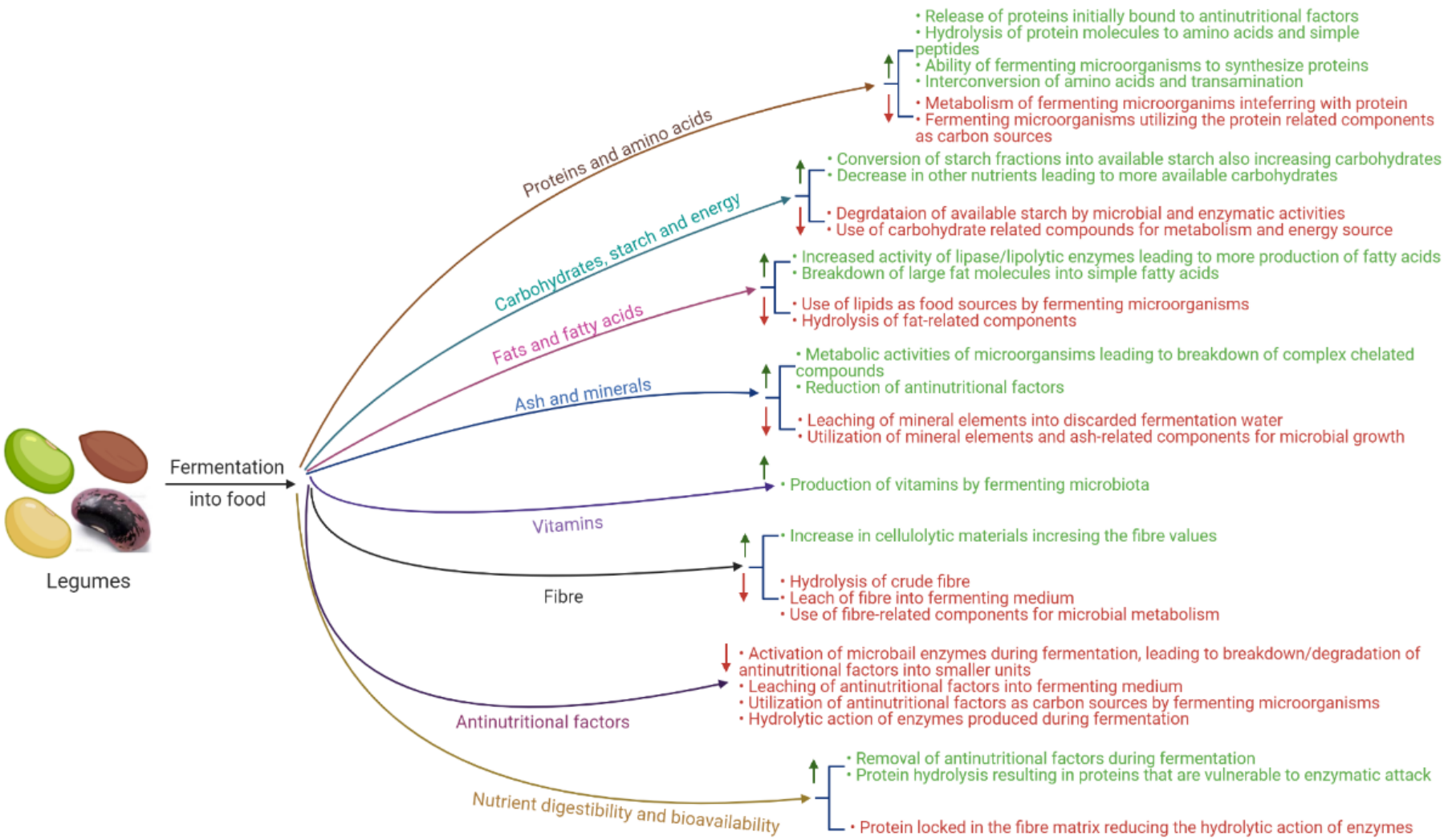

Figure 2. A summarized mechanisms of nutrient modifications in fermented legumes.

Legumes are excellent sources of good-quality proteins and are rich in essential AAs. Fermentation increases the amount of free AA contents in legume-based products, depending on the legume species and cultivars [141], and such an increase could be of advantage in supplementing the nutrients obtained from other food crops and assisting people suffering from protein deficiency attributed to the maintenance and growth of the body. The fermentation of Bambara groundnuts into unhulled *dawadawa* (a fermented condiment) increased the protein content by approximately 18%, and this was attributed to the release of proteins initially bound to the antinutritional factors [142]. The mechanism of the protein increase in this study was also ascribed to an increase in the microbial mass resulting in an extensive hydrolysis of the protein molecules to AAs and other simple peptides. Additionally, in the same study, fermentation was observed to significantly increase all the essential AAs except for lysine and histidine. The trend observed for histidine and lysine was attributed to their distinct basic side chains (which contain nitrogen and resemble ammonia), possibly causing them to have reacted differently during fermentation [142]. Peas (*Pisum sativum*) fermented with *Aspergillus niger* NRRL 334 and *Aspergillus oryzae* NRRL 5590 for 6 h at 40 °C to obtain fermented pea protein-enriched flour through SSF led to an increase in protein (0.5–15%) and AA (1.8–29%) levels [11,143]. It was postulated that the increase in the level of protein was due to the fungi utilizing lipids and starch as well as the ability of these fungi species to produce proteins [11,143]. An increase in the protein (3–25%) through the SSF of legume flours has also been previously reported [144–149], with these studies ascribing such increases to the synthesis of new proteins during fermentation, yeast proliferation, the loss of dry matter, net synthesis of protein by fermenting seeds, increase in fungal biomass that was produced from the fermenting microorganism and partial protein denaturation and pH decrease during fermentation. The mechanism of an increase in the protein content of lupin flours fermented with *Aspergillus ficuum*, *Aspergillus sojae* and their co-cultures could be linked to the microorganisms using the substrate as carbon and energy sources during SSF to produce fungal protein [150]. The formation of soluble products and monomers after fermentation, as well as the interconversion of AAs, was reported to have also enhanced AA levels by up to 13%, though an AA decrease of between 0.3% and 16% was equally reported during the fermentation of African yam bean flour [149]. The increase in AAs might also be attributed to transamination or synthesis taking place during the SSF process [11,143]. Some anabolic processes leading to the build-up of polymer or microbial cell proliferation were also reported to have increased the protein content (5–94%) of soymilk from soybeans [151].

Some studies have reported both an increase and a decrease in protein and AA levels during the fermentation of legumes. Difo et al. [146] recorded both an increase (12%) as well as a decrease of 10% in protein in fermented *Vigna racemose* flour. Such a decrease was suggested to have been due to the metabolism of *Aspergillus niger* with respect to other compounds present in *V. racemosa*, and such a metabolism might have produced some compounds capable of interfering with the protein content. The decrease in AAs in a study by Kumitch et al. [143] over the fermentation time (6 h) could have been due to the fungi utilizing these AAs and reducing the essential AAs further. Another study was conducted on the common bean (*Phaseolus vulgaris*) fermented with *Limosilactobacillus fermentum* for 72 h at 37 °C to obtain fermented bean powder through SmF, leading to an increase in protein (1%) as well as an increase (1–20%) and decrease (3–7%) in AAs [152]. While the increase in AAs was linked to the synthesis of substances by bacteria present in the substrate, the decrease suggested their utilization by the bacteria [152]. The modification of nutritional constituents usually occurs simultaneously with one another. For example, the slight decrease in the crude protein of *Aspergillus ficuum* fermented lupin was suggested to be interrelated to the observed increase in soluble carbohydrate and starch [150]. Noting that food constituents exist together in a food matrix, it could be postulated that a greater dissolution of carbohydrate and starch led the "exposed" proteins to the fermenting organisms, leading to this reported decrease. Asensio-Grau et al. [153] attributed the modification of protein levels to the bioconversion of some carbohydrates

into protein. The differences in the trend of modification (increase/decrease) of protein and AA compositions in fermented cereals and legumes could be associated with factors such as the fermentation conditions used (which differs), growth rate and metabolic capabilities of the microbiota, initial protein content and AA composition of the grains as well as the solubility and molecular structure of the inherent protein and AAs.

2.2. Carbohydrate, Energy and Starch Fractions

Fermentation is an exothermic metabolic process which involves the consumption of food nutrients through the activities of microorganisms (either native or deliberately introduced) that serve as fermenters. These organisms rely on the different nutrients of foods and favourable environmental conditions for their growth and metabolic activities, leading to their survival, proliferation and synthesis of by-products. Fermentation enriches cereal-based food in protein by removing part of the carbohydrates and helping in energy reduction during cooking [153,200,201]. The effect of fermentation on the carbohydrate, energy and starch contents of some cereal-based foods are presented in Table 3. Nnam and Obiakor [137] reported a progressive increase (1.1–2.4%) and decrease (0.3%) in carbohydrate contents of spontaneously fermented rice for 72 h (24 h interval) at 28 °C and ascribed this to changes in the population of the fermenting organism, which could be as a result of continuously changing the fermentation environment, enabled through changes in acidity and chemical balances. A significant increase in the carbohydrate content was also reported in fermented pearl millet flour (3%) [128], fermented oat flour (1%) [130], fermented sorghum flour (0.9%) [139] and *ogi* (5–6%) [140]. Decreases in carbohydrate levels have also been reported in *fura* (0.7%) [129], fermented sorghum flour (0.3–1%) [132], fermented rice flour (0.5–7%) [134], fermented sorghum flour [136], fermented maize flour (4%) [156] and fermented pearl millet flour (3%) [158], with the studies attributing these to the metabolic activity of microorganisms degrading carbohydrates into simple sugars for their growth, as well as hydrolyses of starch by α-amylase. Increases in energy levels have been reported in fermented pearl millet flour (2%) [128] as well as decreases in fermented maize dough (1.6%) [138] and fermented sorghum flour (1.6%) [139] with no mechanisms reported. An increase in the total starch of a fermented cereal starter (from barley and pea) through SSF was ascribed to the decline in amylase activity and the release of trapped starch granules from the fibrous cell wall structure (by crude multienzyme composed of non-starch polysaccharide-hydrolysing enzymes) [18]. Decreases in resistant (20.6–72.9%) and total (12.2–16.8%) starches in fermented sorghum flour were also associated with the natural fermentation of sorghum that led to increased enzymatic reactions [166].

Table 3. Influence of fermentation on the nutritional composition of some cereal-based products.

Raw Material	Fermentation Type	Fermentation Form	Fermentation Conditions	Product	Modification(s) in Nutritional Constituents	Percentage Difference	Key Mechanism(s) Involved	Reference
Barley (*Hordeum vulgare*) and pea (*Pisum sativum*)	SSF	Spontaneous	24 h at room temperature (RT) for 24 h, 72 h at 35–38 °C, 168 h at 40–50 °C, 312 h at 53–60 °C, 456 h at 35–40 °C, 600 h at 28–34 °C and 720 h at RT	Cereal starter	Initial decrease in reducing sugar, increase and afterwards decrease. Initial decrease in total starch and subsequent increase afterwards.	63%↓ in reducing sugar and 3%↑ in total starch.	Increase in total starch ascribed to decline in amylase activity and release of trapped starch granules from the fibrous cell wall structure.	Li et al. [18]
Linseed (*Linum usitatissimum*)	SmF	Controlled using *Lactobacillus acidophilus* MTCC-10307, *Bacillus mesentericus*, *Saccharomyces boulardii*, *S. ellipsoideus* and LAB isolate	48 h at 30 °C	Fermented linseed beverage	Reduction in tannins and cyanogenic glycosides.	22–66%↓ in tannins and 8–66%↓ in cyanogenic glycosides.	Reduction in cyanogenic glycosides due to the breakdown and degradation of ANFs into smaller units by the action of enzymes.	Nivetha et al. [154]
Maize (*Zea mays* L.) Hudeiba 1 and Mugtama 45 cultivars	SmF	Spontaneous	0–32 h (8 h interval) at 37 °C	Fermented maize flour	Increase in crude protein, some essential AAs and IVPD.	0.5–5%↑ and 0.1%↓ in crude protein, 0.95–44%↑ and 9–16%↓ in essential AAs, 3–21%↑ in IVPD for Hudeiba 1. 0.41–5%↑ in crude protein, 0.4–38%↑ and 3–47%↓ in essential AAs and 19–45%↑ in IVPD for Mugtama 45.	Not reported.	Mohiedeen et al. [155]

Table 3. *Cont.*

Raw Material	Fermentation Type	Fermentation Form	Fermentation Conditions	Product	Modification(s) in Nutritional Constituents	Percentage Difference	Key Mechanism(s) Involved	Reference
Maize (*Z. mays*)	SmF	LAB consortium from maize and sorghum	0–48 h (12 h interval) at RT	Fermented maize flour	Decrease in lipid, fibre and CHO. Increase in ash, protein, IVSD and IVPD.	74%↓ in crude fibre, 11%↓ in lipid, 4%↓ in CHO, 67%↑ in ash, 37%↑ in protein, 114–146%↑ in IVSD and 34–44.7%↑ in IVPD.	Lipid reduction due to metabolism of fatty acids and glycerol by fermenting organisms. Fibre reduction due to enzymatic breakdown utilization as carbon source. Increase in IVSD attributed to changes in endosperm protein which increased starch accessibility to digestive enzymes.	Ogodo et al. [156]
Maize (*Z. mays*) varieties yellow-coloured quality protein maize and yellow-coloured normal maize	SmF	Spontaneous	72 h at RT	Maize *ogi* flour	Decrease in crude protein, fat, fibre, ash and most minerals. Increase in CHO.	15–24%↓ in protein, 4.6–18%↓ in fat, 27.3–32%↓ in ash, 46–49.2%↓ in crude fibre, 5.5–5.8%↑ in CHO, 7–548%↑ and 21–96%↓ in minerals.	Protein degradation of due to leaching of protein into the fermenting water and/or action of degrading enzymes.	Oladeji et al. [140]
Maize (*Z. mays*) ZM 607 and Tamira Pool A9 varieties	SmF	Spontaneous	8 h at RT	Fermented maize flour	Increase in vitamins and protein. Decrease in fat and fibre content.	51–141%↑ in protein, 20–30%↓ in fat, 24–31%↓ in fibre and 10-fold↑ in niacin.	Not reported.	Ongol et al. [157]
Oat (*Avena sativa*)	SSF	Starter culture with *Pleurotus ostreatus* CS155 strain	336 h (14 days) at RT	Fermented oat flour	Decrease in minerals, fibre and tannin. Increase in protein, fat, CHO, IVPD, soluble nitrogen and some AAs.	6.6%↑ in protein, 97%↑ in fat, 48%↓ in minerals, 22%↓ in fibre, 1%↑ in CHO, 11%↑ in IVPD, 49%↑ in soluble nitrogen, 50%↓ in tannin, 0.12–90%↑ and 2.4–33%↓ in AAs.	Protein increase attributed to increase in AA synthesis. Decrease in fibre due to enzymatic action. Decrease in tannin was due to action of a tannase.	Espinosa-Páez et al. [130]

Table 3. *Cont.*

Raw Material	Fermentation Type	Fermentation Form	Fermentation Conditions	Product	Modification(s) in Nutritional Constituents	Percentage Difference	Key Mechanism(s) Involved	Reference
Pearl millet (*Pennisetum glaucum*)	SmF	Spontaneous	72 h at 28 °C	Fermented pearl millet flour	Decrease in crude fat and ash. Increase in crude protein, AAs, most minerals, CHO, energy and fibre.	24%↓ in fat, 10%↑ in ash, 6%↑ in protein, 6–78%↑ in amino acids, 3%↑ in CHO, 2%↑ in energy, 6%↑ in fibre, 10–92%↑ and 2–43%↓ in minerals.	Breakdown of lipids and leaching of soluble inorganic salts. Accumulation of proteins, increased activities of hydrolytic enzymes, degradation of complex proteins to AAs and production of additional AAs. Improvement in the extractability of minerals via synthesis and cell wall solubilization.	Adebiyi et al. [128]
Pearl millet (*P. glaucum*)	SmF	Spontaneous	72 h at RT	Fermented pearl millet flour	Decrease in ash, fibre and CHO. Increase in fat and protein.	21%↓ in ash, 55%↓ in fibre, 3%↓ in CHO, 103%↑ in fat and 24%↑ in protein.	Ash reduction due to leaching of soluble inorganic salts. Low crude fibre due to enzymatic degradation. Metabolic activity of microorganisms and enzymes on sugars caused CHO decrease.	Akinola et al. [158]
Pearl millet (*P. glaucum*)	SmF	Spontaneous	48 h at 32 °C	Fermented instant *fura*	Increase in crude fat, protein, fibre and most minerals. Decrease in ash, CHO and PA.	3%↑ in fat, 4%↑ in protein, 8%↓ in ash, 0.9%↑ in fibre, 0.7%↓ in CHO, 100%↓ in PA, 3–33%↑ and 99%↓ in minerals.	Decrease in CHO due to increase in α-amylase activity. Increase in protein due to excess production of some AAs, degradation of storage protein. Mineral increase attributed to breakdown of protein-mineral bonds.	Inyang and Zakari [129]

Table 3. *Cont.*

Raw Material	Fermentation Type	Fermentation Form	Fermentation Conditions	Product	Modification(s) in Nutritional Constituents	Percentage Difference	Key Mechanism(s) Involved	Reference
Pearl millet (*P. glaucum*)	SmF	Inoculated with mixed culture combinations of yeasts and bacteria (*S. cerevisiae*, *S. diastaticus*, *L. brevis* and *L. fermentum*)	72 h at 30 °C	Fermented pearl millet flour	Increase in IVSD and IVPD.	247–362%↑ in IVSD and 54–77%↑ in IVPD.	Not reported.	Khetarpaul and Chauhan [159]
Pearl millet (*P. glaucum*)	SmF	Spontaneous	0–96 h (24 h interval) at 20, 30, 40 and 50 °C	Fermented pearl millet flour	Initial decrease in reducing minerals increase and afterwards decrease in fermentation conditions.	14–63%↑ in calcium, 7–159%↑ in iron, 9–102%↑ in zinc, 118%↑ in copper and 49–102%↑ in manganese.	Not reported.	Mahajan and Chauhan [160]
Rice (*Oryza sativa*)	SmF	Spontaneous using 1% baker's yeast	Optimum conditions of pH 5.5 for 6.26 h at 32 °C	Fermented rice flour	Increase in protein, ash, minerals, some vitamins, total starch, resistant starch, amylose content, insoluble and soluble fibre. Decrease in lipids and PA.	13%↑ in protein, 7%↑ in ash, 0.8%↓ in lipid, 108%↑ in soluble fibre, 16%↑ in insoluble fibre, 39%↑ in resistant starch, 11%↓ in total starch, 1.8%↓ in amylose content, 13–34%↑ in minerals, 3–3617%↑ and 0.99–3.4%↓ in vitamins and 41%↓ in PA.	Protein increase due to accumulation of microbial cells. Increase in ash related to increased mineral solubility and bioavailability. Vitamin B increase due to enzyme interactions and release of the bound forms of the vitamins. Decrease in amylose content due to the breakdown of its chain by α-amylase.	Ilowefah et al. [133]

Table 3. *Cont.*

Raw Material	Fermentation Type	Fermentation Form	Fermentation Conditions	Product	Modification(s) in Nutritional Constituents	Percentage Difference	Key Mechanism(s) Involved	Reference
Rice *(O. sativa)*	SmF	Controlled using 1% baker's yeast	Optimum conditions of pH 5.5 for 6.23 h at 32 °C	Fermented rice flour	Increase in protein, ash, minerals, some vitamins and insoluble and soluble fibre. Decrease in lipids and PA.	9%↑ in ash, 13%↑ in protein, 0.8%↓ in lipid, 17%↑ in insoluble fibre, 106%↑ in soluble fibre, 39%↓ in PA, 13–34%↑ in minerals, 1.3–3617%↑ and 1.4–21%↓ in vitamins.	Increase in mineral contents to reduction in PA.	Ilowefah et al. [161]
Rice *(O. sativa)* bran	SSF	Controlled using *Rhizopus oryzae* CCT 7560	0–120 h (24 h interval) at 30 °C	Fermented rice bran	Increase in ash, protein fibre and a decrease in lipids after 48 h fermentation.	1.1–56%↑ in ash, 11–57%↑ in fibre, 6.1–49%↑ in protein, 1.3–3.3%↑ and 23–51%↓ in lipid.	Decrease in lipid was due to use of fat-related components for mycelial synthesis.	Kupski et al. [162]
Rice *(O. sativa)*	SmF	Spontaneous (microflora)	24–72 h (24 h interval) at 28 °C	Fermented rice flour	Increase in protein at 24 h and decrease afterwards. Decrease in CHO at 24 h and increase afterwards. Decrease in fat, ash, tannin and phytate. Decrease and increase in minerals in fermentation time.	36.6%↑ and 8.6–19.1%↓ in protein, 0.3%↓ and 1.1–2.4%↑ in CHO, 16.4–81%↓ in fat, 16–75%↓ in ash, 50%↓ in tannin, 19–69%↓ in phytate, 3.8–100%↑ and 14–97.9%↓ in minerals.	Fat decrease related to increase in lipase activity, ash decrease due to loss of dry matter. The increase and decrease in the mineral linked to metabolic activities of fermenting organisms which hydrolysed metal-phytate complexes to release free minerals. Tannin decrease attributed to milling which removed most of the tannin-related fractions while phytate reduction ascribed to increased phytase activities.	Nnam and Obiakor [137]

Table 3. *Cont.*

Raw Material	Fermentation Type	Fermentation Form	Fermentation Conditions	Product	Modification(s) in Nutritional Constituents	Percentage Difference	Key Mechanism(s) Involved	Reference
Rice (*O. sativa*) Mentik wangi susu, red cempo merah and black jowo melik varieties	SSF	Controlled using *R. oligosporus*	0–72 h (24 h interval) at RT	Fermented de-husked rice flour	Initial increase in ash, protein and fat with a decrease and increase afterwards. Decrease in CHO.	0.5–14%↑ and 0.5–31%↓ in ash, 3–20%↑ and 0.3%↓ in protein, 3–49%↑ and 0.77%↓ in fat and 0.45–7%↓ in CHO.	Protein increase due to metabolic activity of fungi while decrease due to protein degradation to support fungal growth. Increase in ash due to phytase activation and reduction in PA. Decrease in fat and CHO due to lipid and CHO degradation, respectively.	Suarti et al. [134]
Sorghum (*Sorghum bicolor*)	SSF	Spontaneous and controlled using *L. Fermentum*	72 h at 28 °C and 24 h at 34 °C	*Ting*	Decrease in tannin contents.	29.92–98.71↓.	Tannin decrease due to rearrangement and depolymerization, reduced extractability due to self-polymerization, interaction of tannin with other macromolecules and ability of LABs to metabolize tannins.	Adebo et al. [163–165]
Sorghum (*S. bicolor*)	SSF	Induced fermentation (i.e., back-slopping or inoculum enrichment)	0–36 h (4 h interval) at 37 °C	Fermented sorghum flour	Increase in IVSD. Decrease in total starch and resistance starch.	1.6–54%↑ in IVSD, 12.2–16.8%↓ in total starch and 20.6–72.9%↓ in resistance starch.	IVSD increase attributed to changes in endosperm protein fractions, while decrease in total and resistant starches due to natural increased enzymatic reactions.	Elkhalifa et al. [166]
Sorghum (*S. bicolor*) (HS-B67–2)	SmF	Probiotic micro-organism *L. acidophilus*	12 h at 37 °C	Sorghum flour for sorghum-based food mixture	Decrease and increase fibre content. Increase in vitamins content.	10%↓ in total and insoluble dietary fibre; 49–69%↑ in soluble fibre; 21–50%↓ in β-glucan. ↑53, 67 and 29% in thiamine, riboflavin and niacin, respectively.	Fibre decrease due to increased activity of hydrolysing enzymes.	Jood et al. [167]

Table 3. *Cont.*

Raw Material	Fermentation Type	Fermentation Form	Fermentation Conditions	Product	Modification(s) in Nutritional Constituents	Percentage Difference	Key Mechanism(s) Involved	Reference
Sorghum (*S. bicolor*) (Gobiye and 76T1#23 cultivars)	SmF	Spontaneous	0–48 h (12 h interval) at RT at RT	Fermented sorghum flours	Increase in protein. Decrease in fat, fibre, ash, CHO, phytate, tannin and most minerals.	4.2–16.3%↑ in protein, 2.5–16%↓ in fat, 20.8–40.4%↓ in fibre, 13.1–41.1%↓ in ash, 0.32–1.4%↓ in CHO, 12–70%↓ in phytate, 7.4–59%↓ in tannin, 0.13%↑ and 0.02–7.2%↓ in minerals.	Protein increase attributed to cells of fermenting microorganisms, while decrease in fibre was due to partial solubilisation of cellulose and hemicellulosic type of material by microbial enzymes. Reduction in minerals ascribed to utilization of hydrolysed elements for their metabolic activities and losses during decantation.	Mihiret [132]
Sorghum (*S. bicolor*)	SSF	Starter inoculum	72 h at RT	Fermented sorghum flour	Reduction in ash, protein, fat, energy, polyphenols, phytate and AAs. Increase in IVPD, CHO and some minerals.	6%↓ in ash, 13%↓ in protein, 7%↓ in fat, 0.9%↑ in CHO, 1.6%↓ in energy, 6%↑ in fibre, 18%↓ in polyphenols, 22%↓ in phytate, 21%↑ in IVPD, 0.15–63%↑ and 8.3–48%↓ in minerals, 4.2–54%↓ in AAs, no increase or decrease in tannin	IVPD increase due to ANF reduction.	Mohammed et al. [139]

Table 3. *Cont.*

Raw Material	Fermentation Type	Fermentation Form	Fermentation Conditions	Product	Modification(s) in Nutritional Constituents	Percentage Difference	Key Mechanism(s) Involved	Reference
Sorghum (*S. bicolor*)	SSF	Controlled using LAB consortium from fermented maize and sorghum	0–48 h (12 h interval) at RT	Fermented sorghum flours	Decrease in fat, CHO and fibre. Increase in ash and protein.	0.78–6.40%↑ in ash, 7.03–34.45%↑ in protein, 2.93–9.36%↓ in fat, 1.01–5.25%↓ in CHO and 33–72%↓ in crude fibre for sorghum sample; 1.84–5.62%↑ in ash, 7–32%↑ in protein, 4–10%↓ in fat, 1.22–5%↓ in CHO and 19%↑ and 50–70%↓ in crude fibre for maize.	Fat decrease could be attributed to its use as energy source and production of aroma compounds through the breakdown of fatty acids and glycerol. Decrease in CHO due to starch hydrolysis by amylases, while protein increase can be attributed to activities of proteolytic enzymes. Increase in ash related to mineral increase.	Ogodo et al. [136]
Sorghum (*S. bicolor*)	SSF	Controlled using *L. plantarum*	48 h at 30 °C	Fermented sorghum flour	Reduction in phytates, tannins, oxalate and HCN.	77%↓ in phytate, 96.7%↓ in tannin, 67.85%↓ in oxalate and 52.3%↓ in HCN	Phytate and tannin reduction due to microbial and enzymatic activity.	Ojha et al. [168]
Sorghum (*S. bicolor)*	SmF	Spontaneous	72 h at RT	Fermented sorghum flour	Increase in protein, ash and fat. Decrease in CHO, fibre, tannin and phytate.	34.2%↑ in protein, 25.7%↑ in ash, 13%↑ in fat, 49%↓ in fibre, 17%↓ in CHO, 45%↓ in phytate and 56%↓ in tannin.	ANF reduction due to the ability of microbial action.	Ojokoh and Eromosele [169]
Sorghum (*S. bicolor)*	SSF	Spontaneous	840 h (5 weeks) at RT	Fermented sorghum spent grains	Increase in protein, lipids and decrease in fibre and ash. Increase in nitrogen-free extract and minerals (phosphorus and calcium) and a decrease afterwards.	28.7–34.8%↑ in protein, 66–69%↓ in fibre, 36–41.5%↑ in lipid, 13.6–23%↓ in ash, 42–47.8%↑ in nitrogen extract, 19%↓ and 12%↑ in phosphorus and 7.5%↓ and 50–97.5%↑ in calcium.	Fibre decrease due to breakdown of the cellulose components by microorganisms to utilizable sugars. Protein increase due to protein synthesis.	Onyimba et al. [135]

Table 3. *Cont.*

Raw Material	Fermentation Type	Fermentation Form	Fermentation Conditions	Product	Modification(s) in Nutritional Constituents	Percentage Difference	Key Mechanism(s) Involved	Reference
Sorghum (*S. bicolor*) Karamaka and Mugud cultivar	SSF	Starter inoculum	0–16 h (2 h interval) at RT	Fermented sorghum flour	Decrease in phytate and tannin. Increase in IVPD.	12.4–67.8%↓ in phytate, 12.7–67.3%↓ in tannin and 0.49–31.3%↑ in IVPD.	Phytate reduction due to microbial and phytase activity.	Wedad et al. [170]
Stale rice (*O. sativa*)	SSF	Fermented using *Cordyceps sinensis*	168 h (7 days) at 25 °C	Fermented rice flour	Increase in protein, lipids, CHO, AAs, vitamin E, dietary fibre and β glucan.	60.7%↑ in protein, 252%↑ in lipid, 4.2%↑ in CHO, 576%↑ in dietary fibre, 900%↑ in β glucan, 133%↑ in vitamin E and 83–28,471%↑ in AAs.	Increase in bioactivity and AAs was attributed to transformation of inherent constituents and some mycelia of *C. sinensis*.	Zhang et al. [171]
Tef (*Eragrostis tef*)	SmF	Back-slopping using leftover (ersho: produced from spontaneous traditional fermentation)	1st stage: at RT for 3–4 days; 2nd stage: 2–3 h	Fermented flour to prepare batter and *injera*	Decrease in vitamin (folate content).	12%↓ in folate content in batter and 34%↓ in folate content in *injera*.	Reduced folate content due to folate consumption by other microorganisms or losses during discarding the supernatant.	Tamene et al. [172]
Yellow maize (*Z. mays*)	SmF	Spontaneous	96 h (4 days) at 30 °C and 80% relative humidity (RH)	Fermented maize dough	Decrease in fat, energy, ash, minerals, protein, vitamins (thiamine, riboflavin and β-carotene), minerals (calcium, iron and zinc) and ANFs (TI, phytate and β-amylase inhibitor). Increase in CHO and fibres.	11%↓ in fat, 9%↓ in protein, 54%↓ in ash, 0.92%↓ in energy, 69.4%↓ in thiamine, 81.8%↓ in riboflavin, 66%↓ in β-carotene (retinol equivalent) contents, 38%↓ in calcium, 2.8%↓ in iron, 7.6%↓ in zinc, 9%↑ in CHO and fibres, 61.5%↓ in phytate, 41.6%↓ in TI and 16.5%↓ in amylase inhibitor.	Fibre decrease attributed to partial solubilisation of cellulose and hemicellulose type of materials by microbial enzymes. Fat decrease due to grain variety, fermentation conditions and other processing steps. Vitamin decrease ascribed to mechanical loss during other process and lipid solubilisation.	Ejigui et al. [138]

↓—decrease; ↑—increase; AA—amino acids; ANFs—antinutritional factors; CHO—carbohydrate; HCN—hydrogen cyanide; IVPD—in vitro protein digestibility; IVSD—in vitro starch digestibility; LAB—lactic acid bacteria; PA—phytic acid; SmF—submerged fermentation; SSF—solid-state fermentation; TI—trypsin inhibitor; TIA—trypsin inhibitor activity.

Table 4. Influence of fermentation on the nutritional composition of some legume-based products.

Raw Material	Fermentation Type	Fermentation Form	Fermentation Conditions	Product	Modification(s) in Nutritional Constituents	Percentage Difference	Key Mechanism(s) Involved	Reference
African oil bean (*Pentaclethra macrophylla*)	SSF	Spontaneous	72 h at RT	Fermented African oil bean flour	Decrease in fibre, fat, ash, CHO and energy. Increase in protein.	20%↓ in fibre, 5%↓ in fat, 19.4%↓ in ash, 7%↓ in CHO, 26%↓ in energy and 22%↑ in protein.	Protein increase due to synthesis of new proteins.	Akubor and Chukwu [144]
African oil bean (*P. macrophylla*)	SSF	Spontaneous	12–48 h at RT	Fermented *ugba*	Decrease in ANFs, some saturated and unsaturated fatty acids.	60–73%↓ in HCN, 24–46%↓ in phytate, 71–79%↓ in tannin, 62–77%↓ in oxalate, 2–24%↑ and 2–18%↓ in fatty acids.	ANFs' decrease attributed to leaching during soaking and enzymatic activities in the microflora.	Onwuliri et al. [173]
African yam bean (*Sphenostylis stenocarpa*)	SSF	Controlled using *S. cerevisiae*	24 h at 45 °C	Fermented African yam bean flour	Increase in crude protein, ash, minerals, some AAs and IVPD. Decrease in fat content, fibre, CHO and ANFs (PA and tannin).	17%↑ in protein, 14%↑ in ash, 2–52%↑ in minerals, 0.2–13%↑ and 0.3–16%↓ in AAs, 10%↑ in IVPD, 25%↓ in fat, 15%↓ in fibre, 4%↓ in CHO, 40%↓ in PA, 21%↓ in tannin and 58%↓ in TIA.	Enhanced AA levels due to formation of soluble products and monomers as well as interconversion of AAs. IVPD increase ascribed to proteolysis, increased availability of AAs and reduced ANFs. Decrease in fat attributed to lipase activity and use of lipids as food source by fermenting organisms. Decrease in fibre and CHO due to enzymatic degradation of fibre and use of CHO-related compounds as energy source, respectively.	Chinma et al. [149]

Table 4. *Cont.*

Raw Material	Fermentation Type	Fermentation Form	Fermentation Conditions	Product	Modification(s) in Nutritional Constituents	Percentage Difference	Key Mechanism(s) Involved	Reference
African yam bean (*Sphenostylis stenocarpa*)	SmF	Spontaneous	24 h at 45 °C	Fermented African yam bean flour	Increase in crude protein, CHO and fat. Decrease in ash and fibre.	2.7%↑ in protein, 86%↑ in fat, 1%↑ in CHO, 29.8%↓ in ash and 12.4%↓ in fibre.	Fat increase attributed to fat from dead microflora or the fermenting microflora not using fat as energy source. Decrease in ash due to vegetative loss and leaching into fermentation medium, while fibre reduction due to hydrolysis and use by microflora for metabolism. Protein increase due to hydrolysis of protein-antinutrient bonds, to release free AAs for synthesis of new protein.	Onoja and Obizoba [174]
Bambara groundnut (*Vigna subterranea*)	SSF	Spontaneous	120 h at 35 °C	Fermented unhulled *dawadawa*	Decrease in ANFs (PA, tannin and oxalate). Increase in protein, some AAs as well as minerals.	18.1%↓ in PA, 26.6%↓ in oxalate, 34.2%↓ in tannin, 2.3–43.8%↑ and 12.1–66.7%↓ in minerals, 17.7%↑ in protein, 8.3–25%↑ and 9.6–19.6%↓ in AAs.	Increase in protein attributed to extensive hydrolysis of the protein molecules to AAs and other simple peptides. AA increase ascribed to transamination and AA synthesis of these AAs by microbiota. Increase in minerals linked to ANF reduction, while decrease in other minerals due to their utilization for microbiota physiological and metabolic activities. PA reduction attributed to enzymatic activity.	Adebiyi et al. [142]

Table 4. *Cont.*

Raw Material	Fermentation Type	Fermentation Form	Fermentation Conditions	Product	Modification(s) in Nutritional Constituents	Percentage Difference	Key Mechanism(s) Involved	Reference
Bambara groundnut (*V. subterranea*)	SmF	Spontaneous	48 h at 60 °C	Fermented Bambara groundnut flour	Increase in crude protein, ash, fibre, fat, CHO, some AAs and minerals (except for sodium and phosphorus). Decrease in ANFs.	1.2%↑ in protein, 4.2%↓ in ash, 4.1%↑ in fibre, 2%↑ in fat, 0.32%↑ in CHO, 0.96%↑ in energy, 6–107%↑ and 3–47%↓ in AAs, 16%↓ in oxalate, 26%↓ in TA, 39%↓ in PA, 42%↓ in PP, 37%↓ in trypsin, 4–27%↑ and 29–33%↓ in minerals.	ANF reduction ascribed to biodegradation caused by microbiota.	Ijarotimi and Esho [175]
Bambara groundnut (*V. subterranea*)	SmF	Controlled using spore suspension of *R. oligosporous*	0–72 h (12 h interval) at 32 °C	Fermented Bambara groundnut flour	Decrease in ANFs.	28–75%↓ in tannin, 36–52%↓ in oxalate, 22–96%↓ in PT and 42–87%↓ in TIA.	Tannin reduction caused by the activity of polyphenol oxidase and microflora.	Ola and Opaleye [176]
Black beans (*Phaseolus vulgaris*)	SSF	Controlled using *P. ostreatus* CS155 strain	336 h (14 days) at RT	Fermented black beans flour	Decrease in protein, fat, minerals, fibre and some AAs. Increase in CHO, IVPD, tannin and soluble nitrogen.	3.5%↓ in protein, 20%↓ in fat, 7%↓ in minerals, 59%↓ in fibre, 146%↑ in CHO, 20%↓ in IVPD, 123%↑ in soluble nitrogen, 20%↓ in tannin, 2–139%↑ and 0.85–14%↓ in AAs.	Fibre decrease due to enzymatic activity, which led to conversion of resistant starches to available starches and subsequent increase in CHO contents. Tannin decrease ascribed to fungus-producing tannase.	Espinosa-Páez et al. [130]
Black-eyed pea (*V. unguiculata*)	SSF	Controlled using *Aspergillus oryzae* (MTCC 3107)	0–96 h (24 h interval) at 30 °C	Fermented black-eyed pea flour	Increase in iron, zinc and in vitro bioavailability of minerals (iron and zinc).	11–16.8%↑ in iron, 24–36%↑ in zinc, 6–75%↑ and 8–106%↑ in in vitro bioavailability of iron and zinc, respectively.	Increased mineral digestibility and bioavailability attributed to reduction in ANF and toxic factors.	Chawla et al. [177]

Table 4. *Cont.*

Raw Material	Fermentation Type	Fermentation Form	Fermentation Conditions	Product	Modification(s) in Nutritional Constituents	Percentage Difference	Key Mechanism(s) Involved	Reference
Chickpea (*Cicer arietinum* L.)	SSF	Controlled using *R. oligosporus*	Optimum conditions of 51.3 h at 34.9 °C	Fermented tempeh flour	Increase in crude protein, true protein, available lysine and IVPD. Decrease in lipid, ash, CHO, PA and tannins.	25%↑ in crude protein, 15.2%↑ in IVPD, 30.5%↑ in true protein, 40.5%↑ in available lysine, 5.7%↓ in lipid, 39.4%↓ in ash, 0.72%↓ in CHO, 89.9%↓ in PA and88%↓ in tannin.	Increase in IVPD and lysine due to ANF elimination and protein hydrolysis.	Reyes-Moreno et al. [178]
Chickpea (*Cicer arietinum* L.)	SSF	Controlled using *Cordyceps militaris*	168 h (7 days) at 25 °C	Fermented chickpea flour	Increase in crude protein, true protein, fat, ash, IVPD and AAs, except for arginine. Decrease in CHO.	19.4%↑ in crude protein, 20%↑ in true protein, 1.8%↑ in fat, 6.1%↑ in ash, 6.7%↓ in CHO, 4.4%↑ in IVPD, 3.7%↓ and 7–27.6%↑ in AAs.	Protein increase due to accumulation during fermentation as well as synthesis or transamination. Increase in IVPD ascribed to the unfolding of the proteins and hydrolysis by proteases. CHO reduction due to use for fungal growth.	Xiao et al. [147]
Common bean (*Phaseolus vulgaris*)	SmF	Controlled using *L. fermentum*	72 h at 37 °C	Fermented bean powder	Increase in protein, ash, soluble fibre, soluble nitrogen, starch and some AAs. Decrease in CHO, crude fibre, fatty acids, vitamins, soluble sugar and some minerals.	1%↑ in protein, no increase or decrease in fat, 4%↑ in ash, 8%↑ in starch, 0.5%↓ in CHO, 0.5%↓ in crude fibre, 19%↑ in soluble fibre, 9%↑ in soluble nitrogen, 1–20%↑ and 3–7%↓ in AAs, 1–20%↓ in fatty acids, 1.1–12%↑ and 0.9–24%↓ in minerals, 75%↓ in soluble sugar and 5–41%↓ in vitamins.	Increase in ash due to accumulation of white sugar decrease due to microbial utilization as food source. Increase and decrease in AA suggests synthesis of protein-related compounds and utilization by the bacteria, respectively.	Barampama and Simard [152]

Table 4. *Cont.*

Raw Material	Fermentation Type	Fermentation Form	Fermentation Conditions	Product	Modification(s) in Nutritional Constituents	Percentage Difference	Key Mechanism(s) Involved	Reference
Cowpea (*V. unguiculata*)	SSF	Spontaneous and controlled using *A. niger*	48 h at RT	Fermented cowpea flours	Increase in protein. Decrease in lipid, ash, fibre, ANFs, minerals, raffinose and stachyose, except for decrease and increase in CHO.	21.8–24.9%↑ in protein, 25.3–58.7%↓ in lipid, 11.8–63.3%↓ in ash, 17.3–28.8%↓ in fibre, 3.15%↓ and 6.9%↑ in CHO, 3.8–98.5%↓ in minerals, 28–99%↓ in ANFs, 74.6–85%↓ in raffinose and 59.5–99.3%↓ in stachyose.	Increase in protein attributed to increase in biomass and partial protein denaturation. Decrease in ash, lipid, CHO and fibre linked to microbial metabolism. ANF reduction attributed to degradation by microorganisms.	Difo et al. [146]
Cowpea (*V. sinensis L. var. carilla*)	SmF	Spontaneous and controlled using *L. plantarum*	48 h at 37 °C	Fermented cowpea flour	Increase in riboflavin, decrease in ANFs (raffinose, TIA and stachyose), total starch, available starch and thiamine.	80%↓ in raffinose, 50%↓ in TIA, 96%↓ in stachyose, 5.8%↓ in total starch, 5%↓ in available starch, 69%↓ in thiamine and 106%↑ in riboflavin for spontaneous fermented sample; 94%↑ in riboflavin, 43%↓ in thiamine, 6.2%↓ in total starch, 12%↓ in available starch, 27%↓ in TIA, 88.8%↓ in stachyose and 68.6%↓ in raffinose for controlled fermented sample.	Not reported.	Doblado et al. [179]
Cowpea (*V. sinensis* var. Orutico and *V. sinensis* var. Tuy)	SSF	Spontaneous	48 h at 42 °C	Fermented cowpea seeds	Decrease in available starch and mineral elements.	4.5–22.8%↓ in starch, 42.1%↓ in ash and 4.4–68.8%↓ in mineral contents.	Degradation of available starch by microbial and enzymatic activities, water solubilization and leaching of minerals into steep water.	Granito et al. [180]

Table 4. *Cont.*

Raw Material	Fermentation Type	Fermentation Form	Fermentation Conditions	Product	Modification(s) in Nutritional Constituents	Percentage Difference	Key Mechanism(s) Involved	Reference
Cowpea (*V. unguiculata*)	SSF	Controlled using *R. microspoms*	0–24 h (3 h interval) at RT	Fermented cowpea flour	Increase in protein, fat, ash and CHO.	2.3–8.8%↑ in protein, 100–133%↑ in fat, 30.8–33%↑ in ash and 1.7–5%↑ in CHO.	Ash increase linked to increase in B vitamins.	Prinyawiw-atkul et al. [181]
Guanacaste (*Enterolobium cyclocarpum* (Jacq.) Griseb.)	SSF	Controlled using *A. niger*	0–28 h (7 h interval) at 30 °C	Fermented whole leaves of *Enterolo-bium cyclo-carpum*	Decrease in tannin, saponin, PA, oxalate, neutral detergent fibre and acid detergent fibre. Increase in crude protein and a decrease afterwards.	13.3–42.7%↓ in tannin, 11.7–28.8%↓ in saponin, 10.1–25.4%↓ in PA, 6.6–26.5%↓ in oxalate, 7.2–14.4%↓ in acid detergent fibre, 21.7–25.5%↓ in neutral detergent fibre, 10.2–16.3%↑ and 1.3–8.7%↓ in protein.	Protein increase attributed to addition of microbial protein during fermentation. Decrease in fibres is an indication of cell wall presence. ANF decrease ascribed to enzymatic activities.	Ayuk et al. [182]
Horse gram (*Macrotyloma uniflorum*)	SmF	Spontaneous	48 h at RT	Fermented horse gram flour	Reduction in ANFs (PA, tannin and oxalate).	69.5%↓ in PA, 69.4%↓ in tannin and 66.8%↓ in oxalate.	ANF reduction attributed to leaching, degradation through enzyme activity and utilization of ANF as a carbon source.	Ojha et al. [183]
Kidney bean (*Phaseolus vulgaris*)	SSF	Controlled using *P. ostreatus* CS155 strain	336 h (14 days) at RT	Fermented kidney bean flour	Decrease in fat, minerals, CHO, tannin and fibre. Increase in protein, IVPD, soluble nitrogen and some AAs.	13%↑ in protein, 10%↓ in fat, 13%↓ in minerals, 16%↑ in fibre, 57%↑ in IVPD, 100%↑ in soluble nitrogen, 17%↓ in CHO, 34%↓ in tannin, 0.1–41%↑ and 0.4–18%↓ in AAs.	Protein increase was attributed to AA synthesis. Decrease in tannin attributed to fungal tannase.	Espinosa-Páez et al. [130]

Table 4. *Cont.*

Raw Material	Fermentation Type	Fermentation Form	Fermentation Conditions	Product	Modification(s) in Nutritional Constituents	Percentage Difference	Key Mechanism(s) Involved	Reference
Kidney bean (*Phaseolus vulgaris*)	SmF	Spontaneous	16 h at RT	Fermented kidney bean flours	Decrease in protein, ashes, fat, total starch, available starch, soluble fibre, insoluble fibre, minerals, TIA, tannin and vitamin B1 (thiamine). Increase in resistant starch, vitamin B2 (riboflavin) and IVPD.	1.7–14.5%↓ in protein, 3.8–7.7%↑ in IVPD, 0.63–2%↓ in fat, 5.4–16%↓ in total starch, 10–26.6%↓ in available starch, 4.2–10.6%↑ in resistant starch, 53–64%↓ in ashes, 4.5–25.8%↓ in insoluble fibre, 61–94%↓ in soluble fibre, 15–35%↓ in vitamin B1 (thiamine), 16.7–33%↑ in vitamin B2 (riboflavin), 56–70.9%↓ in TIA, 60.6–69.7%↓ in tannin and 1.8–68%↓ in minerals.	Increase in vitamin due to synthesis during fermentation. Decrease in insoluble fibre attributed to use of cellulose and arabinoxilnase.	Granito et al. [184]
Lentils (Lens culinaris)	SSF	Controlled using *P. ostreatus* strain	336 h (14 days) at 28 °C	Fermented lentils flour	Increase in protein and energy. Decrease in CHO and lipid.	18.5%↑ in protein, 15%↑ in energy, 8%↓ in lipid and 6%↓ in CHO.	CHO decrease due to use as carbon source. Protein increase ascribed to bioconversion of some compounds into protein.	Asensio-Grau et al. [153]
Lentils (*Lens culinaris* L.) HM-1, LL-931 and Sapna	SSF	Controlled using *A. awamori* (MTCC 548)	168 h (7 days) at 25 °C	*Aspergillus*-fermented lentil flour	Increase in minerals and in vitro bioavailability of iron and zinc.	0.07–60%↓ in minerals, 68.3–90.6%↑ and 86.7–100.6%↑ in in vitro bioavailability of iron and zinc.	Higher digestibility of iron and zinc attributed to reduced presence of ANFs.	Dhull et al. [185]

Table 4. *Cont.*

Raw Material	Fermentation Type	Fermentation Form	Fermentation Conditions	Product	Modification(s) in Nutritional Constituents	Percentage Difference	Key Mechanism(s) Involved	Reference
Lima bean (*Phaseolus lunatus*)	SmF	Spontaneous	72 h at 32 °C	Fermented lima bean flour	Increase in CHO. Decrease in crude protein, fibre, fat content, ash, minerals and ANFs.	3%↑ in CHO, 3%↓ in protein, 25%↓ in fibre, 4%↓ in fat, 17%↓ in ash, 5–13%↓ in minerals, 78%↓ in tannin, 89%↓ in PT, 97%↓ in TIA, 75%↓ in lectin, 95%↓ in oxalate and 91%↓ in cyanide.	Decrease in protein due to previous heat treatment during processing. Reduced fat attributed to loss of total solids and fat denaturation. Decrease in minerals contents was due to leaching and reduced ANFs ascribed to microbial degradation.	Farinde et al. [186]
Lupin (*Lupinus albus* and *Lupinus luteus*)	SSF	Spontaneous and controlled using LABs (*L. sakei*, *Pediococcus acidilactici and Pediococcus pentosaceus*)	24 h at 30 °C for *L. sakei*, 32 °C for *Pediococcus acidilactici and* 35 °C for *Pediococcus pentosaceus*	Fermented whole meal	Increase in IVPD.	3.5–17.7%↑ in IVPD for *Lupinus albus*. and 7.8–19%↑ in IVPD for *Lupinus luteus*.	Not reported.	Bartkiene et al. [187]
Lupin (*Lupinus albus* L. *var. Multolupa*)	SmF	Spontaneous fermentation (microflora) and *L. plantarum*	48 h at 37 °C	Fermented lupin flours	Decrease in vitamin content.	6–96%↓ in vitamins (α-, γ- and δ-tocopherols).	Not reported.	Frias et al. [188]

Table 4. *Cont.*

Raw Material	Fermentation Type	Fermentation Form	Fermentation Conditions	Product	Modification(s) in Nutritional Constituents	Percentage Difference	Key Mechanism(s) Involved	Reference
Lupins (*Lupinus angustifolius* L.)	SSF	Controlled using *A. sojae*, *A. ficuum* and their co-cultures	168 h (7 days) at 30 °C	Fermented lupin flours	Increase in fat, ash, crude fibre fractions, protein, starch, calcium and phosphorus. Decrease in IVPD and PA. A decrease and increase in soluble CHO.	53.3–73.2%↓ in PA, 1.40%↓ and 0.64–1.8%↑ in crude protein, 3–11%↑ in fat, 3–7%↑ in ash, 9%↓ and 7–10%↑ in crude fibre, 0.3–15.3%↑ in acid detergent fibre, 11.4–35.2%↑ in neutral detergent fibre, 40–87%↑ in hemicellulose, 21–56%↑ in lignin, 6%↓ and 1.8–14%↑ in cellulose, 7–16.8↓ and 5.6↑ in soluble CHO, 98–700%↑ in starch, 16–32.5%↓ in IVPD, 14–29%↑ in calcium and 10–13%↑ in phosphorus.	Increase protein attributed to production of fungal protein. Reduction in IVPD due to protein being locked within the fibre matrix, reducing the hydrolytic action of enzymes.	Olukomaiya et al. [150]
Lupin (*Lupinus angustifolius* L.) var. 'Vilniai' and 6 hybrid lines (1700, 1701, 1703, 1072, 1734, 1800)	SmF and SSF	Controlled using *L. sakei* KTU05–6	48 h at 30 °C	Fermented lupin seeds	Increase in AAs.	2.7–1287%↑ in AAs for SmF samples and 0.7–613%↑ in AAs for SSF samples.	Not reported.	Starkute et al. [189]

Table 4. *Cont.*

Raw Material	Fermentation Type	Fermentation Form	Fermentation Conditions	Product	Modification(s) in Nutritional Constituents	Percentage Difference	Key Mechanism(s) Involved	Reference
Lyon bean (*Mucuna cochinchinensis*)	SSF	Spontaneous	0–72 h (24 h interval) at 30 °C	Fermented Lyon bean flour	Reduction in oxalate, PA, tannin and CHO. Increase in protein. Increase in fat and decrease at 72 h. Increase in ash and decrease at 48 h. Increase in fibre.	1.1–60.1%↑ and 0.41%↓ in protein, 51.6–111%↑ in fat, 7.1–49.9%↑ and 8.5–13%↓ in ash, 54.3–179.3%↑ in fibre, 5.4–25.9%↓ in CHO, 16.5–68%↓ in oxalate, 13.7–26%↓ in PA and 9.2–25.7%↓ in tannin.	Not reported.	Olaleye et al. [190]
Mahogany Bean (*Afzelia africana*)	SmF	Spontaneous	0, 24, 48, 72 h at 30 °C	Fermented mahogany bean flour	Increase in protein, fat, fibre, ash and CHO.	3–15%↑ in protein, 3–39%↑ in fat, 2.6–7%↑ in fibre, 3–18%↓ in ash and 12–61%↓ in CHO.	Increased protein attributed to increase in microbial mass and extensive protein hydrolysis to AA and other simple peptides. Fat increase ascribed to extensive breakdown of large fat molecules into simple fatty acids. Loss in ash due to leaching of soluble minerals into the processing water. CHO reduction attributed to conversion of oligosaccharides to simple sugars or utilization of CHO for growth and metabolism.	Igbabul et al. [191]
Mung bean (*Vigna radiata*)	SmF	Spontaneous and back-slopping	72 h at RT	Fermented mung bean flour	Decrease in fat, CHO and vitamin A. Increase in fibre, in ash and some minerals.	Fermented and back-slopping: 33 and 38%↓ in fat; 60%↓ in vitamin A of both, 50 and 35%↑ in fibre, 7.2%↓ in CHO, 51.2%↓ and 6.3%↑ in ash and 8.8–22.6%↑ in calcium and iron.	Decreased fat due to activities of lipolytic enzymes. Reduction in CHOs due to its use as energy source.	Onwurafor et al. [192]

Table 4. *Cont.*

Raw Material	Fermentation Type	Fermentation Form	Fermentation Conditions	Product	Modification(s) in Nutritional Constituents	Percentage Difference	Key Mechanism(s) Involved	Reference
Pea (*Pisum sativum*)	SSF	Controlled using *A. niger* NRRL 334 and *A. oryzae* NRRL 5590	0, 2, 4 and 6 h at 40 °C	Fermented pea protein-enriched flour	Increase in AAs, protein and IVPD of the fermented samples over fermentation time but a decrease in AAs of the *A. niger*. Decrease in ash at 6 h fermentation for *A. oryzae* and increase in lipid at 2 h fermentation for *A. niger*.	4–32%↓ in TIA, 0.5–14%↑ in protein, 0.2–8.7%↑ and 0.6–0.9%↓ in ash, 0.6–94%↓ and 20%↑ in lipid, 0.93%↓ and 0.67–8%↑ in IVPD and 0.7–10%↓ and 1.8–29%↑ in AAs.	Increase in protein content attributed to increase in fungal biomass. Decrease in AAs due to fungi utilizing the AAs as food source.	Kumitch [11]; Kumitch et al. [143]
Pigeon pea (*Cajanus cajan*)	SSF	Spontaneous	168 h (7 days at 1 h interval) at RT	Fermented pigeon pea seed flour	Increase in protein and ash. Decrease in fat, fibre, nitrogen free extract and energy.	3.7–9.6%↑ in protein, 16–38%↓ in fat, 6.7–19.7%↑ in ash, 22.5–37.7%↓ in fibre, 0.4–4.3%↓ in nitrogen-free extract and 0.5–3%↓ in energy.	Increase in protein ascribed to synthesis of protein and AAs. Fat reduction due to increased activities of lipolytic enzymes causing fat hydrolysis.	Adebowale and Maliki [145]
Pigeon pea (*Cajanus cajan*)	SSF	Spontaneous and back-slopping	72 h at RT	Fermented pigeon peas flour	Increase and decrease in ash, fat, fibre, protein and CHO. Increase in energy.	0.2%↑ and 17–36.8%↓ in ash, 0.32–8.6↑ and 7–18.6%↓ in fat, 2.2–6.4%↑ and 12–20%↓ in fibre, 5–20.8%↑ and 9.4%↓ in protein, 3.3–7.8%↑ and 1%↓ in CHO and 50.6–57.4%↑ in energy.	Increase in protein attributed to activities of extracellular enzymes.	Odion-Owase et al. [193]

Table 4. *Cont.*

Raw Material	Fermentation Type	Fermentation Form	Fermentation Conditions	Product	Modification(s) in Nutritional Constituents	Percentage Difference	Key Mechanism(s) Involved	Reference
Red bean (*Phaseolus angularis* (Willd.) W.F. Wight.)	SSF	Controlled using *Cordyceps militaris*	168 h (7 days) at 25 °C	Fermented red bean flour	Increase in protein, ash and some AAs. Decrease in fat and CHO.	9.3%↑ in crude protein, 2.7%↓ in fat, 5.6%↑ in ash, 3.2%↓ in CHO and 4.8–43.9%↓ and 7–230%↑ in AAs.	Reduction in CHO due to its use as energy source for fungal growth. Increase in AAs due to synthesis or transamination.	Xiao et al. [148]
Soybean (*Glycine max*)	SSF	Controlled using *L. plantarum* Lp6	72 h at 37 °C	Fermented soybean protein meal and fermented soybean protein meal with added protease	Increase in IVPD and nitrogen solubility.	9%↑ in IVPD and 4.4%↑ in nitrogen solubility for fermented soybean protein meal; 12%↑ in IVPD and 2.2%↑ in nitrogen solubility for fermented soybean protein meal with added protease.	Increase in IVPD related to positive influence of protein degradation by proteases.	Amadou et al. [194]
Soybean (*G. max*) Rudoji and progress varieties	SSF	Spontaneous and controlled using LABs (*L. sakei*, *Pediococcus acidilactici and Pediococcus pentosaceus*)	24 h at 30 °C for *L. sakei*, 32 °C for *Pediococcus acidilactici and* 35 °C for *Pediococcus pentosaceus*	Fermented whole meal	Increase in IVPD.	9–17%↑ in IVPD for Rudoji and 10–15%↑ in IVPD for progress.	Not reported.	Bartkiene et al. [187]
Soybean (*G. max*)	SmF	Controlled using starter organisms *Streptococcus thermophilus* CCRC 14,085 and *Bifidobacterium infantis* CCRC 14,603	24 h at 37 °C	Fermented soymilk	Decrease in saponin and PA.	46.9%↓ in saponin and 28.9%↓ in PA.	Reduction in PA due to phytase and β-glucosidase activities.	Lai et al. [195]

Table 4. *Cont.*

Raw Material	Fermentation Type	Fermentation Form	Fermentation Conditions	Product	Modification(s) in Nutritional Constituents	Percentage Difference	Key Mechanism(s) Involved	Reference
Soybean (*G. max*)	SmF	Spontaneous	Up to 72 h at RT	Fermented soymilk	Decrease in CHO and fat. Increase in ash, protein and minerals. Decrease in energy value but an increase at 6 and 12 h fermentation.	10–99%↓ in CHO, 8.9–222%↑ in ash, 2.2–53%↑ in minerals, 5–94%↑ in protein, 2.3–60%↓ in fat and 7.5–15.5%↓ and 0.1–7.4%↑ in energy value.	Reduction in CHO due to its use as energy source. Release of minerals from chelated complexes, influenced its increase. Protein increase due to anabolic processes causing build-up of protein-related polymers and microbial cell proliferation. Decrease in fat connected to increased activities of the lipolytic enzymes which caused fat hydrolysis.	Obadina et al. [151]
Soybean (*G. max*) curd waste or okara	SSF	Controlled using *Candida albicans* NRRL Y-12, *C. guilliermondii* NRRL Y-2075, *Kluyveromyces marxianus* NRRL Y-7571, *Kluyveromyces marxianus* NRRL Y-8281, *Pichia pinus* and *S. cerevisiae* NRRL Y-12632	72 h at 30 °C	Fermented okara	Decrease in fibre, fat and CHO. Increase in protein and ash.	7.4–45.5%↓ in fibre, 20.1–54.4%↑ in protein, 2.8–27.8%↑ in ash, 3.3–29.2%↓ in fat and 0.71–51.1%↓ in CHO.	Decrease in fibre linked to secretion of cellulose/hemicellulose-degrading enzymes by yeasts.	Rashad et al. [196]

Table 4. *Cont.*

Raw Material	Fermentation Type	Fermentation Form	Fermentation Conditions	Product	Modification(s) in Nutritional Constituents	Percentage Difference	Key Mechanism(s) Involved	Reference
Tamarind (*Tamarindus indica* L.)	SSF	Spontaneous	24, 48 *and* 72 h at RT	*daddawa*-type condiment	Initial increase in CHO and ANFs (phytate, trypsin inhibitor and tannin) and decrease afterwards. Initial decrease in protein, fat, ash, fibre and minerals and subsequent increase afterwards.	1.04–42%↓ in CHO, 6–49%↓ in PT, 0.66–86%↓ in TI, 25–75%↓ in tannin, 1–3%↑ in protein, 3–34%↑ in fat, 5–18%↑ in ash, 2–41%↑ in fibre and 4–33%↑ and 1–17%↓ in minerals.	Decrease in ANFs attributed to enzymatic activity during fermentation. The slight increase in protein due to synthesis of enzymes and degradation of protein-related substrates.	Olagunju et al. [197]
Tamarind (*Tamarindus indica* L.)	SSF	Spontaneous	96 h (4 days) at RT	Tamarind seed flours	Reduction in ash, phytate, tannin, TIA and CHO. Increase in protein, fat and fibre	2.3%↓ in ash, 37–99%↓ in CHO, 4.8–14.3%↓ in phytate, 42.9–85.7%↓ in tannin, 78.7–89.4%↓ in TIA, 9.5–24.6%↑ in protein, 17–48.9%↑ in fat and 15–16.7%↑ in fibre.	Decrease in TIA and phytate due to enzymatic activities. Protein increased attributed to enzyme synthesis and compositional change following degradation of other constituents. Fat increase due to increased activity of lipolytic enzymes that led to production of more fatty-related compounds. CHO reduction linked to their use as carbon source (substrate) in order to synthesize cell biomass.	Oluseyi and Temitayo [198]

Table 4. *Cont.*

Raw Material	Fermentation Type	Fermentation Form	Fermentation Conditions	Product	Modification(s) in Nutritional Constituents	Percentage Difference	Key Mechanism(s) Involved	Reference
Wild *Vigna* species of legume (*V. racemosa*)	SSF	Spontaneous and controlled using *A. niger*	48 h at RT	Fermented *V. racemosa* flour	Increase in protein for spontaneous sample and decrease in the controlled fermentation. Decrease in lipid, ash, fibre, CHO, ANFs, minerals, raffinose and stachyose, except for an increase in CHO of the controlled fermented sample.	12.4%↑ in protein, 9.7%↓ in lipid, 12.3%↓ in ash, 18.4%↓ in fibre, 1.02%↓ in CHO, 2.6–59%↓ in ANFs, 12.5–98%↓ in minerals, 33%↓ in raffinose and 65%↓ in stachyose for the spontaneous fermented sample; 29.4%↓ in protein, 62.8%↓ in lipid, 31%↓ in ash, 0.7%↓ in fibre, 22.9%↑ in CHO, 30–99%↓ in ANFs, 42.6–98.2%↓ in minerals, 59.5%↓ in raffinose and 87.7%↓ in stachyose for controlled fermented sample.	Increase in protein due to increase in biomass brought about by the fermenting microorganisms. Protein decrease attributed to metabolism of *A. niger*. Decrease in ash, fibre, lipid and CHO due to their metabolism by the microorganisms. Reduction in ANFs attributed to degradation by microorganisms. Decrease in mineral contents ascribed to leaching of the minerals into fermentation water and mineral utilization by fermenting microbiota. Raffinose and stachyose reduction could be due to their utilization as energy sources.	Difo et al. [199]

↓—decrease; ↑—increase; ANFs—antinutritional factors; CHO—carbohydrate; HCN—hydrogen cyanide; IVPD—in vitro protein digestibility; IVSD—in vitro starch digestibility; PA—phytic acid; PP—phytin phosphorus; PT—phytate; RT—room temperature; SSF—solid-state fermentation; SmF—submerged fermentation; TA—tannic acid; TI—trypsin inhibitor; TIA—trypsin inhibitor activity.

In legumes, fermentation has been observed to lead to both a decrease and increase in carbohydrate or starch contents (Table 3). A previous study on the determination of available starch contents of two fermented *Vigna sinensis* seed varieties revealed a reduction in the starch content from 24.3% to 22.33% in the orutico variety and from 29.7% to 22.9% in the tuy variety, [180] with the authors attributing this to the degradation of available starch by microbial and enzymatic activities. This trend was also reported by Doblado et al. [179] evident with the reduction in total starch, though with a corresponding increase in sugar contents of fermented *Vigna sinensis* (var carrila) samples. In contrast, an 8% increase in the starch content and a corresponding 0.5% decrease in the carbohydrate content was reported in fermented bean powder (using *L. fermentum*) [152]. Olagunju et al. [197] also reported a reduction in carbohydrate contents of tamarind seeds fermented for 3 days, with values of 1.04–42%. The study related this decrease in carbohydrate content to the decrease in the carbohydrate ratio in the total mass, resulting in the redistribution of nutrient percentages [197]. A 3% decrease in the carbohydrate content reported during the fermentation of red bean (*Phaseolus angularis*) was attributed to the use of carbohydrate as the energy source for fungal growth [148]. Different authors [130,144,146,149,153,178,190,191] have all equally reported reductions in carbohydrate levels during the fermentation of African oil bean (7%), *tempeh* (0.7%), cowpea (3%), mahogany bean (up to 61%), kidney bean (17%), lentil (6%), African yam bean (4%) and Lyon bean (up to 26%), and ascribing such reductions to the use of carbohydrate-related compounds as the energy source by fermenting microorganisms for growth and metabolism as well as the conversion of oligosaccharides to simple sugars. The observed varying decreases in the carbohydrate values of these legumes could be due to differences in the inherent composition (e.g., amylose, amylopectin and the structural composition of carbohydrates), plant varieties, species as well as fermenting microorganisms present during the fermentation process. Furthermore, Obadina et al. [151] reported a progressive reduction in carbohydrate contents (10–99%) of fermented soymilk at 72 h as the fermentation time increased, attributing this to the activities of the fermenting microorganisms which transformed and utilized them into energy for growth and other cellular activities. According to Olagunju et al. [197], protein fermentation is mostly facilitated by *Bacillus* spp., and these organisms are notable producers of enzymes such as amylase, glucosidase, fructofuranosidase and lactanase, which could break down different components of carbohydrates in fermenting legumes, leading to their reduction.

Increases in carbohydrate levels of fermented cowpea (up to 5%) [181], fermented Bambara groundnut (0.3%) [175], fermented black bean (146%) [130], fermented lima bean (3%) [186] and fermented pigeon pea (up to 8%) [193] were reported with such trends linked to activities of enzymes during fermentation that must have led to the conversion of resistant starches to available starches; subsequently, increasing the carbohydrate contents. Different studies have reported increases and decreases in the energy content during the fermentation of legumes (Table 4). An increase in the energy content of fermented pigeon pea flour (50.6–57.4%) [193] and fermented lentil flour (15%) [154] has been previously reported. Decreases in energy contents of fermented African oil bean flour (26%) [144] and fermented pigeon pea flour (0.5–3%) [145] have also been observed (Table 4). Obadina et al. [151] recorded both an increase (0.1–7.4%) as well as a decrease of 7.5–15.5% in energy value in fermented soymilk. While most of these aforementioned studies did not describe the mechanisms of such modifications in energy values, Adebowale and Maliki [145] linked the decrease in the energy value of fermented pigeon pea flour to the decrease in both the nitrogen-free extract and fat values of the samples.

2.3. Fats and Fatty Acids

Most studies on fermented cereal, such as pearl millet and maize-based products [128,156,157], reported a reduction (6–34%) in the fat content. The decrease in the fat content has been associated with the metabolism of lipids by the fermenting organisms and the leaching of soluble inorganic salts. In the study conducted by Ejigui et al. [138], a decrease of 11% in the fat content of fermented maize at 30 °C for a period of 4 days

was attributed to a variety of grains, fermentation conditions and steps, such as washing and sieving, which was involved in the production of dough. In addition, Nnam and Obiakor [137] reported about an 81% reduction in rice fermented for 72 h, whereas in another study on fermented stale rice, Zhang et al. [171] reported an increase (252%) in the fat content. Nnam and Obiakor [137] attributed the reduction in the fat content of fermented rice to an increase in the lipase activity in the fermenting medium. A decrease in the lipid of 6.1–49% was reported in rice bran fermented for 120 h at 30 °C, and this was presumably due to the use of fat-related components for mycelial synthesis [162].

Additionally, in Table 3, most of the studies on the fermentation of legumes, such as African oil bean, African yam beans, black beans, cowpea, kidney beans and lima beans, revealed that fermentation reduced the fat content between 0.63% and 58.7% [130,144,146,149,178,184,186]. Some of the authors attributed these reductions to the metabolism of microorganisms in the fermentation medium, the breakdown of lipids by lipase, the use of lipids as the food source by fermenting organisms, the loss of total solids during soaking and the denaturation of the fat by heat processing as well as the leaching of fat-related components into the processing water. Onwurafor et al. [192] also reported that fermenting mung bean flour using spontaneous and back-slopping methods for 72 h reduced the fat content by 33–38%, and this was due to the activities of lipolytic enzymes during fermentation. A similar mechanism for the decrease in fat contents was reported by Adebowale and Maliki [145] in fermented pigeon peas and fermented soybeans [151], and was also attributed to increased activities of the lipolytic enzymes during fermentation, which hydrolysed fat components into fatty acid and glycerol. In contrast, increases in fat levels of fermented chickpea (1.8%) [147], fermented lupin (3–11%) [150], fermented African yam bean (86%) [174], fermented Bambara groundnut (2%) [175], fermented cowpea (100–133%) [181], fermented mahogany bean (3–39%), [191] and fermented tamarind (17–48.9%) [198] have been reported (Table 4). The mechanisms involved in the increase in the fat content might be linked to the increased activity of lipolytic enzymes that may have produced more fatty acids during the fermentation, the extensive breakdown of large molecules of fat into simple fatty acids, the fat from dead microflora and/or the assumption that fermenting microflora did not use the fat as a source of energy [174,191,198]. In their study, Barampama and Simard [152] reported that fermentation reduced fatty acids (linoleic and linolenic fatty acids) in common bean by about 20%. A decrease of 2–18% and an increase of 2–24% were also observed in fatty acids of *ugba* (fermented African oil bean), and the concentrations of some fatty acids did not change during fermentation. An observed increase as well as a decrease in these fat-related constituents after fermentation suggest selective lipase activities. While these lipolytic enzymes could have contributed to the lipid dissociation and increased the extractability of fat-related constituents, same enzymes could also have selective reductive activities, perhaps using these fat-related components as carbon sources [70,202,203]. Equally important and not highlighted in these studies are the role of other microorganisms involved in fermentation that could have promoted lipid hydrolysis [204,205].

2.4. Ash and Mineral Composition

Varying effects of fermentation on the ash and mineral contents of cereals and legume-based food products have been reported, and these effects are independent of the forms of these foods. For fermented pearl millet, Adebiyi et al. [128] reported a decrease in total ash contents from 1.86% to 1.36% after fermentation for 3 days; however, they reported an increase in mineral elements such as Ca, Na, Cu, Fe, Zn and K. A reduction in ash was attributed to the leaching of soluble salts, while an increase in mineral elements was due to the improved extractability and availability of minerals as a result of fermentation. The study of Nnam and Obiakor [137] reported a reduction in the ash content of rice from 1.5% at 0 h of fermentation to 1% after 72 h, with irregular trends in the values of minerals such as Ca, P, K, Fe, Zn and Cu during time intervals. They attributed the loss in the ash content to a reduction in the dry matter, which was as a result of the breakdown of total solids

during fermentation. A decrease (14–97.9%) and increase (3.8–100%) in minerals were also reported during the fermentation of rice [137]. Both opposing trends were linked to the metabolic activities of the fermenting microorganisms which hydrolyse the metal–phytate complexes to release free minerals for use and losses in dry matter, which led to apparent increases in minerals [137]. An increase of 0.5–14% in ash with a decrease of 0.5–31% were also reported during the fermentation of rice, and were attributed to the activation of phytase which reduces phytic acid [134]. The increase in mineral (13–34%) and ash contents (7%) of fermented rice was reported by Ilowefah et al. [133], and the increase in the ash content was due to the increase in the mineral solubility and bioavailability. In a similar study by the authors, an increase in mineral (13–34%) and ash contents (9%) of fermented rice at 6 h for 32 °C was reported as well as an increase in minerals linked to the reduction in phytic acid contents, which may have formed complexes with the minerals [161].

For legumes, an increase in ash contents (Table 4) was reported for fermented soymilk [151], mung beans flour [192] and tamarind seeds [197]. These products were subjected to different fermentation times and recorded a general progressive increase in ash contents as the fermentation time increased, except for the slight reduction in ash content from 0 to 24 h in fermented tamarind seeds [197]. With an increase in ash contents as the fermentation time increased, a corresponding increase in minerals, such as Ca, Mg, P, Zn, Cu, Mn and Fe, was also reported [197]. This was also similar to the findings of Obadina et al. [151] and Onwurafor et al. [192], who reported increases in Ca, Fe, Mg and Zn contents as the fermentation progressed. An increase in ash and mineral contents in these studies was ascribed to metabolic activities of microorganisms as well as the breakdown of complex chelated compounds within the fermenting lot, leading to an improved synthesis of minerals. On the other hand, Granito et al. [180,184] reported a significant decrease in ash and mineral contents during the natural and submerged fermentation of *Phaseolus vulgaris* and two varieties of *Vigna sinensis*, respectively. They attributed this decrease to the leaching of mineral elements into discarded fermentation water and the utilization of mineral elements for the proper growth of microorganisms during fermentation. The decrease (29.8%) in ash content in African yam bean fermented at 24 h was attributed to vegetative loss, leaching into the fermentation medium as well as the microflora which might have used the ash-related components for metabolism [174]. A decrease (12.1–66.7%) in some minerals present in fermented Bambara groundnut was attributed to their utilization by fermenting microorganisms for their physiological and metabolic activities, while an increase (2.3–43.8%) was linked to the reduction in phytic acids and other antinutritional factors [142].

2.5. Vitamins

Fermentation has been reported to exhibit varying effects on different vitamins such as B vitamins and vitamin E in cereals and legumes (Tables 3 and 4). In most of the studies, especially in the fermentation of maize, buckwheat, rice and sorghum using different starter cultures (LAB species, yeast and fungi), an increase in vitamin B1, B2, B3 and E were reported by up to 10 folds [133,157,167,171]. Ilowefah et al. [134] reported that vitamin B increased in fermented maize flour due to enzyme interactions with starch, protein and other key biosynthetic precursors, which stimulated their synthesis of bound forms of the vitamins. Contrary to these studies, Ejigui et al. [138] and Tamene et al. [172], on the fermentation of maize and tef, reported a reduction in vitamin B1, B2, β-carotene (as retinol equivalent) and the folate content of the resulting flour and their products. A decrease in vitamins was caused as a result of mechanical loss due to processes, fermentation and lipid solubilization, as well as consumption by other microorganisms or losses due to discarding the supernatant [138,172]. In some other studies, fermentation reportedly increased the vitamin B1, B2 and E (α-tocopherols) levels of fermented legumes (cowpea and kidney beans) by 17 to 94% [179,184]. Likewise, levels of vitamin A, B1, B2, B3, α-, γ- and δ-tocopherols reportedly reduced in fermented common bean, cowpea, lupin and mung bean by 5–106% [152,179,188,192]. The level of vitamins after fermentation seemed to be

dependent on the fermenting strain and metabolic activity of these strains. This could have impacted the varying reported trends in the vitamin content.

2.6. Fibre

Studies on rice showed that fermentation increased the fibre content in their resulting flours [171] and, likewise, the insoluble and soluble fibre fractions at 22 °C for 72 h [133]. The increase in fibre in stale rice by *Cordyceps sinensis* was attributed to the transformation mechanisms of corresponding substances in the fermentation process, and some mycelia of *Cordyceps sinensis* possibly attached onto the surface of rice grain [171]. Jood et al. [167] reported about a 10% reduction in the total and insoluble dietary fibre, and the authors suggested that an increase in the activity of hydrolysing enzymes such as cellulase, α-galactosidase, etc., caused the rapid hydrolysis of the insoluble dietary fibre constituents, leading to their conversion into soluble dietary fibres. The mechanism of the decrease in fibre in fermented cereal was attributed to the partial solubilization of cellulose and hemicellulose type of materials by microbial enzymes [30]. Other authors ascribed the reduction in fibre of fermented maize flour (74%) to an enzymatic breakdown by LAB, which utilized the fibre as a carbon source [156]. In addition, the authors explained that due to the enhanced activity of β-glucanases and carboxypeptidases, insoluble β-glucan could be degraded into soluble β-glucan and, further, due to the fermentation activity of other enzymes such as β-glucosidases, cellobiose, etc., it could hydrolyse the soluble β-glucan into glucose. A 55% decrease in fibre was attributed to the enzymatic degradation of the fibre during the fermentation process of fermented pearl millet [158], while a decrease of 40% in fibre levels in fermented sorghum was attributed to the partial solubilisation of cellulose and hemicellulosic type of material by microbial enzymes [132]. Onyimba et al. [135] reported a decrease of 66–69% in fermented sorghum and ascribed this to the action of cellulolytic microorganisms present in the fermenting substrate [135]. Likewise, a 22% decrease in fermented oats was ascribed to the action of enzymes from *Pleurotus ostreatus* such as hemicellulase, xylanases, cellulase and laccase [130].

The fermentation of various legume seeds and their effect on fibre levels have also been reported (Table 3). In legume seeds, such as African yam beans and Lima beans, fermentation reduced the crude fibre content, with other studies equally reporting that fermentation reduced the insoluble and soluble fibres of pigeon pea and kidney beans [149,174,184,186]. The decrease in crude fibre was attributed to hydrolysis and leaching into the fermentation medium, or the microflora used the fibre-related components for its metabolism [174], while a decrease in insoluble fibre was ascribed to the use of cellulose and arabinoxilnase by the fermenting microorganisms [184]. The decrease in the fibre content (59%) in black bean fermented at 336 h (14 days) with the *Pleurotus ostreatus* CS155 strain was attributed to the action of enzymes from *Pleurotus ostreatus*, such as hemicellulase, xylanases, cellulase and laccase [130]. Additionally, a study on curd waste from soybeans fermented with two types of yeasts showed that a decrease in fibre (7.4–46%) was an indication of the secretion of cellulose/hemicellulose-degrading enzymes by the yeasts during fermentation, and the individual preparation of yeast may have different enzyme activities as well as being able to interact differently with soluble and insoluble fibre components [196]. In common beans and lupin seeds, Barampama and Simard [152] and Olukomaiya et al. [150] reported that due to microbial actions, the acid detergent fibre increased about 86%, and others, such as hemicellulose and lignin and cellulose, were approximately 2–14% of the fibre fractions. The increase in cellulose was ascribed to the build-up of acid, alkaline or neutral detergent-insoluble substances causing the fibre values to be overestimated [150].

2.7. Antinutritional Factors

Food fermentation has been shown to effectively increase the nutritional composition of foods as well as decrease the levels of antinutritional factors (ANFs) and toxic constituents, and might be a better alternative in minimizing the adverse effects of these compounds in diets [197,206]. The fermentation of sorghum flour reduced hydrogen cyanide by

52.3% [168], while Nivetha et al. [154] reported a 66% reduction in the cyanogenic glycosides content of a linseed (*Linum usitatissimum*) fermented beverage using *Lactobacillus acidophilus* [154]. The reduction in cyanogenic glycosides was due to the breakdown and degradation of the ANFs into smaller units by the action of the enzymes mobilized during the fermentation period [154]. The inherent phytase activity of sorghum activated by LAB during fermentation degraded phytates, while the decrease in tannin content was due to microbial activity and phytate acyl hydrolases [168]. Likewise, decreases between 30% and 98.7% in tannin levels were reported in *ting* (a fermented product from sorghum), and were attributed to the rearrangement and depolymerization of the tannin structure [163–165]. This can be linked to the acidic environment of the fermentation medium, reduced extractability, self-polymerization, interaction of tannin with other macromolecules (such as starch and AAs) and the ability of LABs to possibly metabolize tannins [163–165]. Indications from these studies suggest that fermentation leads to the production of enzymes, such as tannase [130], that reduce and/or eliminate tannins during this process. In fermented rice, the decrease in tannin (50%) was attributed to milling, which removed most of the tannin-related fractions, while phytate (19–69%) was reduced due to the increased activities of phytases during fermentation [137], and the reduction in ANFs in sorghum fermented for 72 h at room temperature was due to the ability of microorganisms to use them up [169].

For legumes, the decrease in ANFs of fermented African oil bean (24–79%) was attributed to soaking (which caused some of the ANFs to leach out), as well as microflora enzymes which degraded organic complexes to release antinutrients and the subsequent leach out of these components into the surrounding medium [173]. Adebiyi et al. [142] observed significant reductions in ANFs in unhulled *dawadawa* samples from Bambara groundnut—phytic acid (18.06%), oxalate (59.12%) and tannin (34.16%)—, with the reduction in phytic acid attributed to the enzymatic activity of fermenting microorganisms that degrade phytic acid or the complex(es) formed by them. In fermented Bambara groundnut flour, a decrease of 16–42% in ANFs was also observed, and this was due to the effect of the biodegradation of chemicals involved during fermentation [175]. Similarly, the traditional fermentation of tamarind seed for the production of *iru* (*daddawa*) resulted in a significant reduction in ANFs, tannin contents (75%), phytic acid contents (50%) and trypsin inhibitor activity (86%), while *Bacillus pumilus*, *B. subtilis* and *B. licheniformis* were implicated as the organisms responsible for fermenting the legume [89]. A 29% decrease in phytic acid in fermented soymilk was ascribed to the action of phytase and β-glucosidase produced by fermenting microbes [197]. Olaleye et al. [190] reported an increased nutritional content as well as a significant reduction in oxalate (16.5–68%), phytate (13.7–26%) and tannin (9.2–25.7%), following the fermentation of beans for 72 h at 45 °C with no reported mechanism. As described in various studies, the fermentation of cereals and legumes reduces tannins via hydrolysis by tannase, which catalyses the hydrolysis of ester and depside bonds, yielding gallic acid and glucose [168,207,208]. This enzymic degradation of tannins is facilitated by a lower pH, such as that achieved during the fermentation of legumes and cereals. Some researchers have suggested that the reduction in tannins during fermentation may also be attributed to its water solubility; hence, leaching out into the fermenting media, just as all other polyphenolic compounds [207–209]. Elsewhere, the fermentation of tamarind seed for 72 h resulted in up to an 85.7% reduction in tannin, 89.4% reduction in trypsin inhibitor activity and 14.3% reduction in phytate [198]. The decrease in phytate was attributed to a wide range of microflora that is known to possess phytase activity and enzymatic hydrolysis that causes a decrease in trypsin inhibitor activity [198]. Some authors argue that phytate reduction during fermentation is a consequence of plant phytases activated during fermentation, although phytase activity is very variable depending on the plant species [210–212]. According to Licandro et al. [212], fermentation leads to the production of organic acids, decreasing the pH of the substrate and, thus, optimizing conditions for the activity of phytases.

A number of studies have reported reductions in oxalate concentrations after fermentation—27% in *dawadawa* [142], 62–77% in *ugba* [173], 36–52% in fermented Bambara

groundnut flour [176], 67% in fermented horse gram flour [183] and 95% in fermented lima bean [186], with such reductions attributed to the utilization of oxalate as a carbon source of microbes and the microbial degradation of ANF-related components [183,186]. It has also been suggested that the reduction in oxalate content following fermentation can be attributed to the hydrolytic action of enzymes produced during fermentation [213].

2.8. Nutrient Digestibility and Bioavailability

Fermentation is known to enhance nutrient bioaccessibility, bioavailability and digestibility, mainly via the disruption of plant cell wall structures/tissues and the release of enzymes and other bioactive components. Additionally, lower pH values of the food medium attained during fermentation may improve the absorption of certain nutrients, as well as facilitate the decrease in some ANFs which interfere with nutrient bioavailability and bioaccessibility. The quality of protein should not only consider the composition of AAs, but also the digestibility as well as the absorption of the produced hydrolysis products in the human gastrointestinal tract [214–216]. For example, protein might have a very good AA profile, but are unable to absorbed well and/or be digested in the body. Some studies have reported an increase in in vitro protein digestibility (IVPD) during the fermentation of cereals and legumes. An improved protein digestibility during fermentation was attributed to the release of protein from plant tissues by the enzymatic breakdown of dietary fibres, with a simultaneous reduction in/degradation of polyphenols, tannins and phytic acid by the action of microbial enzymes [156,210,215]. Polyphenols are known to bind to recognition/receptive sites of digestive enzymes, or crosslink with proteins; hence, limiting the hydrolysis reaction [211]. Furthermore, during fermentation, insoluble/complex storage proteins undergo perturbations in structural configurations, which render them more accessible and susceptible to attack by pepsin and endopeptidase that breaks down proteins into smaller peptides that are more soluble. Ogodo et al. [134] suggested that lower pH values obtained during fermentation may well promote the enzyme activity of peptidases and activate endogenous proteases, which increases peptides and the free AA concentration; hence, increasing protein solubility.

Wedad et al. [170] reported an IVPD increase of 0.49–31.3% in sorghum fermented with starter inoculum through SSF. Mohammed et al. [139] also reported an increase of 21% in fermented sorghum, and such an increase was due to the reduction in ANF during fermentation. An increase of 10% was reported in IVPD of African yam bean (Table 4), and this was attributed to proteolysis, an increased availability of AAs and reduced ANFs [149]. An increase of 15.2% was reported in IVPD of chickpea fermented into *tempeh* flour and the authors attributed this to the elimination of undesirable factors (i.e., tannins during soaking and phytic acid during fermentation) as well as protein hydrolysis during fermentation, which resulted in proteins that were more vulnerable to enzyme action [178]. Additionally, an increase of 4.4% in IVPD of chickpea fermented with *Cordyceps militaris* was ascribed to the unfolding of the proteins during fermentation; thus, making them more accessible and easier to be hydrolysed by proteases [147]. On the contrary, during the fermentation of lupins into fermented lupin flour, Olukomaiya et al. [150] reported a 16–32.5% decrease in IVPD, with the authors attributing this decrease to protein being locked within the fibre matrix and, thus, reducing the hydrolytic action of the enzymes as well as partial protein denaturation during drying, which might also lower protein dispersibility and solubility; thus, resulting in a reduced IVPD.

An increase in the in vitro bioavailability of iron (68.3–90.6%) and zinc (86.7–100.6%) was reported by Dhull et al. [185] in fermented lentils. The authors attributed this increase to the reduction in ANFs as well as compounds that formed complexes with zinc and iron in the unfermented flour. Significant increases in in vitro starch digestibility (IVSD) have been recorded for maize (*Zea mays*) flour fermentation with LAB-consortium from maize (10.68–49.32%), LAB-consortium from sorghum (10.68–58%) and natural fermentation (20.10–49.45%) [156]. The enhanced digestibility was due to changes in the endosperm protein which allowed starch to become more accessible to the digestive enzymes [156].

The increase in IVSD in fermented sorghum (1.6–54%) was equally attributed to changes in the endosperm protein fractions that allowed starch to become more accessible to the digestive enzymes [166].

3. Conclusions and Future Perspectives

It was evident from the various studies consulted in this review that fermentation, though being an ancient food processing practice, remains an important approach for increasing the level of nutrients, reducing antinutritional factors and enhancing nutrient bioaccessibility/bioavailability of cereals and legumes. Very often, fermentation does not only increase the availability and digestibility of nutrients, but also makes the food more appetizing and acceptable by improving its texture, aroma, flavour, etc., as well as rendering the food safer for consumption by reducing/degrading certain inherent toxins in the food crop. This established fermented foods an important part of diet and nutrition in many cultures around the world, particularly in developing countries, with limited access to sophisticated food processing techniques and infrastructure. Additionally, some of the microorganisms implicated in food fermentation have been linked with important health benefits. Based on inference from the reviewed literature, we see fermentation as an important process in the food production value chain. Indeed, fermentation is a complex process and food components do not necessarily exist in isolation, but as an entity. Accordingly, modifications in these constituents are influenced by the crop specie and cultivar, grain composition, fermenting microorganisms and the metabolism of these organisms. Additionally, important are the prior processing steps before and after fermentation. These intricacies tend to limit the understanding of food fermentation and insights into the mechanisms governing the modification in these components somewhat difficult. Hence, in order to fully exploit the benefits of fermentation, more research should be conducted, particularly focusing on modern microbial and biotechnological techniques, as well as the adoption of advanced techniques, including, but not limited to, metabolomics, metagenomics, metatranscriptomics, proteomics and artificial intelligence models to better optimize, standardize and describe the fermentation process for an overall improved food quality, enhanced nutrition and health as well as other associated socioeconomic benefits.

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