Revisiting the Roles of Microorganisms in Food Sector for Industrial Exploration

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ARTICLE INFO
Received: 18.04.2024;
Revised: 16.07.2024;
Accepted: 18.07.2024

Key Words:
Foodstuff, food additive, bacteria, yeast, mold, algae.

ABSTRACT

From antique periods, humans have intentionally or unintentionally exploited microorganisms for their production of foodstuffs and food additives. Fermentation is an age-old technology utilized by humans to conserve perishable foods and to flourish their nutritional and organoleptic properties. The worldwide geometric rise in population, global climate change impart tremendous pressure on human civilization to shift from traditional sources of food and food ingredients and rely on a futuristic alternative source that not only hampers the orthodox supply of food source but also eco-friendly in nature of its production. And microorganisms fulfilled this demand in all respects. From the beginning of 20th century with the constant innovation in microbial biotechnology, microorganisms such as bacteria, yeast, mold, and algae have been tremendously applied for the production of various kinds of foodstuffs and food additives like-dairy products, beverages, fermented-meat, vegetables, cereals, fish, vitamins, amino acids, polyunsaturated fatty acids, prebiotic, food-colorant, preservatives, thickeners single-cell protein, probiotics; which we are utilized in our daily life. This chapter especially focuses on the applications of microorganisms in the production of foodstuffs, food additives as well as consumable microbial biomass with their genetic manipulation in the food industry.

1. Introduction

Progressing population growth, gradually changing food patterns and global climate change are collectively pushing unprecedented stress on the universal food production system (Linder 2019). The global population increase from 7.7 billion (2020) now to 10 billion in 2050 (World Population Clock, 2019). 70% of additional food will be requisite for our imminent generations by 2050 (FAO United Nations 2009). Increasing temperatures resulting from anthropogenic activities reduce agricultural production of major crops (Zhao *et al.* 2017), including crops destroyed by the pests (Deutsch *et al.* 2018) and extreme climatic conditions (Lesk *et al.* 2016). At this breakneck crisis period in human civilization, an alternative strategy is instantly needed to overcome the deficiency of conventional means of food production. Although humans have taken advantage from microorganisms for synthesizing foodstuffs and food additives for thousands of years (the earliest evidence of utilizing microbes was enlisted earlier than 7000 BC when alcohol produced from sugar with the help of yeast to prepare alcoholic beverages in Sumeria and Babylonia) (Amalaradjou *et al.* 2016), present critical situations enforced humans to become much more dependent on microorganisms for their food requirements. Nowadays microorganisms are exploited not to produce only various type of foodstuffs [fermented food products (dairy/meats/ vegetable/fish/cereal products), and fermented beverages (alcoholic, milk, tea, coffee, honey)] and food additives (preservatives, antifoaming agent, emulsifying agent, thickening agent, organic acids, amino acids, vitamins, flavoring agent, colorant, food-grade enzymes) but also themselves applied as edible microbial biomass (single-cell protein, baker yeast, probiotics).

Foodstuffs are substances suitable for consumption as food. From the ancient times we have consumed a variety of fermented foodstuffs such as dairy-based (curd, cheese, kefir, yogurt, shubat), vegetable and fruit-based (pickles, sauerkraut, soy sauce, natto, , tursu), meat-based (salami, sausages, teewurst, som moo, pepperoni), fish-based (bagoong, rakfish, garum, fish sauce, jeotgal), cereal-based (idli, dosa, kishk, tarhana, ogi, mawe, injera, kiska, dokla); and fermented beverages [alcoholic: beer, wine, whiskey, perry, apfelwein; milk-based: lassi, butter-milk, acidophilus milk; tea-based: goishicha, pu-erh tea, kombucha, doncha; honey-based: mead, metheglin) (Wikipedia 2022). According to the World Health Organization (WHO 2018), food additives are the supplementary substances mixed to food to preserve or enhance the freshness, safety, texture, taste, or appearance of food. Additives or their degradative constituents mostly persist in food, however, sometimes expelled during processing. Microorganisms are vigorously utilized to produce a wide array of food additive components that are involved in the production, processing, packaging, and/or storage without being a major ingredient of the food. The nutritive value of food additives such as vitamins (Vitamin B_{12}, B_2, C), amino acids (glutamic acid, lysine), sweeteners (erythritol, xylitol, mannitol, sorbitol, D-tagatose), prebiotic oligosaccharides (galactooligosaccharides, isomaltooligosacc-harides, chitooligosaccharides, fructooligosaccharides, xylooigosaccharides), polyunsaturated fatty acids (docosapentanoic acid, docosahexanoic acid, gamma linolenic acid, arachidonic acid, eicosapentanoic acid) are utilized to increase the nutritive value of food. The sensory value of food such as color, odor, taste, and consistency or texture enhanced by colorant (canthaxanthin, astaxanthin, prodigiosin, violacein, β-carotene), microbial polysaccharides cum thickening agent (alginate, pullulan, dextran, xanthan gum, gellan), flavoring agent (diacetyl, lactones, esters, methylketones, aldehydes), biosurfactant agent (liposan, rhamnolipids, mannoprotein, trehalolipids, emulsan). The current forms of food production and distribution have increased the demand for longer shelf life which is increased by the incorporation of preservatives (nisin, natamycin, neuterin, bacteriocins, bacteriophages) (Belitz *et al.* 2009). The ingestion of microorganisms by humans is not an innovative concept. From the ancient period of human civilization, humans consume undeliberate or deliberately microbes employing alcoholic beverages, dairy products, etc. During the First World War German soldiers were provided with yeast, especially *Candida utilis* as a protein supplement. Microorganisms provide high quantity and quality of protein in a short period by culturing cheap sources make them a promising substitute to the orthodox sources of food. Humans now globally consumed single-cell protein (SCP), baker yeast, and probiotics, which provide good sources protein, beneficially affect human health in so many ways, and support the production of a variety of bakery products, respectively.

Microorganisms including chiefly bacteria, fungi (yeast and mold), and algae have been enormously applied in the production of a diverse range of foodstuffs, food additives, and microbial biomass. A bioprocess is a particular practice that uses complete living cells (e.g., microbes, plant cells) or their components (e.g., enzymes, chloroplasts) to acquire preferred products (Papagianni 2017). Bioprocesses use present knowledge about live systems to cultivate new biological mediators that can function as a bio-manufacturing hub for value-added products (Nikel *et al.* 2016). The microbial bioprocess carries out both industrially oriented research in the fields of microbial physiology, applied microbiology, and fermentation technology. Microorganisms hold the greatest industrial interest since they have a short generation period and harbor a wide array of enzymes and metabolic processes. Besides, there is a great diversity of microorganisms throughout nature that can be tested for modifying and degrading a range of complex organic molecules (Lopes *et al.* 2017). With the advancement of molecular biology, genetic engineering, system biology, directed evolution bioinformatics, enabled the clarification of the genomics, transcriptomics, and metabolomics of food microorganisms. Also, a superior understanding of microbial biology has facilitated the knowledge-based manipulation of bacteria for food and food ingredient production, metabolic engineering for the production of nutraceuticals, and molecular mining of unknown activities (Gupta and Prakash 2017, Hoskisson 2018).

This review reports up-to-date information about the microbial production of food-related products, additives, and edible microbial biomass, besides also highlighting the genetic manipulation of microbes and prospects in this field.

2. Microbial Bioprocessing Strategies

Fermentation is the principal bioprocessing technique for manufacturing microbial foodstuffs and additives. The word "fermentation" originally comes from the Latin verb 'fervere', means to boil; i.e. bubbles of CO_2 originated from the fermented yeast extract of fruit or malted grain (Stanbury *et al.* 2017). The science of fermentation is known as zymology. Humans have been familiar with the fermentation process to yield foodstuffs and beverages since the Neolithic age (Wikipedia 2022). Microbial metabolites are of two types: primary metabolites and secondary metabolites. Throughout the log period of microbial growth, the products synthesized are either biosynthetically produced anabolites which are necessary for the normal growth of the microbes such as amino acids, nucleotides, proteins, nucleic acids, lipids, carbohydrates, etc. or catabolically produced catabolites such as ethanol and lactic acid (LA). These products are collectively known as primary metabolites. The majority of primary metabolites have substantial economic significance and produced by fermentation. Secondary metabolites such as antibiotics, anticancer agents, pigments do not have any significant role in cell metabolism. They deliver adaptive roles, for example, by functioning as defense compounds or signaling molecules in ecological interactions, symbiosis, metal transport, competition, and so on (Patel 2012, Stanbury *et al.* 2017, Thirumurugan *et al.* 2017).

Mainly bacteria and fungi (yeast and mold) are extensively functional in fermentation technology. There are two basic strategies applied in fermentation technology: solid-state fermentation (SSF) and submerged fermentation (SmF). SSF exploits solid substrates, like wheat or rice bran, sugarcane bagasse, and fruits or vegetables peel. The major benefit of utilizing such waste materials as substrates is to recycle their inherent nutritional potential. Here, substrates are slowly utilized leading to the controlled release of nutrients provisioned for lengthy fermentation periods. Fungi and microorganisms with low water activity support SSF; but unsuitable for microorganisms require high water activity, such as bacteria. (Babu and Satyanarayana, 1996). SmF exploits free-flowing liquefied substrates, such as molasses and broths; therefore, suitable for bacteria or microorganisms with high water activity. The metabolites are released into the fermentation broth and these criteria are particularly helpful for mining of secondary metabolites in a liquid state. Here substrates are rapidly utilized, need to be regularly exchanged/supplemented with nutrients (Mazumder *et al.* 2009, Ravichandran and Vimala 2012, Doriya *et al.* 2016). The benefits of SSF over SmF are economic-friendly, minor risk of contamination, simple recovery of the enzymes, compatible with the natural environment of the fungus, production of a protein-augmented by-product, production of enzymes with intensified enzyme activities, and higher specific activities (Mondal *et al.* 2019). The SSF is well established for the production of several types of value-added products like antibiotics, SCP, polyunsaturated fatty acids, enzymes, organic acids, vitamins, biopesticides, biofuel (Bhargav *et al.* 2008). SmF is generally used for producing a variety of secondary metabolites such as antibiotics, phenolic, steroids, pigments, enzyme inhibitors (Gonzalez *et al.* 2003). SmF in turn is of two types: batch and continuous fermentation. In batch fermentation, the organism is kept in a limited volume of culture medium; therefore, biochemical synthesis is restricted for a definite period. In continuous fermentation, the fresh nutrient medium is continuously or discontinuously fed into the fermentation vessel with the regular withdrawal of a fraction of the medium for retrieval of cells or fermentative products (Malakar *et al.* 2020).

3. Application:

3.1 Foodstuffs: The various kind of microorganisms based foodstuffs are dairy products, fermented-vegetables, meat, fish, honey, etc. The production of fermented foods through microbial fermentation relies on the growth and metabolism of specific cultures present in the starting raw material (milk, vegetables, meat, fish, and grain); known as starter cultures. The starter cultures can naturally be present or are inoculated into food materials to bring about desired changes in the final product; which include enhanced nutritional and functional values, longer preservation period, improved food safety, and increased sensory attributes and economic value. The commonly used starter cultures include bacteria, yeast, and molds. The bacterial starter cultures predominantly include lactic acid bacteria (LAB), which consists of Gram-positive cocci and rods that metabolize sugar via the homofermentative or heterofermentative pathway (Axelsson 2004). Although LAB includes 10 genera, most starter cultures belong to *Lactobacillus, Lactococcus, Leuconostoc, and Streptococcus spp.* The starter cultures must be robust to withstand freeze-drying, and stable under defined storage conditions for several months with no reduction in activity (Hutkins *et al.* 2006 and Amalaradjou *et al.* 2016). Fermentation results in protecting the growth of spoilage and pathogenic organisms, desirable qualities including the production of flavor compounds (diacetyl and acetaldehyde), production of bioactive compounds, and the associated nutritional and health benefits (Ross *et al.* 2002).

3.1.1. Dairy Products: Since primeval periods, dairy products have to nourish human health by providing minerals (calcium, phosphorous, potassium, magnesium), vitamins (A, B2, B12, D), proteins, and other indispensable nutrients. A large array of microbes present in different fermented dairy products consumed in different regions of the world. Microbes ferment the principal milk-sugar lactose to produce lactic acid which in turn precipitates milk protein thicker consistency of dairy products than milk. The acidic pH lowers the growth of spoilage or pathogenic microbes (Kumar and Chordia 2017). The most commonly used dairy products include curd, acidophilus milk, sour cream, yogurt, cheese, buttermilk, and kumis (Wouters 2002).

Yogurt is a semi-solid fermented milk product that originated in Bulgaria. On region basis the consistency, aroma, and flavor of yogurt depend on its composition, either simple or with added ingredients such as fruits, sugar, and gelling agents. The dominant starter culture for most yogurt production is symbiotic thermostable LAB: *Streptococcus salivarius* subsp. *thermophilus* and *Lactobacillus delbrueckii* subsp. *bulgaricus*. The proteolytic rods support the growth of the streptococci by synthesizing amino acids, small peptides; whereas cocci can enhance the rods growth by anaerobically forming formic acid from pyruvic acid with a swift production of CO_2. Initially, the streptococci grow faster utilizing growth factors provided the rods, and cause an initial pH drop (approx. 5.0) to the yogurt. Afterward, the lactobacilli grow faster by exploiting the growth factors (formic acid and CO_2) and responsible for a further decrease in pH to 4.0 (Frazier *et al.* 1971, Prescott and Dunn 2004, Niamsiri and Batt 2009). **Curd** is made by curdling or coagulating the milk. This happens because raw milk contains *Lactobacillus spp.*, which ferment sugars into lactic acid the precipitates milk protein casein; imparts the sour taste and texture to curd. The milk-sugar lactose, a disaccharide (compound sugar) containing β-(1’!4) glycosidic linkage between galactose and glucose (Ledenbach and Marshall 2009). **Cheese** is produced by concentrating milk-protein casein, fat, and minerals through dehydration. The basic steps in cheese making include acidification, coagulation, dehydration, and salting. In the case of cheese, the starter cultures are primarily used for acid production. The most common starter cultures employed in cheese manufacture are *Lactococcus lactis* subsp. lactis, *L. lactis* subsp. *cremoris*, *S. thermophilus, L. helveticus* and *L. delbrueckii* subsp. *Bulgaricus.* The acidic flavor of unripened cheese and milk coagulation is due to the lactic acid production by these LAB. Besides, starter cultures also aid in further flavor enrichment, production of proteolytic and lipolytic enzymes that are critical to ripening and suppression of spoilage and pathogenic organisms (Frazier *et al.* 1971, Johnson 2017).

3.1.2. Fermented fruits and vegetables: Fermentation is one of the primitive food processing techniques to lengthen the shelf life of perishable food. Numerous fermented fruits and vegetable products have documented in our ancient culture (Swain *et al.* 2014). Fruits and vegetables are enriched with water-soluble vitamins C and B-complex, provitamin A, minerals, phytosterols, phytochemicals, and dietary fibers; indispensable for human nutrition (Dhal *et al.* 2005). Low sugar content, neutral pH, and nutrient-rich vegetables afford a natural medium for lactic acid fermentation; which in turn boosts the organoleptic and nutritional features (Heller 2001). Fermented fruits and vegetables have the following benefits anti-cancer, anti-obesity, anti-constipation, and antimicrobial (Thapa and Tamang 2015).

Serofluid dish (or Jiang shui, in Chinese), a thousand-year-old traditional food in the Chinese culture. Serofluid dish is fresh celery and other vegetables into the soup or rice soup after a variety of micro-organisms (*Bacillus subtilis, Saccharomyces cerevisiae*, and *Acetobacter sp.*) co-fermentation of fermented food (Zhao *et al.* 2019). **Sauerkraut** (means sour cabbage) is produced from the lactic acid fermentation of cabbage. Here, fresh cabbage is chopped, add 2.3–3.0% salt, and this mixture now allowing for natural fermentation. Sauerkraut production involves consecutive microbial fermentation through hetero-fermentative and homo-fermentative LAB, generally involving *Leuconostoc sp.*, *Lactobacillus sp.,* and *Pediococcus sp.* The pH of the final product ranging from 3.5 to 3.8, responsible for preserving fermented cabbage for a long period (Swain *et al.* 2014). **Gundruk** is a fermented, unsalted, and acidic vegetable product native to the Himalayas. It is prepared from the fresh leaves of native vegetables such as rayosag (*Brassica rapa* L.), cauliflower leaves (*Brassica oleracea* L.), mustard leaves (Brassica juncea L.), and cabbages (*Brassica sp.*); kept 1-2 days for wilting and now these wilted leaves are slightly crushed, packed in an airtight earthen pot for natural fermentation through indigenous microbes (*Lactobacillus fermentum, L. plantarum, L. casei, L. casei* subsp. *pseudoplantarum*, and *Pediococcus pentosaceus*) for about 15–22 days. After appropriate fermentation, products are takeout and sun-dried for 2–4 days (Tamang and Tamang 2010). **Indian pickles** are produced from dried vegetables or fruits, treated with salt in airtight containers, sundried for several days, and during this period halophilic or salt-tolerant intrinsic microbes metabolize the sucrose in the fruit or vegetables to produce by-products such as acetic acid, lactic acid, and CO_2; responsible for extended shelf life, taste, aroma. LAB imparts its characteristic sourness and imparts a tangy flavor to them. Indians are very much familiar with pickles and regularly consumed in their diet, mainly fruit-based especially mango (*Magnifera indica*), lemon (*Citrus limon*) blended with large varieties of spices, salt, and oil. During the initial period of pickling, at low salt concentration predominant bacterial genera are *Pseudomonas, Bacillus, Flavobacterium* (Shah *et al.* 2014), and subsequently with the advancement of fermentation at high salt concentration, *Streptococcus faecalis*, and *Leuconostoc mesenteroides* begin to flourish (Sharma 2007). Successively, *Lactobacillus brevis*, and *L. plantarum* grows and produces lactic acid. Yeast (*Debaryomyces*, *Pichia*, *Candida spp.*) doing their job at the end of fermentation and lactic acid concentration starts to drop (Mokoena *et al.* 2016). LAB introduces the rapid build-up of organic acids like lactic acid, acetic acid, and citric acid in the raw substrates (Darmayanti *et al.* 2014). Brines utilized for pickle fermentation consisting of high salt concentrations and organic acids with reduced pH level (<4.5), induces inhibitory effect to the pathogenic coliforms, clostridia, pseudomonads, and other non-LAB that deteriorate flavor and texture of the final product (Sohaib *et al.* 2016). **Kimchi** is a Korean ethnic fermented vegetable, characterized by its typical sour, and carbonated taste. Kimchi is a generic term indicating a group of native lactic acid fermented vegetables in Korea. It is prepared fermentation of brined oriental cabbage or radish to decant with numerous spices (red pepper, green onion, garlic, ginger), and other minor requirements (seasonings, salted seafoods, fruits, vegetables, cereals, fish, meats) (Swain *et al.* 2014). Kimchi fermentation is a temperature-reliant process that involves ripening at 15°C for one week and then kept there at 25°C for three days. However, low temperature is favored in kimchi fermentation to avoid the production of a strong acid, extra-ripening, and prolonged period of optimum taste. Mostly identified bacterial genera in kimchi are *Leuconostoc mesenteroides*, *Lactobacillus plantarum*, and others important genera including *L. pseudomesenteroides*, *L. curvatus*, and *L. lactis*; together they cause a gradual decline of pH to 4.0 (Patra *et al.* 2016).

3.1.3. Fermented Meat: Fermentation is a traditional, simple, and inexpensive method for the preservation of meat and meat products. Some well-known fermented meat products across the world are including, salami of Europe, alheira of Portugal, androlla of Spain, nham of Thailand, kargyong, satchu, and suka ko masu of Nepal, arjia, chartayshya and jamma of India, and nem chua of Vietnam (Nguyen *et al.* 2011, Anagnostopoulos and Tsaltas 2019, Rai *et al.* 2010). Based on the ripening period, fermented dry sausage can be distributed in two sets: sausages ripened for above 4 weeks causes a firm texture with a mildly acidic, salty taste or semidry sausages ripened for 7 to 28 days (depending on the product diameter) leading to a strongly acidic, salty, mild taste, and a softer texture. Previously fermented meat products are only produced from pork and beef but present consumers claim for low-fat sausages leading to a concurrent increase in poultry sausage consumption (Stadnik and Kęska 2015, Tamang *et al.* 2020). Fermentation of meat by LAB enhances nutritional and organoleptic properties, improves sliceability, support reddening of these products, and ensure food safety by inhibiting the growth of pathogenic microbes. Changes in organoleptic properties are chiefly due to the acidification (sugar and lipid content of meat degraded to produce lactic acid and free fatty acids, respectively). The acidification process is an important parameter for sausage preparation as it determines the flavor, color, and texture of dry sausage, enhances shelf life. The acidification process is tightly regulated, since a fast pH drop results in a massive protein denaturation that makes the product unacceptable (Pilevar and Hosseini 2017). The dominant LAB in fermented meats are *Lactobacillus curvatus*, *L. paraplantarum, L. plantarum*, *L. sakei*, *L. brevis*, *L. carnis*, *L. casei*, *L. divergens*, *L. sanfransiscensis*, *Leuconostoc carnosum*, L. gelidium, *L. pseudomesenteroides*, *L. citreum*, *L. mesenteroides*, *Pediococcus acidilactici*, *P. pentosaceus*, *Weissella cibaria*, *W. viridescens*, *Bacillus lentus*, *B. licheniformis*, *B. mycoides*, *B. subtilis*, *B. thuringiensis*, *Enterococcus cecorum*, *E. durans*, *E. faecalis*, *E. faecium*, *E. hirae* (Rai *et al.* 2010, Oki *et al.* 2011; Neffe-Skocinska *et al.* 2016); and also the coagulase-negative staphylococci, micrococci, *Enterobacteriaceae* (Marty *et al.* 2011). Besides bacteria, several molds are also used for fermentation of meat and meat products such as *Aspergillus*, *Rhizopus*, *Mucor*, *Actinomucor*, *Amylomyces*, *Neurospora*, *Monascus,* and *Penicillium* spp. (Laranjo *et al.* 2017).

Debaryomyces hansenii is the predominant yeast species widely present in naturally fermented sausages. Based on the availability of oxygen, molds exist on surfaces in fermented sausages while yeasts found internally (Kumar *et al.* 2017). Molds improve organoleptic properties of sausages by synthesizing lipase and proteases, and also produce tiny-pores on the surface of sausages by dehydration (Tamang *et al.* 2020).

3.1.4. Fermented Fish: From immemorial time, fermented fish is a fundamental part of many food cultures throughout the world. Traditionally people of coastal regions preserve fish by adopting various techniques- fermentation, salting, sun-drying, and smoking (Salampessy *et al.* 2010). Some indigenous fermented fish products consumed around the world are hentak, ngari, bordia, karati, lashim, and tungtap of India, jeotgal or jeot or saeujeot of Korea, plaa-som of Thailand, shiokara of Japan, patis of the Philippines, surstromming of Sweden (Majumdar *et al.* 2016). Based on the appearance of the final product, fermented fish can be divided into three categories: whole fermented fish that virtually keeps its original structure (Zeng *et al.* 2013), fermented fish pastes which appear as paste-like products (Giri *et al.* 2010); and in fermented fish sauce, fish is crushed into a liquid form (Zeng *et al.* 2013). Fermentation of fish is usually achieved by the intrinsic microbial community present in the raw fish, known as spontaneous fermentation or by inoculating the fish with starter cultures (Devi *et al.* 2015). Due to uncontrolled fermentation occurs in the spontaneous procedure, sometimes the final product is not acceptable qualities (Capozzi *et al.* 2017). Spontaneous fermentation is optimized by incorporating the inoculum from the previous batch of fermentation. Fermentations of raw fish with starter cultures leading to the well-regulated fermentation process with better qualities of final products (Tamang and Samuel 2010). The well-established microbial genera are including bacteria (*Enterococcus faecalis*, *Lactobacillus plantarum*, *L. reuteri*, *Streptococcus salivarius*, *Bacillus*, *Micrococcus*, *Pediococcus spp.*)' yeasts (*Candida*, *Saccharomyces spp.*), and molds (*Aspergillus*, *Actinomucor spp.*) (Yuliana *et al.* 2018, Yang *et al.* 2019). During fermentation, fishes are either blend with salt or salt with various sources of carbohydrates (mostly rice, predominantly in the North-eastern Asian countries or millet, predominantly in South-eastern Asian countries) (Liang 2016). Carbohydrate residues not only serve as an energy source to quicken the fermentation but also absorb excess moisture and impart a unique flavor to the end product (Sathe and Mondal 2016). Salt prevents the growth of intrinsic or extrinsic spoilage causing microbes to increase the shelf life and enrich the organoleptic qualities of the end product by activating the proteolytic enzymes which in turn attack the internal membranes and muscle, resulting in solubilized protein exudes leading to a nutritious product (Giri *et al.* 2009, Yang *et al.* 2019, Zang *et al.* 2019, Tamang *et al.* 2020).

3.1.5. Fermented Cereal Foods: Globally cereal grains manage around 60% of the world's food production and are considered to be one of the most important dietary sources of proteins, carbohydrates, vitamins, minerals, and fiber. The most famous fermented cereals based products in different countries are idli, dosa, uttapam of India and Sri Lanka, mawe and gowe of Benin, ben-saalga of Burkino Faso and Ghana, kisra of Sudan, kenkey of Ghana, togwa of Tanzania, ting of Botswana, ogi and kunu-zaki of Nigeria, tarhana of Turkey, and trachana of Cyprus and Greece and so on (Blandino *et al.* 2003, Sidhu et al 2007, Guyot 2010). However, the nutritional quality of cereals is sometimes poor in contrast to the dairy products, because of the reduced protein content, the lack of certain essential amino acids (lysine), the occurrence of antinutrients (phytic acid, tannins, and polyphenols) (Verni *et al.* 2019). However, cereals serves as prebiotic, support the growth of LAB as they contain water-soluble fiber (such as β-glucan and arabinoxylan), oligosaccharides (such as galacto- and fructooligosaccharides), resistant starch, many phytochemicals or bioactive substances (phytoestrogens, phenolic compounds, antioxidants, and sterols) (Sidhu *et al.* 2007, Kumari *et al.* 2015, Nkhata *et al.* 2018). The common microorganisms isolated from cereal-based fermented foods are bacteria (*Lactobacillus plantarum*, *L. fermentum*, *L. brevis*, *L. salivarius*, *L. lactis*, *Pediococcus pentosaceus*, *P. acidilactici*, *Leuconostoc mesenteroides*, *Weissella confuse*), yeast (*Saccharomyces cerevisiae*, species of *Candid*a, *Debaryomyces*, *Pichia*), and molds (*Aspergillus*, *Paecilomyces*, *Cladosporium*, *Fusarium*, *Penicillium*, *Trichothecium spp.*) (Guyot 2010, Liptakova *et al.* 2017, Ukwuru and Ohaegbu 2018). Microbial fermentation of cereals impart several important features: reduction in the level of non-digestible poly- and oligosaccharides, resulting in lower abdominal distention and flatulence, significantly lowers the content of anti-nutrients (phytates, tannins, polyphenol), synthesizing flavoring compounds (diacetyl, acetic acid, butyric acid) which makes the end products more appetizing, and availability of certain amino acids (lysine, methionine, tryptophan), B group of vitamins (thiamine, riboflavin, niacin, folic acid), and minerals (zinc, calcium, magnesium) as they are complexed with phytate (Kumari *et al.* 2015, Salmeron *et al.* 2015, Peyer *et al.*

2016 Verni *et al.* 2019). Overall, lactic acid fermentation provides safety, nutritional value, shelf life, and acceptability of a huge array of cereal-based fermented foods (Karovicova and Kohajdova 2007, Jha *et al.* 2011, Ray *et al.* 2015).

3.2. Fermented Beverages: Beverages can be defined as any liquid which is ingested by drinking. Alcohol containing fermented beverages (wines, beers, and other products) have been ingested by humans from the Neolithic period (10,000 BC) (McGovern 2009). Among the alcoholic beverages wines are most ancient and produced by yeast mediated fermentation of grape juice. Brewing yeasts recognized for their ability to impart typical flavor and aroma, are members of the genus *Saccharomyces*: *S. cerevisiae* known as top fermenter utilized for the production of ale, found on the surface of the fermenting wort and *S. pastorianus are* known as bottom fermenter used for lager production, found at the bottom of the fermenter, causes flocculation (Fleet 1998, Walker *et al.* 2016, Anagnostopoulos and Tsaltas 2019).

Wine is commonly prepared from the grape (*Vitis vinifera*) with (red wine) or without (white wine) grape skins. Yeasts ferment (naturally present on the grape surface or starter cultures) the natural sugars in the grape juice for 8-10 days and at a temperature (25°-28°C for red wines and 20°-25°C for white wines) to produce ethanol and CO_2. This CO_2 is generally released to the atmosphere, except in the sparkling wines. Temperature and the oxygen concentration of the must (grape juice) are well maintained during fermentation. During alcoholic fermentation, glycerol, acetic acid, higher alcohols, and acetaldehyde are produced in minute amount, determines final wine quality. Wines are stored for varying periods before consumption depending on the variety. Mead is a wine produced from diluted honey while sake is prepared from rice (Prescott and Dunn 2004, Tamang 2012). **Beer** is the most selling alcoholic beverage throughout the world and is produced by the saccharification of starch (often barley) to extract sugars and followed by fermentation through *Saccharomyces cerevisiae* to ethanol and CO_2. The oldest known barley beer documented at 3400 BC (Tucker 2011). The characteristic flavor of beers comes from the addition of hops (the flowers of Humulus *lupulus*). Most beers are prepared from malted barley and during the malting process, β-amylase synthesized in sprouted grain hydrolyzes β-1-4-glycosidic linkages in starch to produce maltose. (Fraizer *et al.* 1971, Hornsey 2013).

Worldwide **tea** is one of the most consumable nonalcoholic beverages and gaining further popularity as a healthier drink in comparison to other nonalcoholic beverages because of its inherent phytochemicals: polyphenols, flavonoids, epigallocatechin gallate (EGCG), and other catechins (Marsh *et al.* 2014). It is served as morning drink for approximately two-thirds of the human population daily. The largest producers of tea are China, India, Kenya, Sri Lanka, and Turkey (Anagnostopoulos and Tsaltas 2019). There are three kinds of tea consumed by people across the world: green tea, black tea, and kombucha, which is a sweet-sour tea beverage made actually from tea extract supplemented with sugar and fermented with yeast and acetic acid bacteria. **Kombucha** tea is believed to have emerged in China over 2000 years ago. It is conventionally produced from the fermentation of sugared black tea with the help of symbiotic yeast community (*Kloeckera spp., Schizosaccharomyces pombe, Saccharomyces ludwigii, S. cerevisiae, Torulaspora spp., Zygosaccharomyces bailii,* and *Pichia spp.*) and bacteria (*Acetobacter xylinum*, *A. xylinoides*, *A. aceti*, *A. pausterianus*, and *Bacterium gluconicum*) (Ernst *et al.* 2003, Jayabalan *et al.* 2014). The microbial fermentation is done by these yeast and bacteria forming a mat-like structure known as zoogleal mat, which is a thin layer of floating cellulose (primarily synthesized by *A. xylinum*) whether the microbial cell mass attached. Caffeine and related xanthines present in tea stimulate bacteria to synthesize the cellulose layer. In kombucha, yeast ferment sugar to produce ethanol i.e. oxidized by the bacterial counterpart to produce acetaldehyde. On the other hand, acetic acid produced by the bacteria induces yeast to synthesize ethanol. At the end of the fermentation the symbiotic association resulting in the production of following by-products: sugars, polyphenols such as catechins, organic food acids, lysine, fiber, ethanol, amino acids, essential elements such as Na, K, Ca, Cu, Fe, Mn, Ni, and Zn, water-soluble vitamins such as vitamin C, vitamin B, and vitamin B2, catalase, carbon dioxide, antibiotic-related substances, and some hydrolytic enzymes (Bauer Petrovska and Petrushevska Tozi 2000). (Ernst 2003, Jayabalan *et al.* 2014).

The term **coffee** is originated from the Ethiopian word Kaffa. From Ethiopia, coffee was dispersed to Arab, where coffee beans for the first time became roasted and brewed. The most popular species of the genus *Coffea* are *C. Arabica* (Arabica coffee), *C. canephora* var. *robusta* (Robusta coffee) which accounting for 56%, and 44% of world total commercial coffee production, respectively (Thompson 2013). Brazil is the chief producer and exporter of *C. Arabica,* followed by Colombia, Paraguay, Venezuela, Indonesia, Ethiopia, India, and Mexico. Coffee fermentation is critical for removing mucilage from parchment coffee. Coffee mucilage contains polysaccharides (pectin), cellulose, and starch. The mucilaginous layer of the depulped coffee beans comprises of 84.2% water, 8.9% protein, 4.1% sugar, 0.91% pectic substances and 0.7% ash (Schwan *et al.* 2012, dule and Diez-Gonzalez 2019). The microbial community associated with the fermentation of coffee beans is primarily dependent on the diversity of the coffee plant, moisture content of beans, processing method, substrates composition, enzymatic and antimicrobial activity of the colonizing species, and also the environmental features (e.g. humidity, temperature, and soil microbiota). At the start of fermentation, the high water activity (aw 0.9) assists the colonization of bacteria on the coffee fruit but during the end of fermentation, low water activity (aw 0.7) supports the colonization of yeasts and molds. The pectinaceous sugars fermented to produce ethanol and acetic, lactic, butyric, and other higher carboxylic acids (Huch and Franz 2015). Cellulolytic *Bacillus* species (predominantly *B. polymyxa* and *B. subtilis*) produce cellulase and pectinase, causing the degradation of cellulose and pectin, respectively (Haile and Kang 2019) that are present in the skin, pulp and mucilage of the coffee berries. Several Gram-negative bacteria (*Tamutella ptyseos, Pseudomonas putrefaciens, Enterobacter aerogenes, Acinetobacter sp.*, *Provindencia mirabilis*) synthesized pectin lyase, which additionally degrading the pectin exist in the mucilage. LAB such as *Leuconostoc mesenteroides, L. holzapfelii, Lactobacillus plantarum*, and *L. brevis* have also been responsible for decomposition of pectic polymers. The yeast (*Pichia burtonii*, *P. holstii*, *P. anomala, Debaryomyces polymorphus*, *Arxula adeinivorans*) isolated from dry-processed coffee fermentations were also contain pectin lyase whereas *P. kluyveri* and *Hanseniaspora uvarum* were reported to produce polygalacturonase (Murthy and Naidu 2011). *D. hansenii* may prevent the degradation of stored fruits and grains by decreasing the growth of the fungal population (Schwan *et al.* 2012, Lee *et al.* 2015, Doyle and Diez-Gonzalez 2019).

From primordial periods, many communities across the world produce naturally fermented milk (or skimmed milk) from various sources, including cow, camel, goat, sheep, yak and even coconut, milk, and can be either pasteurized or unpasteurized.

Kefir is a fermented, slightly alcoholic, milk beverage originated in Eastern Europe. Raw milk is inoculated with unevenly shaped, gummy white/yellow grain called kefir grains, which have a complex symbiotic microbial community that includes species of yeasts (*Candida lambica, Kluyveromyces marxianus, Saccharomyces exiguous*, *Torula kefir*), LAB (*Lactobacillus fermentum, L.*

acidophilus, L. helveticus, L. casei, L. kefiri, L. lactis, L. parakefiri, Leuconostoc mesenteroides), acetic acid bacteria (*Acetobacter aceti*, *A. rasens*). The microbial composition differs subjected to the origin of grain, method, and substrate. The content of lactic acid is 0.7–1% and alcohol is 0.05–0.5%, depending on the incubation period and storage settings (Witthuhn 2005, Prescott and Dunn 2004). **Buttermilk** is classically prepared from lactic acid fermentation of homogenized, pasteurized low-fat milk or pasteurized skimmed milk. *Lactobacillus. lactis* subsp. *cremoris* and *L. lactis* subsp. *lactis* fermenting the milk sugar lactose and lowers pH of the milk by producing lactic acid leading to curdling or clabbering of milk; as the milk protein casein becomes precipitated. These two species are known as acid producers, whereas *L. lactis* subsp. *lactis* biovar. *diacetylactis* and *Leuconostoc mesenteroides* subsp. *cremoris* synthesized the aroma compound diacetyl which impart buttermilk its characteristic flavor; therefore, denoted to as aroma producers (Niamsiri and Batt 2009). **Acidophilus milk** is cultured milk chiefly produced from lactic acid fermentation, chiefly by *Lactobacillus acidophilus,* and other important LAB in acidophilous milk are: *Lactobacillus amylovorus*, *L. crispatus*, *L. gallinarum*, *L. gasseri,* and *L. johnsonii*. Sterilized milk is inoculated by the starter cultures and final lactic acid content product is reach to 1–2% w/w (Prescott and Dunn 2004, Kandylis *et al.* 2016).

Shubat, ergo, kurut, khoormoog are the fermented milk popular in Asia and amasi, kivuguto, rob, suusac from Africa are well documented. Besides, some distinguished naturally fermented milk of Indian subcontinent are including dahi, lassi, misti dahi, srikhand, chhu, chhurpi, mohi, philu, shoyu, somar (made from cow/buffalo/yak milk) (Alexandraki *et al.* 2013, Oki *et al.* 2014, Anagnostopoulos and Tsaltas 2019).

4.0. Microbial Food Additives: According to FAO (Food and Agriculture Organization), food production output will have to increase by at least 70% over the next few decades to keep up with the expected growth of the world population. Every year 30 to 40 % of consumable food is lost due to spoilage or other food quality issues (safety, taste, appearance texture, and freshness). To reduce spoilage and to maintain food qualities without chemical additives as per rising consumer awareness will become even more perplexing (Msagati 2012). Worldwide in-depth research on microorganisms about their huge diversity of metabolite production makes them the best alternatives to chemical additives, crucial to certifying food safety and quality. Numerous industries (chemical/pharmaceutical/biotechnological/food) have exploited the biochemical ability of microbes to synthesize, metabolize, and transform valuable substances (Serra *et al.* 2005, Lopes *et al.* 2017). To ameliorate safety, nutritional quality, texture, flavor, and appearance of food; food additives (preservatives, sweeteners, colorant, flavor enhancers, nutrient supplements, emulsifiers, texturing agents, acidulants, and enzymes) are added to the food (Molina and Gustavo 2016).

4.1. Amino Acids: Amino acids are the building blocks of peptides or proteins and serve as one of the macronutrients of life. The beginning of fermentative production of amino acids becomes feasible with the discovery of glutamic acid-producing bacterium, *Corynebacterium glutamicum* (*Micrococcus glutamicum*), by Kinoshita in 1957 (Suzuki 2013, Lee 2014). In 1907, The First successful commercial production of glutamic acid was done in 1907 at Tokyo Imperial University by Kikunae Ikeda, who established and patented a method to yield crystalline salt of glutamic acid, monosodium glutamate (MSG); the well-known flavor enhancer. Sodium aspartate and alanine are mixed to fruit juices or glycine to sweeteners to improve the taste. L-cysteine serves as an antioxidant in fruit juices and increases baking quality (Lee 2014, Mahmood 2018). L-tryptophan with L-histidine also performs as an antioxidant to protect powdered milk from rancidity. L-phenylalanine and L-aspartate are used to synthesize dipeptide, low-calorie sweetener, and aspartame. L-methionine, L-lysine, L-threonine, and L-tryptophan are scarce in grain products; therefore, supplemented as food or feed additives. Among the commercially produced amino acids**,** L-glutamic acid and L-lysine have the highest demand. Fermentative production of maximum amino acids is achieved in different microbial auxotroph.

L-Glutamic acid is industrially produced by batch/fed-batch submerged fermentation, using genetically modified strains of Corynebacterium (*C. glutamicum, C. lilium, and C. herculis*) or Brevibacterium (*B. flavum, B. lactofermentum, B. divarticum, and B. ammoniagenes*) (D'Este *et al.* 2018). A significant amount of free glutamic acid, or its salt (MSG) is present in various food products such as cheeses and soy sauces. **L-Lysine** serves as an essential amino acid. It is synthesized by either via diaminopimelic acid pathway (DAP) in the case of bacteria, actinomycetes, cyanobacteria, some phycomycetes, and protozoa or the aminoadipic acid pathway (AAP) in ascomycetes, basidiomycetes, and algae. Industrially, the first microbial production of L-lysine through the decarboxylation of diaminopimelic acid is done by Chas Pfizer and Company Inc. in the United (Ikeda 2003, Wendisch 2006). It is used as an animal feed for boosting the growth of pigs and chickens.

In the food industry, it serves as a dietary or nutritional supplement, utilized by athletes, weight lifters, gymnasts, and even some individuals to lift their energy level and preserved their muscles from weakening. **L-Methionine** is an essential amino acid; therefore, it is required in the diets of humans. The first evidence of methionine production enlisted in the 1970s, an auxotrophic (leucine-) strain of *Ustilago maydis* synthesized 6 g/L of L-methionine on a synthetic medium and a strain of *Pseudomonas sp.* G-132-13 synthesized 13.2 g/L of methionine (Mahmood 2018). Genetically modified strains of *E. coli* or *C. glutamicum* can accumulate up to 35 g/L methionine. **L-Tryptophan** is an essential amino acid used as a supplement in grain based foods and livestock diet. With the help of genetically modified strains of *Corynebacterium spp.* and *E. coli*, now tryptophan is mostly synthesized by fermentation (Wendisch 2006, Patel 2012). **L-Valine** is a branched-chain amino acid used as a moisturizing agent in cosmetics, and for chemical synthesis of antibiotics, antiviral agents, and herbicides. Genetically engineered strains of *E. coli* and *C. glutamicum* has produced 60 g/ and 172 g/L valine through glucose fermentation, respectively. L-**Arginine** has been industrially produced through metabolically engineered *C. glutamicum* at 92.5 g/L (Hirasawa and Shimizu 2016).

4.2. Organic Acids: From the antique time, organic acids have been served as an additive to increase the shelf life of foodstuffs. Organic acids share a noteworthy portion of the world fermentation market, and with growing awareness towards food safety microbial production of organic acids is gaining importance. During fermentation, several types of microorganisms (bacteria, yeast, or mold) produce organic acids including lactic, acetic, citric, malic, fumaric, itanoic and kojic acids, and so on (Naraian and Kumari 2017).

Acetic acid (ethanoic acid) popularized as vinegar (French: vinaigre, means sour wine) is the most familiar edible organic. Vinegar used in foods must be of biological origin. In general, acetic acid occurs naturally in trace amounts in fruits, such as pears. Acetic acid was first manufactured in 1794 in Germany using grapes. In vinegar fermentation, Acetobacter oxidized mild concentrated ethanol in the presence of oxygen of the air to produce acetic acid and water. Several industrially important strains for vinegar fermentation are: bacteria (*Acetobacter aceti, A. pasteurianus*, *A. peroxidans*. and *Gluconobacter oxydans*), yeasts (*Saccharomyces cerevisiae, Dekkera bruxellensis, Brettanomyces bruxellensis*, *B. intermedius*, *B. custersianus,* and *B. clausenni*) There are several types of vinegar are used worldwide: cider vinegar (apple), malt vinegar (malt or cereal), rice vinegar (rice), etc (Prescott and Dunn 2004, Khan *et al.* 2017). **Citric acid** has been first isolated from lemon juice in 1874, and is the principal acid found in citrus fruits and also in many vegetables. More than 90% world requirement of citric acid is manufactured by fermentation. Global production of 70% (approx.) citric acid is utilized as additives in the form of acidulant, antioxidant, preservatives, and flavor enhancer in the food and beverage industry. Auxotrophic strains of *Aspergillus niger* growing on carbohydrates (sucrose or molasses) or *Candida lipolytica* growing on paraffin substrates are used in the commercial production of citric acid (Prescott and Dunn 2004). A solid-state (Koji) and submerged fermentation are commercially applied for citric acid production (Soccol *et al.* 2008, Sauer *et al.* 2013). Among the organic acids, **lactic acid** is first produced by microbial fermentation, started in 1880, and using lactobacilli of three species: *L. delbrueckii*, *L. leishmanii*, and *L. bulgaricus*. *Leuconostoc mesenteroides*, a lactic acid bacterium, produces optically pure lactic acid using different carbon and nitrogen sources. Lactic acid is used as a preservative in various foods and also during meat processing. It is used in beer brewing to maintain the wort pH to reduce some undesirable substances such as tannins into an extent to give off-flavors and increase the body of the beer and during wine production, it is often used to convert the naturally present malic acid to lactic acid, to reduce the sharpness and for other flavor-related reasons (Ly *et al.* 2019). Ammonium lactate is an outstanding non-protein nitrogenous source used for livestock diet (Soccol *et al.* 2008, Khan *et al.* 2017). **Malic acid** (Latin: malus, means apple) is used as an acidulant, enhancing the sourness or sweetness of fruit juices, carbonated soft drinks or candies. It is also used in processed cheese, chocolate milk and pudding, commercially prepared additives, processed meat, and cereal-based foods. Commercial production of malic acid (in the form of calcium malate) is done by *Aspergillus flavus* (Ly *et al.* 2019). **Fumaric acid** is used as a food acidulent in beverages and baking powders, as a color fixative in cured meat and poultry products, and also used for the production of L-malic acid by fumarase, and L-aspartic acid by aspartase. From the early 1940s, commercial production of fumaric acid is started mainly with the fungal strains of *Rhizopus oryzae* (Patel 2012). **Itaconic acid** has been first recognized by Baup (1837) as a thermal breakdown product of citric acid. In 1932 Kinoshita isolated *Aspergillus itaconicus*, an itaconic acid producer from dried salted plums. Although several microbes such as *Ustilago zeae*, *U. maydis*, *Candida sp.*, and *Rhodotorula sp.* synthesized itaconic acid. *Aspergillus* *terreus* is a preferred source for industrial production of itanoic acid (80 g/L). Itanoic acid is highly recommended for food packaging (i.e., as packages that interact with foods to prevent the growth of microbial pathogens and food spoilage; thereby, extend the shelf life of food) (da Cruz *et al.* 2017). **Kojic acid** (Japanese: Koji-kin i.e. *Aspergillus oryzae*, chief producer) has been recognized as a by-product in the fermentation of malting rice during the production of sake. It is used as a flavor enhancer, and as color fixatives (acts as a mild inhibitor of pigment development in a plant and animal tissues) for cut fruits or seafood to prevent color changes (Sauer *et al.* 2013, Singh *et al.* 2017).

4.3. Vitamins: Vitamins take part in many enzymatic reactions as a coenzyme, indispensable for normal growth and nutrition, and should be present in minute quantities in our regular diet. Vitamins are broadly classified as fat soluble vitamins (A, D, E, and K), and water soluble vitamins (C, biotin/B7, thiamine/B1, riboflavin/B2, niacin/B3, pantothenic acid/B5, pyridoxine/B6, folic acid/B11, and cobalamin/B12). Water-soluble vitamins serve as coenzymes for transferring chemical groups in enzymatic reactions, whereas fat soluble vitamins act as a constituent of cell membranes. Humans are metabolically unable to synthesize most vitamins; therefore, they must be supplied exogenously. With increasing knowledge of food safety in consumer, microbial production of vitamins commercially outcompete chemically synthesized pseudo vitamins (Ledesma-Amaro *et al.* 2013, Gupta *et al.* 2017).

Vitamin A is a group of compounds namely retinoids, retinol, retinal, retinoic acid, and retinyl esters. Vitamin A is taken up from dietary source as a retinyl ester or carotenoid and metabolized into an active vision compound, 11-cis-retinal, and an active form of vitamin-A exist in the body, i.e. all-trans retinoic acid. Two pro-vitamins (retinol and retinyl ester) are mainly found in fish, meat, milk, and eggs, although higher amounts present in fish oil and liver. The green microalga *Dunaliella* and the fungus *Blakeslea trispora* efficiently synthesize beta-carotene. *Saccharomyces cerevisiae* has been genetically developed to express carotenogenic genes from *Xanthophyllomyces dendrororhous*, producing beta-carotene (6.3 mg/g of dry cells) (Ledesma-Amaro *et al.* 2013, Gupta *et al.* 2017). **Vitamin D** is a fat-soluble vitamin that originated from cholesterol and ergosterol. Cholesterol is metabolically converted to 7-dehydrocholesterol i.e. breakdown by UV-emission to produce cholecalciferol (vitamin D3). While, on UV exposure ergosterol is converted to ergocalciferol (vitamin D2). Neither the D2 nor the D3 is the metabolically active form, and they must go through two successive hydroxylation reactions; first one in the liver, where vitamin D is converted into 25-hydroxyvitamin D (calcidiol), which in turn transformed into 1, 25-dihydroxyvitamin D (calcitriol) in kidney. Vitamin D is normally synthesized in humans by exposure to sunlight, and also found in the flesh of fatty fish and fish liver oils, beef liver, cheese, egg yolks (D2) and some mushrooms (D3). Ergosterol is industrially synthesized the yeasts such as *Saccharomyces cerevisiae, S. uvarum* and *Candida utilis* (10–30 mg/g dry cells) (Ledesma-Amaro *et al.* 2013, Ly *et al.* 2019). **Vitamin E** is available in cereals, meat, vegetable oils, poultry, wheat germ oil, fruits, eggs, and vegetables. Photosynthetic microorganisms are found to accumulate tocopherols and *Euglena gracilis* have been identified as best producer (7.35 mg/g of dry cells) organisms (Ledesma-Amaro *et al.* 2013, Ly *et al.* 2019). **Vitamin K** naturally found in two forms: vitamin K1 (phylloquinone), acts as an electron acceptor in the plant; and vitamin K2 (menaquinone), present in microorganisms. Vitamin K1. In fermented foods are enriched with this vitamin as the producer microbes of those foods accumulate menaquinones; for example, cheese produced by *Proprionibacterium*, soy foods enriched with *Bacillus subtilis*. Auxotrophic strains of *Flavobacterium sp.* has been identified as efficient producer (produce 249 mg/L extracellularly and 40 mg/L or 2.7 mg/g of dry cells) (Ledesma-Amaro *et al.* 2013, Ly *et al.* 2019). **Vitamin B12** is a group of water-soluble vitamins, also known as cobalamines. *Propionibacterium shermanii* synthesized vitamin B12 (25–40 mg/L) in a corn steep liquor medium supplemented with glucose and $CoCl_2$. *Pseudomonas denitrificans* synthesized vitamin B12 (150 mg/L) in a medium containing sugar beet molasses and 5, 6-dimethylbenzimidazol (Patel 2012, Ledesma-Amaro *et al.* 2013). **Folic acid** (Latin: folium means leaf, the dietary source is green leafy vegetables) is the synthetic form of **folate (vitamin B9)** and it is found as additives in fortified foods. It is also available in fruits, beans, and peas, etc. *Ketogulonigenium vulgare, Lactobacillus lactis* has been genetically engineered to overexpress the folate operon to reach the desired level of folate production. (Ledesma-Amaro *et al.* 2013, Ly *et al.* 2019). **Biotin (vitamin B7)** exists in a large diversity of foods such as egg, liver, soybeans, nuts, Swiss chard, or whole wheat. *Serratia marcescens* genetically manipulated by introducing a plasmid having an extra copy of the mutated biotin operon facilitates the production of biotin (600 mg/L) (Ledesma-Amaro *et al.* 2013). **Pantothenic acid (vitamin B5)** is present in brewer's yeast, corn, tomatoes, beef (especially liver and kidney), and salmon. Genetically modified strains of *Escherichia coli* have been reached to the desire level of vitamin B5 production (66 g/L) (Ledesma-Amaro *et al.* 2013, Ly *et al.* 2019). **Riboflavin (vitamin B2)** is the principal component of the FAD and FMN cofactors massively functioned in oxidation-reduction reactions. The highest quantity of riboflavin is present in crimini mushrooms and spinach, but also in asparagus, green beans, yogurt, and cow's milk. Vitamin B2 is naturally synthesized by several microorganisms such as molds (*Ashbya gossypii, Eremothecium ashbyii*), yeasts (*Candida flaeri* and *C. famata*), and bacteria (*Bacillus subtilis* and *Corynebacterium ammoniagenes*). Industrial production of riboflavin (13g/L) is achieved in genetically modified strains of *A. gossypii* by overexpressing all six genes of the riboflavin synthetic pathway (Patel 2012, Ledesma-Amaro *et al.* 2013, Gu and Li 2016). **Thiamine (vitamin B1)** is present in the diet, particularly in wheat germ, soybeans, dried beans, and peas. Although it is prevalent in foodstuffs, its physiological concentration is often low as it is destroyed during cooking. Therefore, in backward countries rice and flour are generally fortified with vitamin B1. *Saccharomyces carlsbergensis* has been reported to produce relatively high amounts (1.036 mg/g dry matter) of vitamin B1 (Ledesma-Amaro *et al.* 2013, Lee 2015). **L-ascorbic acid (vitamin C)** is an important antioxidant, found mainly in fruits and vegetables: citrus fruits, tomato, green chillies, and potatoes are major suppliers of vitamin C. The mutant green alga *Chlorella pyrenoidosa* have been synthesized L-ascorbic acid ranging from 1.05 to 1.46 g/L through fermentation in glucose medium. High yields of L-ascorbic acid are also achieved using a *Gluconobacter oxydans* or mixed-culture fermentation with *Gluconobacter* and *Bacillus megaterium* (Patel 2012, Lee 2015).

4.4. Food Grade Enzymes: Enzymes are a specific type of globular proteins having catalytic activities, necessarily present in all living beings to accelerate biochemical reactions (Raveendran *et al.* 2018). Earlier evidence of microbial enzymes for food applications documented around 6000 B.C., when Neolithic people fermented grapes to produce wine, and Babylonians utilized microbial yeast to produce beer. The commercial production of food processing enzymes have been started in 1874, when Christian Hansen extracted rennin (also known as chymosin) from calf stomachs, later applied to clot milk in cheese manufacturing (Mishra *et al.* 2017, Ramos and Malcata 2017). Food-grade enzymes facilitating both food processing as well as food additives. For the production of food-grade enzymes generally, several factors come into play: minimal production cost, trying to produce from GRAS (genetically recognized as safe) organisms, safety issues regarding the consumable final product and workers of the food industries, retain enzymatic activity during storage, maintaining enzymatic activity in an applicable range of pH and temperature, and also effective in food environment (Ladics and Sewalt 2018, Nigam 2013, Hellmuth and van den Brink 2013).

Food grade enzymes targeted at food processing:

Amylases are hydrolase classes of enzymes, generally categorized into three types: α-amylases (EC 3.2.1.1), β-amylases (EC 3.2.1.2), and glucoamylases (EC 3.2.1.3) (Raveendran *et al.* 2018). Both α- and β-amylases produce dextrins and maltose from starch: the former attacks α-(1'!4) linkages randomly, whereas β-amylase removes maltose from the nonreducing end of the chain by breaking alternate glucosidic linkages. Glucoamylase can hydrolyze α-(l'!6) and α-(l'!3), as well as α-(l'!4) linkages to form glucose. Initially isolated from malt, amylases are prevalent among higher plants and animals, as well as several microorganisms; *Aspergillus niger*, *A. oryzae*, represents the predominant producer (Van Der Maarel *et al.* 2002). In bakery industries α-amylases are added to the dough for converting starch to smaller dextrins, which are later fermented by yeast. It develops the taste, crust color, and toasting properties of bread. α-Amylases are helpful in the production of high-molecular-mass branched dextrins; applied as a glazing agent for the manufacture of rice cakes and powdery foods. To prepare glucose and fructose syrups from starch requires highly thermostable enzymes, obtained from *Bacillus amyloliquefaciencs*, *Bacillus stearothermophilus* or *Bacillus licheniformis* (Ramos and Malcata 2017, Mondal *et al.* 2020). **Cellulases** catalyzes the hydrolysis of cellulose required synergistic action of three enzymes: endoglucanase or CMCase (EC 3.2.1.4), which cleaves internal β-(1'!4)-glucosidic bonds randomly; cellobiohydrolase (CBH) (EC.3.2.1.91), which cleaves off cellobiose units from the ends and β-glucosidase (EC.3.2.1.21), which transforms cellobiose and cellodextrins into glucose (Mondal *et al.* 2019). Cellulases from the mold (*Aspergillus spp.* and *Trichoderma spp.*) and bacteria (*Bacillus spp.* and *Paenibacillus spp.*) are commercially used for the production of food. In the juice industry, a mixture of cellulases with other macerating enzymes is used for improved production by better extraction methods, reduce the viscosity of nectar and puree from fruits, extraction of flavonoids from flowers, and seeds, enhanced clarification and stabilization of juices. Such enzymatic cocktail has also been reported to lower bitterness of citrus fruit, thus improving aroma and taste, and proficient in olive oil extraction (Ramos and Malcata 2017, Raveendran *et al.* 2018). Cellulases are used for the production of good quality of a wine by improving maceration, color development, must clarification and wine stability (Singh *et al.* 2016a). Oksanen *et al.* (1985) reported that cellulases can significantly lower wort viscosity. The flavor of wines as well as fruit juices can be improved by β-glucosidases. **Proteases** (EC 3.4) catalyze the breakdown of protein molecules to peptides and finally to free amino acids; besides they also synthesized active enzymes from proenzymes (zymogens) associated with fat or sugar metabolism. Depending on their point of action on polypeptide chains, proteases are classified into two groups: exopeptidases (act on the ends of polypeptide chains) and endopeptidases (act randomly in the inner regions of polypeptide chains) (Singh *et al.* 2016b). Based on the catalytic moiety of the active site, the endopeptidases are additionally divided into six groups: serine, aspartic, cysteine, metallo, glutamic acid, and threonine protease. Plant proteases (bromelain, ficin, and papain) are widely used in brewing to improve the flavor, tenderization of meat, coagulation of milk, and as a digestive aid by enhancing nutritional value, solubility, and digestibility of food proteins (Sumantha et al 2006). In the baking industry, endo- and exoproteases from *Aspergillus oryzae* have been used to transform wheat gluten via limited proteolysis; resulting in reduced time for dough preparation, and also improve its texture and loaf volume (Li *et al.* 2013, Raveendran *et al.* 2018). Fungal proteases which are effective at low pH used to enhance the fermentation of beer by maintaining its amino acid profile. Protease from *Bacillus thermoproteolyticus* are now utilized for enzymatic production of aspartame. In the cheese-making industry, chymosin is an ideal protease, as its high specificity toward casein, particularly the Phe105–Met106 bond of k-casein; the first step of milk clotting in cheese making (Ramos and Malcata 2017). **Lipases** (EC 3.1.1.3) hydrolyzed triacylglycerols to produce glycerol and free fatty acids. Commercial lipases are usually manufactured from animal sources (pancreatic and pre-gastric tissues of ruminants) or fungal sources (*Penicillium, Aspergillus, Rhizopus, Rhizomucor, Mucor, and Candida spp*.). Microbial enzymes capture around 90 % of global lipase market (Verma *et al.* 2012). Lipases from different sources are applied for cheeses processing to improve texture and softness; camembert cheese utilizes lipase from *Penicillium camemberti* and cheddar cheese to utilize *Aspergillus niger* or *A. oryzae* (Raveendran *et al.* 2018). Lipases are used for aroma augmentation in butter and margarine, and also to increase the shelf life of various baking products (Sharma *et al.* 2009, Hellmuth and van den Brink 2013). **Pectinases** (EC 3.2.1.15) catalyzes the breakdown of pectins into simpler molecules such as galacturonic acid. The pectinases are a group of enzymes: pectin methylesterase eliminates the methoxyl residues from pectin, polygalacturonases cleaved α-(l'!4) glycosidic linkages between galacturonic acid molecules, and pectin transeliminases, producing galacturonic acids (Raveendran *et al.* 2018). Pectic enzymes are industrially employed for clarification, and concentration of fruit juices, clarification of wines; and also for the extraction of oils, flavors, and pigments from plant ingredients (Ramos and Malcata 2017, Mondal *et al.* 2019). **Xylanases** (EC 3.2.1.8.) is a group of enzymes, mainly endoxylanases, exoxylanases, and β-xylosidases, which acts synergistically to catalyze the breakdown of xylan backbone in hemicellulose. Endoxylanases internally cleaves the β-(1'!4) glycosidic bonds of xylan backbone. Exoxylanases hydrolyze β-(1'!4) glycosidic bonds of xylan from the non-reducing ends and release xylooligosaccharides. β-Xylosidases splits the xylobiose and xylooligosaccharides to release xylose (Menon *et al.* 2010, Mondal *et al.* 2020). The predominant producer of xylanase is *Streptomyces*, *Bacillus*, *Pseudomonas*, *Aspergillus, Fusarium, and Penicillium spp*. Xylanase derived from fungi shows higher enzymatic activity that bacteria or yeast originated. The xylanolytic enzymes can increase the specific bread volume as they cause the breakdown of hemicellulose of wheat; improves the water binding capability of dough, and the dough becomes softer, crumb formation is late, dough volume is increased, resulting in better qualities of bread, biscuits. Along with other enzymes xylanases contribute better recovery of aromas, essential oils, vitamins, mineral salts, pigments from plant sources. In beer making industries, xylanases improved the viscosity of beer by degrading barley cell wall leading to the release of arabinoxylans and low molecular weight oligosaccharides (Mandal 2015, Raveendran *et al.* 2018). **β-Galactosidase** or **lactase** (EC 3.2.1.23) catalyzes the hydrolysis of milk sugar lactose produce glucose and galactose (Rosenberg 2006). It is predominantly synthesized from *Lactobacillus bulgaricus, Leuconostoc citrovorum, Streptococcus cremoris,* and *Saccharomyces cerevisiae*. Lactase is utilized in milk and milk-based products to reduce lactose levels. The creaminess of ice creams amended significantly after the hydrolysis of lactose with lactase. It is also used for the production of galactooligosaccharides (GOS) from lactose, used as prebiotic food additives (Raveendran *et al.* 2018).

Food grade enzymes targeted at food

preservation:

Lysozymes (EC 3.2.1.17), or N-acetylhexosaminidases, catalyzes the hydrolysis of β-(1'!4) glycosidic linkages of the peptidoglycan of the bacterial cell wall. Lysozyme is especially active upon Gram-positive bacteria, as they contain a higher amount of peptidoglycan in their cell wall in comparison to Gram-negative bacteria. But is effective against the Gram-negative bacteria when it is applied with ethylenediaminetetraacetic acid (EDTA). Lysozyme is highly effective against *Clostridium tyrobutyricum*, which causes late gas blowing of hard cheeses. Lysozyme is also operative against *Listeria monocytogenes* that exist in dairy and meat products (Fuglsang et al 1995, Raveendran et al 2018). **Glucose oxidase** (EC 1.1.3.4) catalyzes the oxidation of β-D-glucose to gluconic acid, using molecular oxygen as an electron acceptor, with simultaneous production of H_2O_2. The major producer of glucose oxidase is *Aspergillus niger* and *Penicillium glaucum* (Banker *et al.* 2009). In the baking industry it is used to produce strong dough by utilizing its oxidizing potentiality. It is applied to remove glucose and oxygen from diabetic drinks and egg white. Due to its oxygen removing capability and inhibit the growth of several foodborne pathogens namely *Salmonella infantis, S. aureus, Clostridium perfringens, Bacillus cereus, Campylobacter jejuni*, and *Listeria monocytogens*; it is used for food preservation (Ramos and Malcata 2017). **Lactoperoxidases** (EC 1.11.1.7) catalyzes the oxidization of thiocyanate (SCN–) to hypothiocyanate (OSCN–) or $(SCN)_2$, via H_2O_2. The lactoperoxidase system is bacteriocidal against several Gram-negative bacteria with low cell density (*E. coli*, *Pseudomonas aeruginosa*, and *Salmonella typhimurium*); but exhibits bacteriostatic activity Gram-negative bacteria and also toward Gram-positive bacteria (*Bacillus cereus, Staphylococcus aureus, and Listeria monocytogenes*) with high cell density. It is used for the preservation of raw milk throughout storage (Bafort *et al.* 2014, Raveendran *et al.* 2018). **Laccase** (EC 1.10.3.2) oxidized several compounds such as phenolics, aromatic amines, and ascorbate. Different species of white-rot fungi (*Phlebia ostreatus, P. radiata, Trametes hirsuta, T. versicolor,* and *T. ochracea*) have widely used for laccase production. Laccase is applied to dispel haze formation in alcoholic beverage fermentation through polyphenol oxidation. (Mondal *et al.* 2019), and also utilized for oxygen removal in the final step beer production; thereby prolongs the shelf life of beer. In baking industries it is used to enhance stability, strength, and decreases stickiness leading to better machinability of bread batter (Raveendran *et al.* 2018, Mondal *et al.* 2019). **Chitinases** (EC

3.2.1.14) are synthesized from both fungal (*Trichoderma harzianum, Aphanocladium album, Aspergillus fumigatus*) and bacterial (*Aeromonas hydrophila, Bacillus cereus, Serratia marcescens*) sources. Chitinases are used as food additives to increase the shelf life of foods (Ramos and Malcata 2017).

4.5. Prebiotic Oligosaccharides: According to the FAO (2007), a prebiotic is defined as a non-functional food ingredient that prompts health benefits to the host by modulating microbiota present in the host. It has been reported that the population of the microbial community present in per gram of human colon ranges from 10^{10}–10^{12}. An oligosaccharide is a molecule having a small number (2 to about 10) of monosaccharide moieties linked by glycosidic linkages (IUB-IUPAC, 1982). The well-known prebiotics extensively used in the food industry are including fructooligosaccharides (FOS), galactooligosaccharides (GOS), soyoligosaccharides (SOS), xylooligosaccharides (XOS), isomaltooligosaccharides (IMO), pectinoligosaccharides (POS), and chitosanoligosacharides (COS). The health benefits obtained from the consumption of prebiotics are due to following physiological consequences: the provocation of the immune system (curtailed incidence or duration of infection), perfection in the blood lipid profile (decrease of total cholesterol and triacylglycerol level) and glycemic index, reduce the occurrence of the type of cancers (e.g., colon cancer), balance endocrine mechanisms regulating food ingestion and energy usage, satiety (lowering total dietary calorie intake), absorption of calcium (upgraded bone health) and other minerals (magnesium, zinc, and iron), and maintaining of bowel movements and defecation, resulting in reduce fecal transit time (Glibowski and Skrzypczak 2017). Prebiotic oligosaccharides are low-calorie, undigested sweeteners (sweetness declines with lengthier chain length); commercially used in dairy products, bread, jams, confectionery, beverages and infant milk formula (Nguyen and Haltrich 2013).

Galactooligosaccharides (GOS) are oligosaccharides having β-(1’!3) and β-(1’!4) bonds among the galactose moieties, synthesized by transgalactosylase activity of β-galactosidase mostly isolated from *Kluyveromyces* and *Aspergillus spp.* (Vera *et al.* 2016, Meyer *et al.* 2015). GOSs can prominently stimulate the growth of *Bifidobacteria* and *Lactobacilli*. It can stand at high temperature and low pH; make it as a favorite additive in food products. The combination of 90% short-chain GOS with 10% long-chain FOS are introduced in human milk to mimic the molecular size of natural oligosaccharides (Singh *et al.* 2017). **Xylooligosaccharides** (XOS) are oligosaccharides containing two to six xylose residues linked through β-(1'!4) bonds ((Glibowski and Skrzypczak 2017). XOSs are produced from xylan (extracted corn cobs), employing xylanase from *Aspergillus spp.* (Nguyen and Haltrich 2013). XOSs are sweet in taste, thus suitable for diabetic patients as they cannot increase blood glucose level, and normalize insulin secretion from the pancreas (Samanta *et al.* 2015). **Isomaltooligosaccharides** (IMO) is a mixture of a short-chain oligomer of glucose residues mainly linked by α-(1'!6) glycosidic bonds. IMOs with a degree of polymerization of up to 2 to 6 can be synthesized from corn starch by sequential reactions of starch with α-amylase, β-amylase, and transglucosidase originated from *Aspergillus niger* or *Leuconostoc spp*. (Zhang *et al.* 2009). IMOs selectively induce the growth of *Bifidobacterium* and *Lactobacillus* (Glibowski and Skrzypczak 2017). **Chitooligosaccharides** (COS) are synthesized from chitosan, a derivative of chitin, consisting of D-glucosamine and N-acetyl-D-glucosamine linked together by β-(1'!4) glycosidic bonds. COSs are produced through chemical (high temperature with low pH) or enzymatic (chitosanases from *Aspergillus, Bacillus spp.*) hydrolysis of the chitosan polysaccharides (Bouhnik *et al.* 2004, Singh *et al.* 2017). Heavily deacetylated COSs were efficiently preventing the growth of *Staphylococcus aureus, Escherichia coli, Pseudomonas aeruginosa, Streptococcus fecalis*, and *Samonella typhimurium*. COSs have also contributed beneficial effects on the gut probiotic bacteria (*Lactobacillus* and *Bifidobacterium spp.*) (Meyer 2015). **Fructooligosaccharides** (FOS) are obtained from sucrose using the transfructosylation activity of the β-fructofuranosidase, industrially produced from *Aspergillus spp*. β-fructofuranosidase also isolated from the yeast (*Saccharomyces cerevisiae, Schwanniomyces occidentalis, Rhodotorula dairenensis*) and Bifidobacterium (*B. adolescentis, B. longum, B. breve*) (Nguyen and Haltrich 2013). It influenced the growth of gut microbiota; therefore, preventing pathogenic organisms. FOS is helpful in the absorption of water and electrolyte through the gut mucosa. It has been reported that the combination of FOS and GOS declined the symptoms of phenylketonuria in infants (Patel and Goval 2012, Singh *et al.* 2017).

4.6. Flavoring products: Flavour is a unique character of a substance (non-volatile or volatile) affecting the both olfactory and gustatory systems. It may be defined as the multitude of properties of a compound, received by mouth or nose, identified in the form (sense) of taste and smell, and understood by the brain. The non-volatile compounds influenced taste, while the volatile ones stimulate both taste and aroma. Microorganisms can synthesize flavors as secondary metabolites during fermentation on nutrients such as sugars and amino acids. This capability may be used in two different ways. In some food or beverage (cheese, yogurt, beer, wine) flavoring compounds are intrinsically synthesized which ultimately determines the typical organoleptic character of the end product. Through fermentation flavor compounds are separately synthesized by the dedicated microbes and applied later in food manufacture. (Longo and Sanroman 2006, Bhari and Singh 2019).

Diacetyl has been used to impart buttery flavor with yellow color to dairy products and also induced this flavor to popcorns, chips, candies, and pastries. This compound is mainly produced by *Lactococcus lactis*, *Lactobacillus* sp., *Streptococcus thermophilus*, *Leuconostoc mesenteroides*. In bakery products LAB perform dehydrogenation reaction through the enzyme acetoin dehydrogenase to produce diacetyl. The dairy products *Streptococcus lactis*, *S. cremoris* and *S. diacetilactis* produced high amounts of diacetlyl along with acetaldehyde. During beer fermentation diacetyl contribute off-flavors. Diacetyl reductase from *Aerobacter aerogenes* removed diacetyl and 2,3-pentadione from beer by converting flavorless acetoin (Bicas *et al.* 2010, Ogbodo and Ugwuanyi 2017). **Lactones** (cyclic esters of primarily γ- and δ-hydroxy acids) are ubiquitously found in food, providing fruity, coconut-like, buttery, creamy, sweet or nutty flavor. The compound 6-pentyl-2-pyrone delivers a coconut aroma, the major volatile components in cultures of the mold *Trichoderma viride*. Other molds such as *Tyromyces sambuceus* and *Cladosporium suaveolens* synthesize the coconut-flavored lactones γ-decalactone and δ-dodecalactone from ricinoleic acid and linoleic acid, respectively. Yeasts such as *Candida tropicalis* or *Yarrowia lipolytica* degraded ricinoleic acid to accumulate δ-decalactone, which exhibits fruity and oily notes important for peach, apricot or strawberry aroma formulation. The yeast *Sporobolomyces odorus* produced 1.6 mg.L–1 of δ-decalactone, leading to an extreme peach aroma (Longo and Sanroman 2006, Bicas *et al.* 2010). **Esters** chiefly provide fruity flavor to the products (candies, jellies, jams, baked goods, wines, cultured butter, sour cream, yogurt, and cheese). Ethyl, methyl, propyl, butyl, isobutyl, amyl, and isoamyl esters are popularized in the food industry. Hexyl-2-methylbutyrate contributes golden apples, ethyl butyrate provides pineapple flavor, methyl, and ethyl cinnamates attributes strawberry flavour. The yeasts *Hanseniaspora guilliermondii* and *Pichia anomala* are the potent producer of 2-phenylethyl acetate and isoamyl acetate, respectively. In cheese production, ethyl or methyl esters of short-chain fatty acids give fruity flavor while thioesters derived from thiols impart cabbage or sulfur flavor (Serra *et al.* 2005, Ogbodo and Ugwuanyi 2017). M**ethyl ketones** (2-heptanone, 2-nonanone, and 2-undecanone) are employed in blue cheese production and providing the stale aroma to UHT milk. It was first noticed in the blue cheese inoculated with *Penicillium roqueforti*. These are produced by *Aspergillus bisporus*, *A. niger*, *Trichoderma viride*, and *Penicillium roquefortii* through their β-oxidation pathway (Bicas *et al.*2010). **Terpenes** obtained by distillation of resins from certain trees, having general formula $(C_5H_8)n$, where n=2 for monoterpenes, n=3 for sequiterpenes, n=4 for diterpenes, n=6 for triterpenes and n=8 for tetraterpenes. The mold *Ceratocystis moniliformis* produces several aroma products such as citronellol and geraniol (Serra *et al.* 2005, Carroll *et al.* 2016). **Pyrazines** are heterocyclic, nitrogen-containing compounds having nutty and roasted flavor. They are naturally formed in Maillard reaction during conventional cooking/roasting of food. *Corynebacterium glutamicum* synthesized tetramethylpyrazine from amino acids (Gupta *et al.* 2015). **Alcohols** are produced as a result of microbial fermentation (bacteria or yeast). Yeast produces long-chain alcohols which have characteristic organoleptic properties. Several specific strains of yeast such as *Kluyveromyces marxianus, Saccharomyces cerevisiae, Hansenula anomala* are capable of producing 2-phenylethanol (rose-like aroma) from 2-phenylalanine (Bhari and Singh 2019). **Aldehydes** (vanillin, benzaldehyde, acetaldehyde, anisaldehyde, and phenyacetaldehyde) produce desirable creamy, buttery flavors at low concentration while at high concentrations, they produce oxidized off-flavors. Benzaldehyde provides cherry and almond flavor. Alcohol oxidase from *Pichia pastoris* oxidizes benzyl alcohol to benzaldehyde. Threonine aldolase from *Streptococcus thermophilus* and *Lactobacillus bulgaricus* catalyses the bioconversion of threonine to acetaldehyde and glycine. Vanillin (4-hydroxy-3-methoxybenzaldehyde) is a typical flavor compound found in Vanilla planifolia beans; widely used in foods and beverages. Several bacterial and fungal genera (*Pseudomonas putida, Aspergillus niger, Corynebacterium glutamicum, Arthrobacter globiformis*, and *Serratia marcescens*) having the ability to produce vanillin from eugenol and isoeugenol (essential oil) (Carroll *et al.* 2016).

4.7. Food preservatives: Up to 30 to 40 % of edible food products still have been lost due to spoilage and other sensory quality issues leading to noteworthy economic losses. Foodborne diseases remain to have severe socioeconomic consequences. Lowering the influence of spoilage microorganisms and food pathogens in foods will become even become more challenging as customer demand for food products without chemical preservatives (Ben Said *et al.* 2019). Although the availability of plant and animal-derived preservatives, microbial food preservatives gain special attention due to their cost-effective production in a short time-period without disturbing the natural ecosystem.

Nisin is isolated from *Lactococcus lactis* and used to improve shelf-life and safety purposes of different heat-treated and low pH products, including dairy products, processed meats, and vegetables (Galvez *et al.* 2008). It is a cationic, amphiphilic peptide molecule, which has a relatively broad-spectrum activity against a vast range of pathogenic Gram-positive bacteria. The antimicrobial activity of nisin have been first noticed in 1928 by observing the inhibition of a dairy starter culture by a strain of *L. lactis*, not to do by bacteriophages (Elsser-Gravesen and Elsser-Gravesen 2013). Nisin categorized as lanthionine containing bacteriocins, grouped under class I bacteriocins. Nisin is a linear lantibiotic that shown its antibacterial activity by inhibiting cell wall formation as well as creating membrane pores; additionally it is effective against spores. Several alternates of nisin present naturally; among them two become commercially available, nisin A and nisin Z, which vary in one amino acid, resulting in different charges and solubility (Sobrino-López and Martín-Belloso 2008). Although the synthesizer microbe being a Gram-positive bacteria; it protects itself by an inherent immune system incorporated with the biosynthesis genes (Alkhatib *et al.* 2012). **Natamycin** (previously pimaricin) has been first isolated from *Strepyomyces natalensis* in the 1950s and is still commercially produced from that organism. Natamycin is heat-stable, macrolide polyene group of the antifungal agent; characterized by a macrocyclic lactone-ring having several conjugated carbon-carbon double bonds (Chen and Ji 2002). It is active against all types of fungal food pathogens (binds to the ergosterol or other sterols of the fungal cell wall; disrupts it, leading to osmotic imbalance) but ineffective against bacteria and viruses (Delves-Broughton and Weber 2011). Natamycin is particularly for treating surfaces of hard cheese and salamitype sausages to protect from superficial contamination. (Elsser-Gravesen and Elsser-Gravesen 2013). **Reuterin** is a water-soluble, non-proteinaceous, antimicrobial agent produced by *Lacotobacillus reuteri*. It shows a broad range of antimicrobial activity against Gram-negative or Gram-positive bacteria, molds, and yeast. It is effective in a wide range of pH and unaffected from proteolytic and lipolytic enzymes (El-Ziney *et al.* 1999). It displays bacteriostatic activity against many foodborne pathogenic bacteria (*Listeria monocytogenes*) (Saeed *et al.* 2019). **Bacteriocins** are ribosomally produced exogenously secreted antimicrobial peptides having a bactericidal or bacteriostatic activity. Bacteriocin production is a natural characteristic of food-grade LAB (Smid and Gorris 2007). Nisin is the first bacteriocins to be discovered grouped into Class I (lantibiotics), and class II, the unmodified bacteriocins (with the class IIa pediocin-like antilisterial bacteriocins), organize the most plentiful, best characterized, and most useful of the food-grade bacteriocins (Gould 2012). IIa bacteriocins are synthesized by a variety of microorganisms (*Bifidobacterium bifidum, B. infantis, Bacillus coagulans, Listeria innocua, Pediococcus*, *Lactobacillus*, *Enterococcus, Carnobacterium, Leuconostoc, Streptococcus*, and *Weissella spp*.). The IIa bacteriocins specifically bind to the mannose phosphotransferase system (man-PTS), and consequently form membrane pores and kill the sensitive cells. Since they are usually effective against many foodborne pathogens (*Listeria*, *Clostridium, Enterococcus, Carnobacterium, Lactobacillus, Pediococcus, Streptococcus* and *Leuconostoc spp.*); now widely applied as harmless preservatives in a variety of food products for prolonging shelf life as well as to inhibit spoilage (Burke *et al.* 2013). **Bacteriophages** (Greek phage meaning eater i.e. bacteria-eater) are innocent to humans, animals, and plants; now applied as food preservatives since they specifically target bacteria to propagate and ultimately cause death (Elsser-Gravesen and Elsser-Gravesen 2013). Phages have been reported to reduce *Campylobacter* and *Salmonella* on chicken skin (Garcia *et al.* 2010). An amalgamation of phages and bactericidal strains of *Lactobacillus sakei* have been successfully employed to prevent the outgrowth of *Listeria monocytogenes* in prepared ham (Holck and Berg 2009).

4.8. Food colorant: Colorant delivers color on something in the form of dye, pigment, or other substance (Ogbodo and Ugwuanyi 2017**).** The ancient practice of food colorant has been started in Egyptian cities around 1500 BC, where toffee producers used plant extracts and wine to amend the outlook of their products (Downham and Collins 2000). Color performed as an influencing role in the food sector, providing sensory traits of food. It indicates freshness, safety aspect, nutritional quality, and aesthetic value of food, directly emphasize the commercial background of colored food production (Sen *et al.* 2019). Recent concern emerged from the consumer front regarding the potential carcinogenicity or teratogenicity of chemical colorant (Babitha 2009) induces food industries to depend on microbial food colorants. The dominance of microbial food colorant over chemical or plant-mediated colorant are due to rapid growth, easy to handling, color variety, higher light steadiness, heat tolerance, nutritive quality, safety issues, and whether independence as well as some indispensable biological features such as antioxidant, antimicrobial and anticancer activity (Rao *et al.* 2017, Ogbodo and Ugwuanyi 2017). Microbial food colorants are derived from yeast, fungi, bacteria, and algae groups (Chattopadhyay *et al.* 2008).

Canthaxanthin is an antioxidative, lipid-soluble (inhibit the oxidation of lipids in liposomes) orange to deep pink colored carotenoid, isolated from *Bradyrhizobium Spp*. It is permitted as a food colorant and used in a large array of foods; especially in salmon and poultry feed (FDA 2011, Chuyen and Eun 2017). **Astaxanthin** is a lipid-soluble, red-orange pigment, applied as a coloring agent in flesh-foods. Naturally it is available in yeast, microalgae *(Haematococcus pluvialis*), and also in salmon, crustaceans, red shrimp, crayfish, and feathers of some birds (Pogorzelska *et al.* 2018). **β-Carotene** is an antioxidative red-orange colored carotenoids group of pigment, chiefly extracted from the algae, *Dunaliella salina* (Ogbodo and Ugwuanyi 2017). Fermentative production of β-carotene from *Blakeslea trispora* produces a pigment equivalent to chemically synthesized pigments and is an acceptable food coloring agent. The majority of microbes reported synthesizing carotenoids belonging to *Myxococcus*, *Serratia*, *Streptomyce*s, *Mycobacterium*, *Agrobacterium*, and *Sulfolobus spp*. (Malik 2012, Sen *et al.* 2019). **Prodigiosin** is a red pigment having antimicrobial, antiparasitic, and antineoplastic activity, isolated from several strains of *Serratia marcescens*. It has been fruitfully used as a food colorant in yogurt, milk, and carbonated drinks (Namazkar and Ahmad 2013, Akilandeswari and Pradeep 2017). **Violacein** is a purple pigment having antimicrobial and anticancer activity, principally obtained from *Chromobacterium violaceum*. It has potential applications in food, cosmetic, and textile industries (Dufosse 2018). **Riboflavin** (vitamin B2) is water-soluble vitamins cum yellow colored pigment and utilized in dairy items, breakfast cereals, baby foods, sauces, fruit drinks, and energy drinks (Dufosse 2018). **Melanins** are naturally present as pigments in animals, plants, and microorganisms (*Saccharomyces, Neoformans spp*.). They are used in food products, cosmetics, pharmaceuticals, and others (Sen *et al.* 2019). **Lycopene** is a brilliant red-colored carotenoids group of pigment typically present in tomatoes. It has been obtained from a wide array of microbes (*Fusarium, Sporotrichioides*, and *Blakeslea trispora*). It can mitigate some long-lasting diseases (some form of cancers and coronary heart disease). In western countries it is used as a meat coloring agent (Malik 2012, Ogbodo and Ugwuanyi 2017).

4.9. Low-calorie sweeteners: Worldwide low-calorie sweeteners (since their metabolism cannot release significant amounts of energy) become enormously popularize as the incidence of diabetic increases in the population as well modern trend towards healthy lifestyle (Granström and Leisola 2013). The harmless nature of low-calorie sweeteners makes them applicable in a wide variety of foods and beverages (Patra *et al.* 2017).

Erythritol is a four-carbon sugar alcohol naturally found in fruits (grapes, pears, melons), and fermented foods (soy sauce, cheese, and wine). More than 90% of erythritol consumed is not metabolized and released as an unchanged form through the urine; therefore, it cannot interfere with body blood glucose or insulin level (Lin *et al.* 2010). It is not metabolized by oral bacteria, therefore, it cannot induce tooth decay. At present, it is the only known sugar alcohol that is predominantly manufactured by fermentation. Many microorganisms, especially yeasts such as *Zygosaccharomyces, Debaryomyces, Hansenula,* and *Pichia spp.* synthesize erythritol through their pentose phosphate pathway (de cock *et al.* 2002). Lin *et al.* (2010) have been reported a mutant strain of *Moniliella sp.*, and under optimizing conditions it can synthesize up to 189.4 g/L of erythritol in fed-batch fermentation. **Mannitol** is naturally present in pumpkins, celery, onions, grasses, olives, mistletoe, and lichens. Mannitol is partially metabolized and cannot induce hyperglycemia; therefore, it is appropriate for diabetics. It is widely applied for the preparation of candies, chewing gums, flavored jam or jellies, confections, frostings, and cough drops. The *Lactobacillus intermedius* NRRL B-3693 synthesized up to 198 g/L of mannitol by fermenting a high-fructose (300 g/L) medium (Patra *et al.* 2017). **Xylitol** is commercially applied in the production of chocolates, chewing gum, soft drinks, ice cream, toothpaste, and also in pharmaceutical preparations (Patra *et al.* 2017). It is mainly synthesized by the microorganisms (yeasts, molds, and bacteria) but especially by *Candida spp.* Microbes synthesize xylitol by reducing xylose by the action of xylose reductase enzyme in the pentose phosphate pathway. Jiang *et al.* (2016) have been reported a novel strain of *Candida maltosa* CHH65 synthesized up to 100 g/L of xylitol within 48 h by using corncob hemicellulosic hydrolyzate and xylose. **D-Tagatose** is an epimer of D-fructose isomerized at C-4. It naturally exists in the gum of cacao tree (*Sterculia setigera*) as well as a constituent of an oligosaccharide found in lichens (*Rocella* *spp.*). It is synthesized during the lactose metabolism in bacteria (*Thermotoga maritima, Thermus sp., Geobacillus thermodenitrificans, G. stearothermophilus, Lactobacillus plantarum* NC8*, L. sakei 23K,* and *Pediococcus pentosaceus* PC-5) from galactose by the enzyme L-arabinose. Because of its diabetes and tooth-friendly nature, commercially it is used to manufacture breakfast cereals, soft drinks, ice cream, yogurt, confectioneries, frostings, chewing gum, and dietary supplements (FAO 2004, Rhimi *et al.* 2011, Patra *et al.* 2017). Xu *et al.* (2016) produce a genetically modified strain of *E. coli* by co-expressing an L-arabinose isomerase from *L. fermentum* CGMCC2921 and a β-galactosidase from *Thermus thermophilus* HB27*,* which under optimal condition synthesized up to 101 g/L tagatose in 16 h. **Sorbitol** (D-glucitol) is a non-metabolized (low calorific value), diabetes, and tooth-friendly, alcoholic sugar naturally available in many fruits (berries, cherries, plums, pears, and apples) (Ladero et al 2007). Sorbitol can tolerate high temperatures and cannot take part in Maillard (browning) reactions. Its commercial applications are including chewing gums, candies, frozen desserts, confectioneries, and many oral products (toothpaste, mouthwash, icings, and fillings of the tooth) (Jan *et al.* 2017). It is shown *in vivo* prebiotic potentiality by specifically influencing the growth of gut-lactobacilli as well as inducing butyrate production in the intestine (Sarmiento-Rubianoet *et al.* 2007). *Zymomonas mobilis* is capable to synthesize sorbitol and gluconic acid from fructose and glucose, respectively in a one-step reaction catalyze by glucose-fructose oxidoreductase. *Candida boidinii* and *Saccharomyces cerevisiae* are also able to produce sorbitol (Granström and Leisola 2013). **D-Psicose** is a C-3 epimer of D-fructose, naturally present in wheat, itea plants, and processed cane and beet molasses (Mu *et al.* 2012). It serves as an efficient alternative to sucrose as sweeteners having the low postprandial glycaemic response and better insulin sensitivity and glucose tolerance (Hossain *et al.* 2011). Itoh *et al.* (1994) firstly described the enzyme D-tagatose 3-epimerase isolated from *Pseudomonas sp.* ST-24; responsible for epimerization of D-fructose at C-3 to produce D-psicose and this enzyme is utilized for commercial production of D-psicose (150 g/L) (Li *et al.* 2013). Although this enzyme is also synthesized by several microorganisms such as *Rhodobacter sphaeroides* SK011, *Agrobacterium tumifaciens*, *Clostridium cellulolyticum* H10, and *Clostridium scindens* 35704, (Patra *et al.* 2017).

4.10. Polyunsaturated fatty acids (PUFA): PUFAs executes essential physiological roles in maintaining flexibility, fluidity, and selective permeability of biological membranes. The two major families of PUFAs are differentiated by the distance between the methyl or ω end of the fatty acyl chain and their last double bond. The omega-3 and omega-6 PUFA having their last double bond situated at the third or sixth carbon, respectively, from the ω end of the fatty-acyl chain. Several PUFAs of the omega-6 types are including gamma-linolenic acid (GLA) and arachidonic acid (ARA) and the omega-3 types, eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA) (Bellou *et al.* 2016, Nelson and Cox 2017). Omega-3 PUFAs contribute several beneficial effects to human health, such as anti-inflammatory, anti-coagulating activity, lowering triglyceride, blood pressure, and blood sugar levels and also reducing certain types of cancer (Gupta *et al.* 2012). Omega-6 PUFAs serve as a metabolic precursor to synthesize the number of physiologically active eicosanoid hormones, prostaglandins, leukotrienes, and thromboxanes (Ji *et al.* 2014). The ratio of omega-6 to omega-3 PUFA within the range between 5:1 and 3:1 has been suggested as a beneficiary to human health (Simopoulos, 2008). The conventional animal and plant sources of omega-3 fatty acids are including fish oil and fatty fish like salmon, trout, tuna, and flaxseeds, walnut, chia seeds, Brussels sprouts, and hemp seeds; respectively. While, the standard animal and plant sources of omega-6 fatty acids are including egg, and avocado oil, walnut, sunflower oil, peanut butter, almonds, respectively. Microbial lipids in the form of single-cell oils (SCO) are generally marketed to provide health benefits of PUFAs to the consumers. Several microorganisms such as microalgae, bacteria, fungi, and yeasts synthesize omega-3 and omega-6 polyunsaturated fatty acids (Gupta *et al.* 2012).

In the 1990s, a UK based biotechnology company (J. & E. Sturge, N. Yorks, UK) has been started the fermentative production of GLA from *Mucor circinelloides* and synthesized up to 60 kg m^{-3} of cell mass (cells oil density 25%) within 72–96. Kyle *et al.* (1992) reported the production of DHA from the nonphotosynthetic dinoflagellate, *Crypthecodinium cohnii*. The proposed level of DHA as a supplement in infant formulas is within 0.32% and 0.64% of the total fatty acids (Birch et al 2010.). Infant formulas containing the DHA oil derived from *C. cohnii* is marketed under the trade name of 'Life's DHA' (Ratledge 2013). Efficient producers of another omega-6 fatty acid, DPA (docosapentaenoic acid) is *Schizochytrium, Aurantiochytrium, Oblongichytrium*, and *Labyranathula spp.* (Wong *et al.* 2008). Japanese researchers for the first time have been reported the production of oil containing ARA in high amount (50% oil harvest from per kg biomass) from the filamentous fungus, *Mortierella alpine* within 9-10 days of fermentation (Totani *et al.* 1987, Ratledge 2013). Several microorganisms such as *Cylindrotheca fusiformis, Navicula pelliculosa,* and *Nitzschia laevishave* have been reported to produce EPA (Wen and Chen 2010). Algisys LLC (Cleveland, OH) and Photonz (New Zealand) are well-known companies that especially manufacture EPA-only oil through the heterotrophic cultivation of microalgae. Several genetically engineered strains of yeast (*Yarrowia lipolytica,* and *Saccharomyces cerevisiae*) have been well documented for high yield production of EPA (Ratledge 2013).

4.11. Biosurfactants: Surfactants are amphipathic substances having both hydrophobic and hydrophilic components that enable them to incorporate within the oil/water or air/water interphases, lowering the surface or interfacial pressures, and producing microemulsion in which hydrocarbons and water mixed (Banat *et al.* 2000). Both biosurfactants and bioemulsifiers have emulsification qualities and also they often fall in the same group, but bioemulsifiers unable to reduce lower surface tension (Karanth *et al.* 1999). Structurally microbial surfactants may be present in one of the following forms: mycolic acid, glycolipids, a polysaccharide–lipid complex, lipoprotein or lipopeptide, phospholipid, or the microbial cell surface itself. Biosurfactants have the number of benefits in comparison to the chemical surfactants, such as bulky and complex structure, advanced biodegradability and minor toxicity, reduce CMC (critical micelle concentration) and developed surface activity, improved ability to produce molecular assemblage and liquid crystal, biological potentiality (antimicrobial, antitumor, etc.), tolerate to adverse levels of pH, salinity, and temperature; and manufactured from renewable resources (Ranasalva *et al.* 2014). Applications of biosufactants in food industries are including improved maintenance of agglomeration of fat globules (dairy industries), sustain aerated systems within the foods to ameliorate texture and consistency (Campos et al 2013), bakery and ice cream industries utilize it to control consistency thus reducing staling and also solubilizing the flavor oils. Liposan has a property to lower surface tension and is applied to emulsify edible oil. The antifungal activity of *B. Subtilis* (effective dose 50-100 ppm) makes them as an efficient microflora eliminator, used in the warehoused grains of corn and cottonseeds (Manif *et al.* 2016).

Glycolipids are well-known biosurfactants structurally consists of sugar moieties with long-chain aliphatic acids or hydroxyaliphatic acids. Efficient glycolipids as biosurfactants are rhamnolipids, trehalolipids, and sophorolipids (Kitamoto *et* *al.* 2009). **Rhamnolipids** are initially isolated from *Pseudomonas aeruginosa*, chemically consists of one or two molecules of rhamnose are adhered to one or two molecules of β-hydroxydecanoic acid. Rhamnolipids along with niacin prolong the shelf life and prevent the growth of hemophilic spores in ultrahigh treated soymilk. It is widely used in bakery industries to improve dough volume, shape, texture, and shelf life (Sinumvayo and Ishimwe 2015). **Trehalolipids** are constructed from the disaccharide trehalose linked to mycolic acid and synthesized by the several strains of *Mycobacterium, Nocardia*, *Rhodococcus*, and *Corynebacterium spp.* (Bages-Estopa *et al.* 2018). It is efficiently stabilized oleophilic emulsions and bases for creams, oily films, and pastes applied in food industries (Kuyukina and Ivshina 2010). **Sophorolipids** are chiefly produced by yeasts (*Torulopsis bombicola, T. petrophilum, T. apicola,* and *Candida bogoriensis*; and structurally consist of a dimeric sugar sophorose associated with an elongated-chain of hydroxy fatty acid. In bread-making it is used to produce bread with better volume, appearance, and shelf life. 1% sophorolipids in germicidal formulas are highly effective against pathogenic Gram-negative bacteria (*Escherichia coli, Salmonella typhimurium, Erwinia chrysanthemi,* and *Xanthomonas campestris*) and used to curtailed microbial spoilage and extend shelf life in fruits and vegetables (chikoos, tomatoes, lemons, and cucumber) (Oliveria *et al.* 2015). **Cyclic lipopeptides** are amphipathic compounds having a fatty acid tail bonded to a short oligopeptide, producing a macrocyclic ring structure. Three well-known lipopeptides from *Bacillus spp.* are Surfactin, Iturin, and Fengycin. Surfactins having seven amino acid ring structure (Glu-Leu-Leu-Val-AspLeu-Leu) linked to a 3-hydroxy13-methyl tetradecanoic acid, are applied in the baking industry to maintain the texture, stability, and volume of dough and also induces emulsification of fat to regulate the aggregation of fat globules (Meena and Kanwar 2015). Serratamolide, an aminolipid biosurfactant has been derived from *Serratia marcescens* NS.38 used as an antifungal agent to preserve stored grains (Singh 2012). **Phospholipids** are amphipathic lipids in which C1 and C2 of glycerol moiety esterified to two fatty acids, and a charged group is attached to the C3 through phosphodiester linkage. The quantitative synthesis of phospholipids has been detected in some strains of *Aspergillus spp.*, *Thiobacillus thiooxidans*, *Arthrobacter spp.* and *P. aeruginosa*, which are used as emulsifiers, wetting, viscosity modifier, extrusion aid, separating agent, and nutritional supplement in the food industry (Gautam and Tyagi 2006, Nischke and Costa 2007). The well-known

polymeric biosurfactants used in the food industry are including emulsan, alasan, liposan, and lipomanan synthesized from *Acinetobacter calcoaceticus*, *A. radioresistens*, *Candida lipolytica*, and *C. tropicalis*, respectively. (Chakrabarti 2012, Nitschke and Silva 2018). Mannoprotein from *Saccharomyces cerevisia*e is used to stabilize water-oil interphase and producing emulsions appropriate for the manufacturing mayonnaise, cookies, and ice creams (Campos *et al.* 2013).

4.12. Microbial polysaccharides: The well-known microbial polysaccharides are including curdlan, dextran, gellan, levan, pullulan, scleroglucan, alginates, and xanthan (Kirtel *et al.* 2017). Microbial polysaccharides may be intracellular or extracellular, and the extracellular polysaccharides (EPS) are chiefly utilized in the food industry in comparison to intracellular polysaccharides (Patel and Prajapati 2013).

Xanthan gum is water-soluble, heteropolysaccharides composed of a backbone of glucose units linked by β-(1'!4) glycosidic bond along with the branched chains of mannose and glucuronic acid residues; and can withstand at high pH and salt concentrations. It is synthesized by *Xanthomonas campestris, Xanthomonas axonopodis,* and *Xanthomonas pelargonii* through the aerobic fermentation of glucose or sucrose media (Niknezhad *et al.* 2016). In food industry xanthan gum is used to contribute to improve viscosity, texture, appearance, flavor, and water balance (Palaniraj *et al.* 2011). When xanthan gum is mixed with guar or locust bean gum (singly or both) it serves as a stabilizer for ice cream, sherbet, milkshakes, and ice milk. The mixture of xanthan gum and methylcarboxymethyl cellulose is widely used in frozen dairy and yogurts (Kirtel *et al.* 2017, Jindal *et al.* 2018). **Gellan gum** is a high molecular weight, anionic polysaccharide, derived from the bacterium *Sphingomonas paucimobilis*; and consists of linear repeating tetrasaccharides units of β-D glucose, L-rhamnose, and D-glucuronic acid in a molar ratio of 2:1:1 with two acyl groups, acetate, and glycerate linked to the glucose residue nearby to glucuronic acid (Ahmad *et al.* 2015). Gellan gum is widely used in food industry especially in confectionery products to reduce the setting time and prevents them from sticking together in a warm environment, acts as a thickening agent in the production of jams, jellies, and dairy products such as ice cream, milkshakes, cheese, and yogurt (Mariod and Fadul, 2013, Jindal and Khattar 2018). **Curdlan** is a linear β-(1'!3) glucan, partially esterified with succinic acid; and commercially manufactured from *Agrobacterium biobar* and mutants strains of *Alcaligenes faecalis* (Zhang and Edgar 2014). As a thickening agent curdlan is used in the production of jellies, desserts, confectionery products, dietetic foods (salad dressings, desserts, and pasta), and also as an edible coating to increase the shelf life of the food products (Nishinari *et al.* 2009, Ramalingam *et al.* 2014). **Pullulan** is a type of exopolysaccharide derived from *Aureobasidium pullulans*, commonly known as black yeast. The building block of pullulan is maltotriose units, linked through α-(1'!6) bonds (Ramalingam *et al.* 2014, Jindal *et al.* 2018). Applications of pullulan in industrial-scale are including: as a coating material in microencapsulated food, as a consumable and safe food packaging material, as a low-viscosity filler in beverages, as a prebiotic dietary fiber, as a modifier in soups and sauce, as a binder and stabilizer in food pastes, as a protective glaze, and as cholesterol and fatty acid substitute agent in fatty emulsion stabilization (Park and Khan 2009, Kirtel *et al.* 2017). **A dextran** is a group of glucans containing α-(1'!4) and α-(1'!6) linkages, synthesized extracellularly by the species of *Lactobacillus, Leuconostoc,* and *Streptococcus*; although commercially prepared from the fermentation of sugar cane or beet syrups by *Leuconostoc mesenteroides* (Park and Khan 2009). It is the first microbial polysaccharide that has commercialized and approved for application in food. It is utilized in confectionery products for maintaining moisture, viscosity, and prevent sugar crystallization, as a gelling agent in gums and gels, and in pudding mixture to prompt texture and mouth feel (Morris and Harding 2009, Ramalingam *et al.* 2014).

4. Microorganisms as a food source: To secure the demand for our future need in terms of food resources in a sustainable way make our search for an alternative way of constant food supply chain and this requirement is largely addressed by the microbial sources of food production within the ecological safety boundaries. Production of consumable microbial biomass obtained from bacteria, yeasts, molds or microalgae is an encouraging substitute to traditional sources of food and feed. Microbial biomass has high protein content, beneficial lipids, vitamins and often contains a wide array of health benefits (Ritala et al 2017). Commercial production of edible microbial biomass does not depend on agricultural land and accommodated within a minimal area, exist even more in a hostile environment (Linder 2019).

4.1. Microbial protein as feed: The global requirement of animal-derived protein in 2050 reaches 1,250 million tonnes per year at a present scale of consumption rate. Single-cell protein (SCP) is an efficient alternative to trace this necessity (Matassa *et al.* 2016, Ritala *et al.* 2017). The SCP is a rich source of protein and extracted from various microbial sources such as yeast, mold, algae, and bacteria, which are cultured on inexpensive agricultural waste residues for mass production to provide food for humans or animals in the form of a dried or whole microbial cell (Najafpour 2007). Although SCP has high nutritional value, there is a risk of allergic response due to the higher amount of nucleic acids from a high density of cells. Production of SCP from microbial sources containing similar kinds of amino acid profile as from animal or plant sources (Najafpour 2007, Bajpai 2017).

Microalgae harvested for human or animal consumption contributes high protein (60–70%), ω-3 fatty acids, carotenoids, vitamins A, B, C, and E, mineral salts, and chlorophyll (Gouveia *et al.* 2008) along with relatively low nucleic acid content (3-8%) (Nasseri *et al.* 2011). The established industrial producer is including *Arthrospira platensis* and *Arthrospira maxima* (sold as spirulina), *Chlorella*, *Dunaliella salina* (primarily for β-carotene) and *Aphanizomenon flosaquae* (Gouveia *et al.* 2008). **Fungal** (yeast and mold) sources of SCP are commercially prepared from the species of *Saccharomyces, Fusarium*, and *Torulopsis*. The protein content of fungal SCP is within the range of 30–50% (Nasseri et al 2011). Besides, it provides some of the B-complex group of vitamins (thiamine, riboflavin, biotin, niacin, pantothenic acid, pyridoxine, choline, streptogenin, glutathione, folic acid, and p-aminobenzoic acid), dietary fiber, and moderate nucleic acid content (7–10%); therefore, need to be processed before human consumption (Ritala *et al.* 2017, Nasseri *et al.* 2011). **Bacterial** SCP has 50–80% protein content (dry weight basis) (Anupama and Ravindra, 2000), high nucleic acid content (8–12%, especially RNA) and thus entail processing before consume (Nasseri et al 2011). Several important bacterial genera of SCP production are *Bacillus licheniformis, B. subtilis, Corynebacterium glutamicuma, Rhodopseudomonas palustris, Brevibacterium spp., Methylococcus capsulatus* (Suman *et al.* 2015).

4.2. Probiotics: Probiotics (Greek: 'pro' means 'assistance' and 'biotics means 'life') are live microbes which, when incorporated in appropriate quantities, imparts a health benefit to the host (FAO/WHO 2002). The idea of probiotics has been first disseminated in the early 20th century by the Russian Nobel laureate Elie Metchnikoff (Pfeiler and Klaenhammer 2013). The most extensively used probiotics are lactobacilli (*L. plantarum, L. reuteri, L. casei, L. acidophilus, L. delbrueckii, L. helvesticus, L. acidophilus*), bifidobacteria (*B. bifidum, B. lactis, B. animalis, B. longum, B. infantis, B. adolescentis*), bacilli (*B. lichenifirmis, B. subtilis, B. clause, B. coagulans, B. tequilensis)*, and yeasts (*Candida humilis, Debaryomyces hansenii, D. occidentalis, Kluyveromyces*

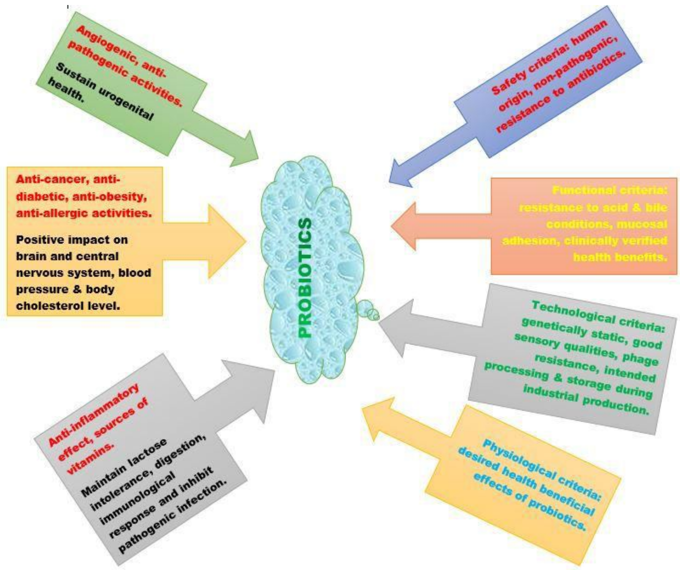

Fig. 1: Heath beneficial properties (left-side) and selection criteria (right-side) of probiotics.

lactis, K. lodderae, K. marxianus, Saccharomyces cerevisiae, S. baulardii, Yarrowia lipolytica) (Kumar *et al.* 2004, Maragkoudakis *et al.* 2006, Anandharaj *et al.* 2017, Elshaghabee *et al.* 2017, Ouwehand *et al.* 2018). A probiotic microorganism should be tolerate tough physicochemical environment during their journey through stomach and small intestine and persist in the gut to reveal its beneficial effects (FAO/WHO 2002). Microbial community present throughout the human body is estimated to be 10^{14} cells, 10-fold more cells than the mammalian cells (10^{13}) comprising the human body itself, with most residing in the gastrointestinal tract (GIT). The evolutionary established composition of the GIT microbial community is complex, dynamic, and specific to each host and can change markedly with diet, age, and lifestyle. Probiotics deliver their benefits to the host in three ways (Pfeiler and Klaenhammer 2013). First, the GIT is a prominent part of the immune system and constantly interacts with consumed foods as well as the commensal microbiota. Some probiotics can alter cytokine production by exposed macrophages and dendritic cells and can shift the production of cytokines from the inflammation-inducing interleukin-12 (IL-12) pathway to the anti-inflammatory IL-10 pathway (Galdeano 2019). Second, the GIT functions as a semipermeable barrier that allows the selective passage of certain molecules. Dysfunctional barriers are involved with several diseases of the GIT, including inflammatory bowel disease. Some probiotic strains can reinforce and repair this barrier by stimulating the production of protective proteins, such as mucins, by intestinal epithelial cells (Wilkins and Sequoia 2017). Third, it has been proposed that prior binding of probiotics to receptor sites blocks pathogen adhesion. Further, stimulation of host cells to produce mucin and thereby to tighten the mucosal barrier likely acts to block infection by pathogenic species (Reid and Hammond 2005, Kechagia *et al.* 2013, Kerry *et al.* 2018).

4.3. Bakery yeast: From the ancient documents it has been proposed that bread is baked in Egypt as early as 10000 BC (Jensen 1998). Generally baker's yeast has several important features such as tolerance to sugars and chemicals, cryo-resistance, sugar fermentation activity, and high leavening capability leading to high-quality baking products (Giannone and others 2010). Commonly, *Saccharomyces cerevisiae* serves as baker's yeast. It provides leavening of the dough, as well as for the formation of desired sensorial characteristics (Cukier de Aquino and others 2012). Yeast cells may be recycled for use in succeeding batches of beer or wine fermentation. Baker's yeast used in bread-making cannot be reused since the yeast is destroyed during baking. Therefore, the production of baker's yeast can be carried out on a very large industrial scale (Reed and Nagodawithana 1991). Cane or beet molasses supply not only sugars as a carbon and energy source but also some organic nitrogen, phosphate, sulfur, minerals (Ca, Mg), vitamins, and trace elements. Yeast is grown in large fermenters by the fed-batch process. The fermenters are equipped with cooling coils and with means for vigorous aeration to maintain highly aerobic growth. In the fermenter liquid 4-6% of yeast solids can be produced. Post-fermentation processing begins with centrifuging to produce a concentrate (yeast cream) with 18-20% solids. The yeast cream is washed and either pressed or filtered to a semisolid yeast mass of 30% solids. This press or filter cake is packaged as a crumbly mass in bags or extruded in blocks that are wax wrapped. It is cooled and shipped refrigerated to bakeries (Reed and Nagodawithana 1991, Ali *et al.* 2012, Reale *et al.* 2013).

5. Genetic or metabolic manipulation of traditional strains: Fermentation has thousands of years of a long history as a food preserving practice and traditionally every culture in the world used this technique to produce a variety of milk, meat, vegetable, fruit, or cereal-based products. From the last few decades the manufacture of microbial food products is increased since the common people become more health-conscious and they are well known about the nutritional values and health benefits provided by the microbial foods. In microbial food products, microbes enrich the quality of food by improving the bioavailability of nutrients, texture, flavor, and also deliver some inhibitory compounds that prevent food deterioration; therefore, extend the food value and security (Tamang *et al.* 2016). Besides, microbes also insert or improve several biological activities (probiotic qualities, antimicrobial, antioxidant, peptide production, degradation of antinutritive compounds, and fibrinolytic activity) to the fermented foods, which ultimately increase the biofunctionality of food products, and inducing potential health benefits to consumers. The global population becomes steadily rise, and peoples are now become more engaged in their routine work; hence, this situation needs nutritious readymade or instant foods. Since the wild microbial cultures are unpredictable in their ability to produce desired products, biotechnologists facing problems to provide quality food products to the customers. Sometimes microbes are unable to survive within the fermenter, because of surrounding environmental factors (pH, temperature, salinity, osmotic pressure, water activity) or the metabolites they produce become lethal to themselves. In food processing industries, raw substrate cost for fermentation media and slow growth rate of the fermentative microorganism, in turn, increases the production cost of the final product. As a result of these complications, food industries suffered from financial crisis. Therefore, a physiologically stable microbe is needed that can withstand in fermenter conditions, able to utilize inexpensive and renewable substrates such as lignocellulosic biomass, organic waste from municipalities, biotech industries as well as increase production rate. With the advancement of genetic or metabolic engineering, the scientists have prepared genetically modified microbes (GMM) with desired properties such the ability to resist a wide range of environmental factors (pH, temperature, osmotic stress, water activity), increased growth rate, improved metabolic activities, able to use low priced and renewable substrate, and produced enhanced nutrient-rich end products (flavor, texture, aroma, color, and shelf life). Industrially beneficial traits of GMM are including improved sensory quality (flavor, aroma, visual appearance, texture, and consistency), able to produce antimicrobial compounds (H_2O_2, bacteriocins) to inhibits the growth of undesirable microorganisms, breakdown or inactivation of natural toxins (cyanogenic glucosides in cassava, mycotoxins in cereal fermentations) and anti-nutritional factors (phytates). To reach the intended demand for food products, scientists develop various methods of genetic or metabolic engineering for GMM production (Adrio and Demain, 2006). Table-1 represented various approaches genetic and metabolic engineering approaches to develop genetically modified microorganisms.

Table 1: A comparative account of the various genetic and metabolic engineering approaches involved in microbial food production.

Name of the microorganism	Engineering strategy	Highlight of the process	Outcome	References
Saccharomyces boulardii	CRISPR-Cas9	Production of auxotrophic mutants (*leu2, ura3, his3, and trp1*)	Heterologous expression of *lacZ* gene, human lysozyme, and xylose-assimilating pathway	Liu *et al.*, 2016
Lactobacillus plantarum	Overexpression	Overexpression of pyruvate carboxylase (PC), phosphoenolpyruvate carboxykinase (PEPCK), and malic enzyme (ME)	22-fold higher production of succinic acid	Tsuji *et al.*, 2013
Lactococcus lactis	Mutagenesis	Adaptive laboratory evolution (ALE) mediated mutagenesis	12% increased lactic acid production and also thermotolerant, useful for cheese production	Chen *et al.*, 2015
Aspergillus niger	CRISPR-Cas9	Deletion of the genes: gluconic acid (*GOX*) and oxalic acid (*OAH*) followed by overexpression of efficient C4-dicarboxylate transporter and a soluble NADH-dependent fumarate reductase	17 g/L succinic acid production	Yang *et al.*, 2020
Leuconostoc mesenteroides	Adaptive evolution	Mutation of ATPase ε subunit and upregulation of intracellular ammonia buffering system	70 g/L lactic acid, helpful for sauerkraut and pickles production	Ju *et al.*, 2016

Kluyveromyces marxianus	Rational engineering	Redirect the metabolic flux towards phenylalanine production	800 mg/L of 2-phenylethanol (2-PE)	Rajkumar, and Morrissey, 2020
Pichia pastoris	Heterologous expression	*Rhizomucor pusillus* glucoamylase (*RpGla*) gene was cloned in *Pichia pastoris*	1237 U/mL of thermostable gamma amylase, useful for baking products preparation	He *et al.*, 2014
Rhodotorula mucilaginosa	Mutagenesis and heterologous expression	Physical (ARTP)-chemical ($NaNO_2$)-physical (UV) mutagenesis followed by exogenous expression of 3-hydroxy-3-methylglutaryl coenzyme A (HMG-CoA) reductase (HMG1) from *S. cerevisiae*	19.14 mg/L	Wang *et al.*, 2017
Saccharomyces cerevisiae	Heterologous expression	*Kluyveromyces lactis* LAC4 (β-galactosidase) *and* LAC12 (lactose permease) genes cloned in *S. cerevisiae*	Ability to utilize lactose, useful for the production of baking products	Rubio-Texeira *et al.*, 2000
S. cerevisiae	Heterologous expression	Exogenous expression of cyclo-DOPA glucosyltransferase from *Mirabilis jalapa* in *S. cerevisiae*	16.8 ± 3.4 mg/L of betanin	Grewal *et al.*, 2018
Candida famata	Overexpression	Increased expression of GTP cyclohydrolase II (*RIB1*) and 3,4-dihydroxy-2-	Up to 28% riboflavin production	Petrovska *et al.*, 2022

Lactobacillus plantarum	Heterologous expression	Construction of pSIP expression vectors with the selection marker alanine racemase gene (alr) and utilized this to overexpress β-galactosidase genes from *L. reuteri* L103	Antibiotic marker free final food grade products formation and utilize lactose	Nguyen *et al*., 2011
Candida aaseri	CRISPR-Cas9	Elimination of six copies of acyl-CoA oxidases genes related to *β*-oxidation	60% efficient lipase-2	Hilmi Ibrahim *et al*., 2020
Lactobacillus brevi	Physiology-oriented engineering	F_0F_1-ATPase deficient strain NRA6 with higher glutamate decarboxylase system (GAD) activity	43.65 g/L GABA	Lyu *et al*., 2017
Escherichia coli	Heterologous expression	Expression of single chain monellin gene in *E. coli* under T7 promoter	50% enhanced production of monellin	Chen *et al*., 2005
Yarrowia lipolytica	Mutagenesis	Atmospheric and room temperature plasma (ARTP) mutation of *Y. lipolytica*	169.3 g/L erythritol	Liu *et al*., 2017
E. coli	Heterologous expression and overexpression	Glucansucrase gene (DSRLM34) from *Leuconostoc mesenteroides* LM34 overexpressed in *E. coli*	43.5% glucansucrase, used as a thickening agent in sucrose-supplemented milk	Kang *et al*., 2014
S. cerevisiae	Global transcription machinery engineering	Mutation of the transcription factor, *SPT15* gene (TATA	34.9% reduced production of ethanol, helpful for wine	Du *et al*., 2020

Y. lipolytica	Codon optimization and promoter engineering	Codon-optimized ? *6-desaturase* gene from *Mortierella alpina* was expressed in *Y. lipolytica* under the control of the strong promoter hp4d	60.9% gamma-linolenic acid (GLA)	Sun *et al.*, 2017
A. niger	Cre-*lox*P mediated gene editing	Expression of copies of oxaloacetate acetylhydrolase–encoding gene (*oah*A)	3.1-folds increment in malic acid	Xu *et al.*, 2019
Pediococcus acidilactici	Heterologous expression	Expression of feruloyl CoA synthetase (*fcs*) and enoyl CoA hydratase (*ech*)	4.01 g/L vanillin	Chakraborty *et al.*, 2017
P. acidilactici	Heterologous expression	Expression of synthetic *ala*D Gene cassette under the control of auto-inducible P289 promoter	217.54 g/L L-alanine	Sharma *et al.*, 2021

Various strategies of genetic and metabolic engineering are exploited for microorganisms-based food productions. Among these approaches, mutagenesis is the primitive one. Limited exposure of chemical or physical mutagenic agents (nitrosoguanidine (NTG), 4-nitroquinoline-1-oxide, methylmethane sulfonate (MMS), ethylmethane sulfonate (EMS), hydroxylamine (HA), and ultraviolet light) to microorganisms led to a change in their genetic makeup that ensure the production of a desired product (Mallikarjuna and Yellamma 2019, Deckers *et al.* 2020). CRISPR/Cas9 (clustered regularly interspaced short palindromic repeats/ CRISPR-associated protein 9) is one of the modern genome-editing tools, working with two primary components: a Cas9 endonuclease and a single chimeric guide RNA (sgRNA). The designed gRNA brings the Cas9 to the target site, allows it to execute a double-strand break (DSB) in the target DNA, followed by renovating this DSB by the host cell inherent repair system. This system permits Random insertions and deletions within the target sequence permits this system as a prolific apparatus to insert and delete desired genes (Kun *et al.*, 2020, Mondal *et al.*, 2022a). Promoters performs as a starter of transcription, regulating gene expression. Placing a strong promoter upstream of the apt gene allows the desired level of gene expression (Mondal *et al.*, 2022a). Codon bias is the basis of codon optimization, in which a specific codon among the other codons of an amino acid is utilized in a particular organism. When existing codon for an amino acid of a microorganism is altered with infrequent codons of that amino acid, resulting in ameliorated gene expression (Karaoglan and Erden-Karaoglan, 2020). A modern approach of mutagenesis is atmospheric and room-temperature plasma (ARTP) in which radio-frequency atmospheric-pressure glow discharge plasma is applied to execute a higher rate of mutation in the target cells while maintaining them at a low temperature (Ottenheim *et al.*, 2018). Adaptive laboratory evolution (ALE) is a mechanism to assess the evolutionary history of a microorganism in a regulated laboratory microenvironment. During ALE, a microorganism is cultivated under defined environmental conditions for prolonged time that allows the assortment of advanced phenotypes (Mavrommati *et al.*, 2021). Heterologous strain production dependent on the expression of a gene (to get favourable products) or fragment of it in a microorganism that does not have the gene in its genome naturally (Mondal *et al.*, 2022). Directed evolution mimic the process of natural evolution, and selected the mutants with preferable features from the mutant libraries. Two major tactics are usually adopted for directed evolution, either randomly recombining a set of similar sequences (e.g., gene shuffling) or introducing random changes in a particular protein sequence (e.g., error-prone PCR). The main advantage of directed evolution is that no previous structural knowledge is compulsory. However, the alterations are largely minor and require several rounds of evolution to produce a huge number of mutants. Finally, high-throughput experimental screening performed to recognize the mutants with required features (Schmidt *et al.*, 2019). Rational design based on the site-directed mutagenesis mediated mutation in a microbial genome and such mutation executed from the evaluation of biochemical, protein structural, and molecular modelling data. The primary benefit of the rational design tactic is a greater possibility of picking advantageous mutations, beneficial for easy screening within a shorter version of mutational library (Mondal *et al.*, 2022b). Still, majority of cellular and metabolic manipulation strategies are almost solely dependent on the removal or over-expression of single genes due to technological restrictions in vector creation, transformation competences, and screening proficiencies. In bacterial genetic system, sigma factors play a major role in recognition of promoter by RNA polymerase and initiation of transcription, thus sigma factors are chosen for mutation that allows the reprogramming of transcriptome at a global scale (Tan *et al.*, 2016; Du *et al.*, 2020). Cre (Cre recombinase) is one of the tyrosine site specific recombinases (first time isolated from the bacteriophage P1) and it identifies the specific DNA fragment sequences called *lox*P (locus of x-over, P1) site and facilitates site-specific excision of DNA sequences between two *lox*P sites (Kim *et al.*, 2018). Several editing tools are now available to reprogram microbial genome in order to achieve desired level of product but due to lack of knowledge regarding the microbial physiology; rate, titre, and yield-these three basic criteria, which are prerequisite to run any microorganisms-based industry are still challenging. In microbial physiological engineering, for successful accomplishment of genetic or metabolic engineering of a microbial strain following factors-cell growth, substrate utilization, metabolism ability, stress tolerance, and product transformation are strictly maintained (Liu *et al.*, 2021).

However, traditional probiotic strains face several challenges such as exposure to low pH during fermentation as well as in the human stomach, survival under oxygen concentration during refrigeration and storage, and persistence to gut microenvironment. Moreover, sensory acceptance of foods supplemented with probiotics to the consumer end is another prime concern to the industrialization of probiotics. Genetic or metabolic engineering of probiotic strains allows to overcome such impediments. The tailoring of conventional probiotics via genetic or metabolic engineering is not only improved their functional spectrum such as targeting pathogens or toxins, imitating cell surface receptors, boost immune system, add novel dimension to the drug or vaccine delivery system but also mitigates their pathogenic properties like introduction of antimicrobial resistance, infection. Table-2 represented various strategies to develop genetically and metabolically engineered probiotics.

Table 2: A comparative account of the various genetic and metabolic engineering strategies implicated in probiotic strains development.

Microorganism	Highlight of manipulation	Outcome	References
Saccharomyces boulardii	Expression of tetra-specific VHH (Single-domain variable fragments of heavy-chain antibodies) fusion (designated as ABAB)	Neutralizing *Clostridium difficile* exotoxins-TcdA and TcdB, responsible for mild diarrhea to fulminant colitis	Chen *et al.*, 2020
Lactococcus lactis	Expression of *L. lactis* hybrid receptor (HR) that was composed of the transmembrane ligand binding domain of CqsS (specific to *Vibrio cholerae* autoinducer CAI-1 and also modulates the histidine kinase receptors) and the signal transduction domain of NisK (a two-component receptor in *L. lactis* responsible for regulating the lantibiotic nisin production). Besides, the HR tagged with an upstream ribosome binding site (RBS), and a fluorescent protein mCherry followed by Glu-to-Gly mutation at residue 182 (HR4M) to detect CAI-1. Furthermore, introduced transcriptional repressor TetR downstream to the HR4M-regulated nisA promoter that allows constitutive repression of xylA-tetO promoter from engineered *Bacillus subtilis* and mCherry replaced with β-lactamase.	Manipulated *L. lactis* strain specifically identify quorum-sensing signals of *V. cholerae* in the gut and also *in situ* identify V. cholerae in the fecal samples	Mao *et al.*, 2018

Escherichia coli Nissle 1917 (EcN)	Exogenous expression of 3-hydroxybutyrate synthesis system comprising the *phaA*, $phaB_{TD}$, and *tesB* genes encoding acetyl-CoA acetyltransferase from *Cupriavidus necato*r H16, 3HB-CoA dehydrogenase from *Halomonas bluephagenesis* TD01 and thioesterase from *E. coli* MG1655 in EcN	Production of 2.9 g/L 3HB, that improved colitis	Yan *et al.*, 2021
E. coli Nissle 1917 (EcN)	Heterologous expression of multiple copies of *pheP* (phenylalanine-specific permease) and *stlA* (phenylalanine ammonia-lyase) under the regulatory control of the anaerobic-inducible promoter P_{fnrS}	Mitigates phenylketonuria	Isabella *et al.*, 2018
E. coli Nissle 1917 (EcN)	Expression of the gene *argA215*, encoding N-acetylglutamate synthase enzyme ArgA ($argA^{fbr}$) under the control of the *fnrS* promoter (P_{fnrS}) with the concomitant deletion of arginine repressor ArgR and thymidylate synthase gene *thyA*	Ameliorates hyperammonemia	Kurtz *et al.*, 2019

Saccharomyces cerevisiae	Following the directed evolution, express the human P2Y2 receptor incorporated in the yeast mating pathway by a chimeric yeast Gpa1–human $G\alpha_{i3}$ protein tagged with mCherry florescence repoter under the control mating-responsive FUS1 promoter	Alleviate inflammatory bowel disease by reducing pro-inflammatory extracellular ATP (eATP)	Scott *et al.*, 2021
E. coli Nissle 1917 (EcN)	Heterologous expression of an anti-biofilm enzyme, dispersin B (DspB) [glycosyl hydrolase activity] in an *E. coli* Nissle Δ*alr* Δ*dadX* strain	Avert *Pseudomonas aeruginosa* gut infection	Hwang *et al.*, 2017
Lactobacillus casei	Exogenous expression of the Listeria adhesion protein (LAP) from a non-pathogenic Listeria (*L. innocua*) and a pathogenic Listeria (Lm) on the surface of *L. casei*	Complete elimination colonization of *Listeria monocytogenes* (Lm) from gut, amends the Lm-mediated intestinal barrier dysfunction by blocking the nuclear factor-κB and myosin light chain kinase-induced redistribution of the major epithelial junctional proteins. Besides, it also rises intestinal immunomodulatory roles by employing $FOXP3^{+}T$ cells, $CD11c^{+}$ dendritic cells and natural killer cells.	Drolia *et al.*, 2020

E. coli Nissle 1917 (EcN)	Heterologous expression of *mchAXIBCDEF* (microcin H47) and the *ttrRS* (tetrathionate)	Inhibition of *Salmonella* induced gut inflammation	Palmer *et al.*, 2018
Lactobacillus gasseri	Heterologous expression of GLP-1 (glucagon-like peptide-1) under the control of SlpA promoter	Amend hyperglycemia by editing intestinal cells into glucose-responsive insulin-secreting cells	Duan *et al.*, 2015
E. coli Nissle 1917 (EcN)	Heterologous expression of GLP-1 GM [modified GLP-1 (7-37)] in EcN	Potential anti-obesity effect	Ma *et al.*, 2020
E. coli Nissle 1917 (EcN)	Heterologous expression of a series of expression cassettes: PROP-Z (programmable probiotics with lacZ) composed of both (i) an erythromycin-resistant luxCDABE cassette responsible to emit a luminescent signal from endogenous production of bacterial luciferin and luciferase and (ii) a pTKW106alp7A plasmid that introduce kanamycin resistance, isopropyl-β-D-thiogalactopyranoside (IPTG)–inducible lacZ expression, and an engineered plasmid maintenance system	Detect liver metastasis indication in urine	Danino *et al.* 2015

Lactobacillus reuteri	Heterologous expression of *agrCA* gene (*agr*QS) under the control of p3 promoter and also integrated the reporter gene GusA with the RBS site	Potential to detect autoinducer peptide-I (AIP-I), a quorum sensing molecule synthesized by *Staphylococcus aureus*	Lubkowicz *et al.*, 2018
E. coli	Exogenous expression of codon-optimized sequence for the A4 anti-CD47 nanobody with an C-terminal hemagglutinin tag in *E. coli*	Accelerates the activation of tumor-infiltrating T cells, induce rapid tumor regression, and inhibits metastasis	Chowdhury *et al.*, 2019
Lactobacillus lactis	Three antimicrobial peptides-Alyteserin, CRAMP and Laterosporulin, were genetically merged to a guiding peptide MM1 (multimerin-1, a protein expressed on the surface of human platelets), which specifically binds to Vacuolating Toxin A (VacA) of *Helicobacter pylori* and cloned 22 into an excretory vector pTKR inside L. lactis.	Prevent the growth of *H. pylori*	Chowdhury *et al.*, 2021

6. Future trends and Conclusion: It is crucial to understand the future demand of food from the consumer end and up to what extent of this demand is accomplished by the continuously flourishing microbial biotechnology. We have just statistically predicted the global population in the future few decades but we cannot properly estimate the quantity or quality of food we need and the amount of food we produce in future environmental situations. From the end of the 20th century, there is sudden change noticed in food behaviour of the people throughout the world, which may be due to their health consciousness, lack of time, and lots of physical or mental consequences related to modern-day life as well as the impact of global climate change. Although there is huge scope still to be open in the microbial world with currently operating genetic or metabolic manipulation approaches such as CRISPR/Cas9, rational strain engineering, adaptive laboratory evolution and high-throughput screening strategies along with futuristic technologies in this field should allow us to smoothly counter these challenges.

Diversity in microbial foods with food additives play an incredible role for our forthcoming generations in terms of providing nutritional requirements. Futuristic biomanipulated microorganisms will be swift in productivity at a reasonable cost, sufficiently specific to the target, measurable inside biological system with the suitable nutritional benefits and sensory features. Gradual genetic or metabolic manipulation in microorganisms makes them a resilient opponent to our regular custom of food harvesting from plant and animal sources. With the constant scientific advancement it will not so far away, when a major portion of our daily nutritional need fulfilled by microbial foods. Along with encountering our cumulative demand for food supply, it is also our paramount liability to strictly regulate food safety and quality. Attention is also enforced to regulate environmental issues to the manipulated microorganisms.

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