Review

Next-generation sequencing approaches for improvement of lactic acid bacteria-fermented plant-based beverages

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Abstract: Plant-based beverages and milk alternatives produced from cereals and legumes have grown in popularity in recent years due to a range of consumer concerns over dairy products. These plant-based products can often have undesirable physiochemical properties related to flavour, texture, and nutrient availability and/or deficiencies. Lactic acid bacteria (LAB) fermentation offers potential remediation for many of these issues, and allows consumers to retain their perception of the resultant products as natural and additive-free. Using next-generation sequencing (NGS) or omics approaches to characterize LAB isolates to find those that will improve properties of plant-based beverages is the most direct way to product improvement. Although NGS/omics approaches have been extensively used for selection of LAB for use in the dairy industry, a comparable effort has not occurred for selecting LAB for fermenting plant raw substrates, save those used in producing wine and certain types of beer. Here we review the few and recent applications of NGS/omics to profile and improve LAB fermentation of various plant-based substrates for beverage production. We also identify specific issues in the production of various LAB fermented plant-based beverages that such NGS/omics applications have the power to resolve.

Keywords: beer; cereal; fermentation; fruit juice; genomics; lactic acid bacteria; legume; metagenomics; soy; transcriptomics; wine
1. Introduction

Application of generally-regarded-as-safe or GRAS lactic acid bacteria (LAB) to fermented foods is typically done in pursuit of four goals: flavor modification (including production of alcohol), texture modification, increased nutritional quality (e.g., probiotic LAB strains), and improved food safety and stability (shelf-life). Wide-ranging literature review of these attributes and capacities of LAB in various food and beverage fermentations are performed with reasonable frequency, however, available data is skewed in two respects. First, the bulk of available data is physiological in nature for specific LAB strains, with many singular studies investigating metabolic characteristics of LAB fermentations under narrowly specific conditions. This results in limited understanding of the true microflora and metabolic capacities of LAB associated with these fermentations and stunted ability to identify appropriate starter strains and/or modifications to the fermentation environment in pursuit of improved product. Second, of all fermentations that LAB participate in, dairy fermentations are the most thoroughly studied, due in part to the long involvement of LAB in commercial production of liquid and solid milk products. Consequently, the dairy industry has been subject to the widest application of next-generation sequencing (NGS)/omics to the LAB involved (Table 1), yielding the benefit of well-developed and characterized starter cultures that allow for increased control and optimization of dairy fermentation processes.

Though LAB-fermented dairy products are well studied, milk alternatives produced from raw plant substrates are growing in popularity as increasing numbers of consumers now avoid dairy products for medical or ethical reasons [1,2]. Such dairy-alternatives can be produced from various cereal or legume sources; however, these substrates can have nutritional or qualitative shortcomings. For example, plant-based beverages can have anti-nutritional issues such as raffinose-family oligosaccharides (raffinose, stachyose, and verbacose), which can cause gastrointestinal discomfort, or phytic acid, which can reduce mineral availability. Most importantly, plant-based proteins may have poor digestibility and often lack some essential amino acids, such as lysine (cereals) or methionine (legumes) [3], and plant substrates may lose some of their water-soluble vitamins during processing [1]. Finally, plant-based milk alternatives can suffer from structural instability caused by a large amount of insoluble compounds like starch, proteins, and dietary fibre [4], to which LAB with their diverse oligosaccharide and protein degrading enzymes can offer remediation. Application of LAB to these products, and other functional beverages (such as those resulting from fruit and vegetable fermentations), thus can often improve upon these quality issues, while maintaining a label-free and natural status.
Table 1. Next-generation sequencing/omics approaches.

| Approach              | Aim                                                      | References^1 |
|-----------------------|----------------------------------------------------------|--------------|
| Genomics              | NGS sequencing of the DNA content of a single organism   | 17–22, 37, 62, 106 |
|                       | To understand the genetic content and coding capacity of a given organism |              |
| Functional genomics   | NGS sequencing or other means of interrogation of specific genes of known function in single organisms and/or a mixed microbial community | 82, 85 |
|                       | To understand the presence and distribution of functional genes or known genetic attributes within isolates or a microbial community |              |
| Metagenomics          | NGS sequencing of a mixed microbial community via sequencing a specific genetic marker (i.e., 16S rRNA amplicon) or the total DNA content of a community | 28, 39–44, 80, 81, 83, 84 |
|                       | To understand the composition (what microbial species are present) and complexity of a microbial community. Provides information as to potential metabolic capacity of the community |              |
| Transcriptomics       | NGS sequencing of mRNA transcripts of a single organism growing in a given condition | 23–25, 36 |
|                       | To understand what genes are expressed and/or required for growth or survival in a given condition |              |

^1 Examples of papers that have utilized the given NGS/omics approach.

In considering LAB in this context, two things must be remembered. First, production of beverages from grains and pulse crops starts with extracting constituents from milled raw material [1], which means that fermentation by LAB will often occur in higher consistency systems (e.g., slurries of raw substrate) than actual beverages. Second, LAB fermentation of milled raw plant materials to develop products with thicker consistency (e.g., yogurt-like non-dairy alternatives) is likely to grow in popularity in coming years. In order to tailor LAB fermentations to achieve desired outcomes, increased application of NGS/omics technologies is required to better understand the variable nature of LAB fermentations of different plant raw substrates from the perspective of what such fermentations can truly accomplish.

Interestingly, although LAB-fermented, dairy-alternative beverages are starting to have an increased omics-research focus, it is LAB involved in plant-based alcoholic beverages such as beer and wine that to date have received the most, albeit still limited, NGS/omics attention. Here we review the specific challenges related to LAB fermentation in production of different types of plant-based beverages - initially beer and wine, and then legumes, cereals, and fruit/vegetables. Additionally, where available, we present recent evidence for using NGS/omics approaches for improving the quality of the products involving LAB fermentation and indicate important future directions for such research.
2. Beer

The fermentation of barley, rye, or wheat grain to produce beer is arguably one of the oldest biotechnological processes carried out by humans [5], with perspectives on the role bacteria (and most importantly, LAB) play in brewing shifting over time. For instance, in the production of most beer products available on the market today, LAB are viewed as spoilage organisms, with *Lactobacillus brevis*, *Lactobacillus lindneri*, and *Pediococcus damnosus* being the most commonly encountered bacteria that spoil beer [6–10]. Ironically, however, the production of some beer styles, such as Lambic or Flemish sour beers, rely on the free entrance of all manner of microorganisms into the brew (an *open* fermentation) and/or requires purposeful addition of LAB to *sour* the beer by lowering the pH through acid production [11,12].

Given that LAB have long been viewed as beer-spoilage organisms, extensive literature is available that characterizes the spoilage characteristics of the bacteria involved. This includes detailed description of LAB-induced alterations of the sensorial profile of beer, such as off-flavour formation (diacetyl, acetoin), unwanted acidification, and haze and sediment formation [13]. Unfortunately, to date, the underlying genetic mechanisms of LAB beer spoilage have not been widely resolved, except for the production of rope or slime (exopolysaccharide) by various pediococci species via the *gtf* gene [14], and production of biogenic amines (BAs) by LAB in general [15,16].

Due to the significance of LAB as spoilage agents of beer, there has been a recent increase in sequenced brewing-related LAB genomes that are publicly available, including the genomes of five *Lactobacillus backii* isolates [17], *L. brevis* BSO 464 [18], *Lactobacillus malefermentans* KCTC 3548 [19], six *P. damnosus* isolates [20,21], and *Pediococcus clausenii* ATCC BAA-344T [22], as well as upwards of twenty publically available genome projects of isolates associated in some manner to the brewing environment (as of November 1, 2016, via NCBI). Application of transcriptomics to the virulent beer-spoilage organism *L. brevis* BSO 464 (capable of growing in packaged beer with dissolved CO₂ content/pressure) [23], and to beer-spoiling *P. clausenii* ATCC BAA-344T (can grow in partially degassed beer) [24] has revealed multiple insights into LAB genetic mechanisms in relation to beer-spoilage. And, more recently, both bacteria were analyzed for gene expression when grown in the presence of hops [25]. Notably, these transcriptomic analyses have shown that active metabolism of putrescine and histamine, multiple cellular membrane and wall modifications, and complex transcriptional regulation all occur during active LAB growth in beer. This transcriptomics data, in conjunction with multiple comparative genome studies, also indicates that pentose uptake and utilization of the pentose phosphate pathways is a significant niche adaptation of brewing-related LAB, which is perhaps not surprising given that these sugars are among the major nutrients remaining after yeast-fermentation is finished [23,25,26]. Thus, phosphotransferase systems (PTS) genes specific for gluconate and related to the pentose phosphate pathway distinguish beer-spoilage *L. brevis* strains from non-spoiling isolates [23,26]. In addition to transport proteins with specific action for hop iso-α-acids [9,27], the plasmid-harbored *fabZ* operon related to fatty acid synthesis can discriminate beer-spoilage *P. damnosus* strains [20]. Further, de novo folate synthesis genes have been found to be common to beer-related pediococci [21] and polygalacturonase, a gene involved in pectin metabolism (i.e., degradation of plant material)
distinguishes those isolates capable of growth in beer from isolates not capable of growth in beer [26]. Because of this research, the brewing field has advanced its ability to better identify LAB beer-spoilage strains.

Thus far, only one metagenomic sequencing study has been done in the brewery setting; i.e., on a mixed-culture-fermented beer [28]. However, other techniques such as marker gene detection and LAB-specific terminal restriction fragment length polymorphism have been used to profile the populations of LAB found throughout breweries over time [29]. Similarly, PCR-dependent denaturing gradient gel electrophoresis has been used to detect LAB populations during craft beer production [30]. These studies have revealed greater than anticipated LAB diversity and ubiquity within breweries. This, in turn, has interesting implications for improving process hygiene within the brewery setting and points to the likelihood of parallel LAB diversity in facilities used for production of other LAB-fermented plant beverages.

In an ironic twist, this recent genomics, transcriptomics, and metagenomics data has promise for application in efficiently selecting appropriate starter cultures for the craft fermentations leading to sour beers. As craft beers are emerging popular beverages, their commercial success represents an intriguing opportunity to profile LAB diversity, LAB and yeast co-fermentation, and LAB succession in beer. Further, given the general popularity of beer, opportunities exist to utilize NGS/omics approaches and available NGS/omics data to also improve the functional health (i.e., probiotic) properties of beer [5]. Given that LAB have proven capable of overcoming the harsh growth environment of beer, these bacteria are logical candidates to screen for potential probiotic function and to be involved in both future beer and health research. To date, however, no such follow-up research has been performed.

3. Wine

Although malolactic fermentation (MLF) by Oenococcus oeni is considered critical for quality wine production, other LAB in the genera Lactobacillus and Pediococcus can be detected throughout MLF in varying succession patterns [31]. Properties of enological LAB have been well studied, such as the glycosidase enzymes capable of liberating varietal aroma precursors [32,33] and the esterase enzymes that contribute to fruity aroma and flavour compounds [34]. Indeed, single LAB strains have been profiled for their specific enzymatic activities and the possible impacts on aroma profiles [35]. Despite the knowledge that interactions between yeast and LAB influence the modification of aroma compounds and overall MLF [34,36], only the genetics underlying O. oeni contribution to the taste of wine has been genomically characterized [31]. Indeed, the earliest and most extensive application of genomics technology to plant-based LAB fermentations occurred in the wine industry, with release of the O. oeni PSU-1 genome in 2005 [37]. This genomic analysis revealed much about the carbohydrate, nitrate, amino acid, and organic acid (citrate and malate) metabolism of this O. oeni isolate. Additionally, the possible stress response of O. oeni PSU-1 during growth was determined. Currently, over seventy O. oeni genomes and/or genomic projects are publicly available through NCBI [as of November 1, 2016]. At this point, investigation has evolved beyond the genomic study of single O. oeni isolates to include the production of a partial proteome reference map for O. oeni ATCC BAA-1163 [38]. This approach has pointed to important enzymes
and proteins coded by the core genome, as well as isolate-specific enzymes such as tributyrin esterase (putatively involved in the development of fruity flavor compounds) that require further investigation. Importantly, the writ large potential applications of the wealth of genomic information available for *O. oeni* will begin to be revealed only when coupled with transcriptomics analysis of the bacterium growing under different conditions.

Metagenomic studies have also increased in frequency within the wine industry subsequent to 16S amplicon sequencing being used to determine bacterial diversity in botrytized wine [39]. Similar sequencing methodologies have been employed since to reveal the effect of fermentation and biogeographical influence on both fungal and bacterial communities in grape and wine musts [40], as well as to show how cultivar, vintage and climate condition the microbial populations of wine grapes [41]. Very recently, this type of data has been used to assess the link between wine microbiota, fermentation success and wine properties with the goal of developing new early indicators of quality [42].

Influence of the soil microbiome on grapevine-associated microbiota has also been recently investigated [43], with the finding that the microbiota of leaf and grape correlated with soil carbon. The microbial profile of grape vines was influenced by multiple parameters, with the distribution of microbial taxa again observed to be influenced by biogeographic factors and vineyard management [43], further adding to the body of evidence that grape bacterial communities influence the organoleptic properties of regional wines. As well, metagenomic analysis of grape marc identified *Lactobacillus fabifermentans* as a key organism in the breaking down of residual complex carbohydrates into fermentable sugars during storage-fermentation for the potential production of distilled spirit beverages [44]. This bacterium has one of the largest LAB genomes yet sequenced and possesses a diverse carbohydrate utilization toolbox, with coding for complex gene expression regulation and biofilm formation as important adaptation features related to growth in (fermentation of) grape marc [44].

In addition to identified important carbohydrate, nitrogen, and enzymatic activity, which all contribute important flavour compounds to wine, undesirable metabolic activities of enological LAB have also been identified. For instance, *Oenococcus, Lactobacillus, Leuconostoc* and *Pediococcus* all can contribute to the histamine synthesis occurring during wine production [45]. Thus, the danger exists that BA-producing strains might be used as a MLF starter without prior knowledge of their BA-production potential. Consequently, the detection of histidine decarboxylase (or ornithine and/or tyrosine decarboxylase) genes by PCR or DNA probes is now done as a means of wine quality control [46], similar to hop-tolerance genes being screened for as an indication of spoilage-potential for LAB found in beer [47]. Research has also been conducted to identify the genes related to production in wine of ethyl carbamate, a known carcinogen [48], that can be manufactured by LAB in wine during MLF from precursors produced by arginine degradation, such as urea, citrulline, and carbamyl phosphate [48].

Overall, genomic data has clearly aided in the understanding the complex microbial process of wine production. This data, however, has yet to be tapped to streamline and improve the selection of LAB strains with probiotic potential. As with brewing-related LAB, enological LAB must contend with harsh environmental selection pressures such as high sugar content and low pH in grape must, and high ethanol, acidity, SO2 content, and limited nutrients in wine [31]; thus, it has been proposed
that these LAB may be potential probiotic candidates [49]. This research is within its infancy, with investigation of the in vitro immunomodulatory activities of \textit{O. oeni} and \textit{Pediococcus parvulus} finding that some \textit{O. oeni} strains have measurable immunomodulatory potential, though at a level below conventional probiotics [50]. Other results have documented the capacity of 11 wine-related LAB strains to resist lysozyme, gastric juice, and bile to be at levels equal or higher to those observed in the control probiotic strains \textit{Lactobacillus fermentum} CECT5716, \textit{Lactobacillus plantarum} CLC 17, and \textit{Pediococcus pentosaceus} CIAL-86A [51]. As with beer, further application of genetic profiling of candidate probiotic enological LAB can be expected to aid in the development of wine with better functional and even added probiotic properties.

4. Legume Beverages

Legumes, particularly soy, offer a popular alternative to traditional dairy products such as milk, yogurt, and cheese; thus, it is not surprising that multiple studies have been conducted analyzing the growth and metabolic behavior of LAB in soy milk [52,53]. Consequently, the general metabolic and physiological attributes of soy-fermenting LAB have been well established and demonstrated, however, there is limited available research on underlying genetic mechanisms. For instance, many LAB strains possess the metabolic tools to degrade raffinose-family oligosaccharides, a major anti-nutritive issue in legume foods, through $\alpha$-galactosidase activity of the \textit{mleA} gene [54,55,56]. Beyond the identification of this one gene, however, there is limited research on the genetics of raffinooligosaccharide degradation; furthermore, little is known about sequence variability and regulation of \textit{mleA}.

In a similar vein, it is known that the proteolytic specificities of LAB starters for cereal and legume proteins are quite diverse and differ from specificities towards milk proteins [54,57,58]. Despite this, little genomic characterization of these proteolytic activities has been performed. This contrasts with the well-studied proteolytic capabilities of LAB and their importance in sensory quality of dairy products [59]. Understanding the genetic mechanisms of proteolytic activity of LAB is important, as this ability can often be exploited to solve quality issues of fermentations. For instance, proteolysis of soy proteins can increase their digestibility or even prevent allergenic problems related to soy [57]. Furthermore, release of lysine from soy protein by some LAB can be used to supplement lysine-deficient cereal foods, thus making nutritionally complete soy-cereal products possible [57]. In this context, genomic, transcriptomic, and metagenomic analysis all have a role to play in selection of specific LAB strains for appropriate proteolytic activity.

Interest in soy beverage production has led to development of strategies to improve the health or nutritional value of product and, in this regard, genetic analysis of specific LAB strains is beginning to demonstrate benefits. For instance, the genetic characterization of riboflavin (vitamin B$_2$) biosynthesis pathway of \textit{L. fermentum} has been applied to fortify B$_2$ content in soy milk [60], and in soybean matrix by fermentation with a \textit{Lactobacillus reuteri} strain for which a genome sequence was recently published [61,62]. Other physiological studies that are worthy of genetic exploration include those which demonstrate that specific LAB and \textit{Bifidobacterium} strains improve specific health-related properties of soy, including increasing the antioxidant character [63] and the immunomodulatory bioactivity of LAB-fermented soy beverage on human intestinal epithelial cells [64].
As an alternative to soy and due to widespread availability, various legumes have been suggested as raw substrates for production of new plant-based beverages and semi-solid foods. For example, fermentation of lupine milk base with *Bifidobacterium animalis* and *L. plantarum* has been shown to obviate the issues posed by both the raffinose family of oligosaccharides and phytic acid, respectively, through degradation of these molecules [65]. Creation of yogurt-like consistencies through LAB fermentation of lupine milk also has been explored [66]. Such important quality improvements of legume substrates by LAB fermentation are paralleled in work where LAB fermentation in sourdough production and effect on phytic acids levels was explored, and phytate degradation by individual strains of *Lactobacillus sanfranciscensis*, *Lactobacillus pentosus*, and *L. plantarum* was found [67,68,69]. Also of note, peanut milk has been established as a suitable growth medium for the LAB yogurt starter cultures *Lactobacillus delbrueckii* subsp. *bulgaricus* and *Streptococcus thermophilus*, with fermentation by these organisms interestingly found to deplete n-hexanal, one of the compounds responsible for the undesirable green and beany flavor of peanut milk [70,71]. More recently, there has been report of increased antioxidant activity in peanut flour fermented with various *Bifidobacterium* and *Lactobacillus* strains [72]. Although not legume substrates, it should be noted that almond and hazelnut milks also have been demonstrated as potential platforms for fermentation by probiotic LAB strains [73,74]. Despite these promising studies, and the attractiveness of LAB fermentation to improve the quality of legumes (and nuts) for human consumption, the genetics of LAB in relation to these substrates remains uncharted territory.

### 5. Cereal-based Beverages

Cereal-based, fermented beverages and foodstuffs are traditional and important dietary staples worldwide; see [75] for a comprehensive summary of traditional LAB-fermented cereal foods found in diverse geographic locations, the cereal substrates used, and the LAB involved. Another recent review [2] discusses how LAB can improve cereal-based functional beverages. Despite in-depth and wide-ranging study of metabolic and functional attributes, an unknown degree of variability in the genetics and metabolic capacity of participating LAB remains.

Development of defined LAB starter cultures is of key interest for cereal-based fermentation as it allows for improved product quality, as noted for *Kununzaki* (a non-alcoholic Nigerian beverage) [76,77], with the use of a defined starter culture resulting in a beverage with improved nutritional quality, aroma, and taste relative to the product produced with spontaneous cultures. However, it has been noted that the replacement of spontaneous or back-slopped starter cultures with defined starter cultures or single strains can result in different sensorial profiles and/or the loss of important flavor characters in cereal-based products [78], specifically so when yeast are not included in the *designer* starter culture [78,79]. To circumvent this uncertainty, application of metagenomic analysis should be used to initiate the appropriate genomic characterization of natural starters, leading to an understanding of the specific organisms (and their genetic attributes) necessary for successful fermentation such that appropriate designer cultures can be defined.

Recent successful applications in this regard include the metagenomic characterization of the yeast-LAB population for improved production of Chinese rice wine, with the study also demonstrating that product spoilage resulted from the rapid growth of *L. brevis* too early in the
fermentation [80]. Metagenomics analysis of the microbial diversity of xaj-pitha (also a rice wine) has assisted the development of a suitable fermentation starter culture for this beverage [81], and sequence-based screening approaches have been used to select for rice wine starter cultures with reduced capacity to form BA [82]. Similar analysis of the bacterial diversity and community profile of a traditional fermented Chinese yellow rice wine indicated that LAB comprised a considerably smaller proportion of the population than expected, and that there may be associated safety issues with the microbial community present [83]. Metagenomics have also been used to profile which members of the microbial community of rice wine are responsible for production of volatile compounds in rice wine [84]. Furthermore, functional genomics has been used to analyze fermented pearl millet slurry, a base for several foods in Western Africa, targeting amylolytic, vitamin production, and probiotic survival-related genes to assess the technological potential of the naturally occurring flora [85]. Finally, expression of several amylolytic genes in a L. plantarum isolate has been monitored during fermentation of pearl millet slurry [86], providing insight into the required metabolic capacity of LAB during fermentation of this plant substrate.

While metagenomic analysis gains traction within the field of cereal-based beverages, an emerging area of interest is application of this technology to profile the capacity of LAB to produce exopolysaccharides which can be used to improve product texture and stability, as has been studied extensively at the genetic level for sourdough [87,88]. Recently, Russo et al. [89], demonstrated increased initial viscosity of a fermented oat product by using a genomically characterized potential probiotic L. plantarum Lp90 [90]. Other studies have utilized a sequenced strain of Weisella cibaria MG1 in production of barley- and soybean-based products to improve both mouth-feel and structural stability [91,92,93]. As with legumes, the raw substrate, geographic location, and LAB microflora involved will influence the functional utility of a LAB isolate to a considerable degree. Thus, the genetic characterization of participating LAB is essential for improving specific attributes of each beverage type produced.

6. Fruit and Vegetable Juices

Fermented fruit and vegetable juices have favourability and popularity with consumers of all ages and thus make ideal functional beverages. Importantly, raw fruit and vegetable substrates contain beneficial nutrients such as minerals, vitamins, dietary fibers, and antioxidants, and do not contain dairy allergens [94,95]. LAB fermentation of fruit and vegetable substrates can improve levels of desirable flavour compounds and enrich for specific metabolites (e.g., lactic acid, amino acids), while minimizing negative flavour compounds and detoxifying pathogens [96,97]. However, much remains to be answered about the genetic qualities of LAB that confer appropriate properties to fruit and vegetable-fermented products.

As with cereal-based beverages, fruit and vegetable juices substrates are heterogeneous and diverse, with properties differing across geographic location and fermentation/storage conditions; nonetheless, the general microbial profile of various fruit and vegetable juices have been characterized and reviewed [98]. Many physiological studies are available which have examined production of probiotic juices using a variety of different substrates and LAB strains: orange, pineapple, and cranberry juices with Lactobacillus casei, Lactobacillus rhamnosus and Lactobacillus
paracasei [99]; mango juice [100] and noni juice [101] with L. plantarum; tomato juice [95] with Lactobacillus acidophilus, L. casei, L. delbrueckii, and L. plantarum; red beets with L. acidophilus and L. plantarum [102]; and cabbage juice with L. delbrueckii and L. plantarum [103]. In some cases, more detailed analysis has been performed; e.g., the gene-expression of L. plantarum in carrot and pineapple juices was studied via micro- and macro-array platforms to understand physiological processes involved in adaptation to the specific juice environment [104,105] and the importance of carbohydrate and amino acid metabolism regulation, acid tolerance, and pH control was shown. Recent application of genomics and metagenomics have also occurred, with the recent genome announcement for a Leuconostoc mesenteroides strain isolated from the Mexican fermented beverage Pulque [106] then allowing for possible probiotic properties associated with this organism to be unravelled [107]. The genome of Lactobacillus farcimis, the key organism in the Japanese fermented health beverage kōso, has recently been released, underpinning future studies of this bacterium’s probiotic and interesting proteolytic capabilities [108]. The same authors have also used metagenomic analysis to profile the microbial community throughout kōso fermentation [109]. This analysis revealed the community to be markedly diverse and notably different from the community profile revealed using traditional culture methods, importantly showing that difficult-to-culture bacterial species participate in this fermentation [109].

While metagenomics has begun to reveal specific characteristics of LAB fermentation, it was noted previously that the microflora of juice (and other products) establish in the following sequence as fermentation progresses and growth inhibitory qualities increase in strength: non-fermentative psychrotrophic Gram-negative bacteria → fermentative Gram-negative bacteria → LAB → yeasts → filamentous fungi [110]. Thus, one area that has been explored physiologically is how LAB from fruit might be exploited for production of anti-fungal compounds, as has been shown for L. fermentum, L. plantarum, and spoilage fungi in tomato fruit [111], and for other LAB strains in plum, pear, and grape models [112]. A detailed description of the anti-fungal compounds produced has not been made and, most importantly, their production by LAB has not been genetically characterized. The result is that screening of LAB for production of antifungal compounds is still reliant on laborious large-scale growth and physiological studies.

### 7. Conclusions

Plant-based beverages produced via LAB fermentation can consist of a nearly infinite number of compositions and associated issues. This means the LAB involved must possess specific capacities to confer desirable (improved) properties to these beverages. Selecting appropriate LAB and/or developing designer LAB starter cultures for such fermentations can only be done with detailed knowledge of attributes individual LAB possess. In this context, the identification and basic characterization of the native microbial flora involved in spontaneously fermented foods and then determining their individual isolate metabolic capacity through traditional microbiology research is a useful starting point. Available nucleotide sequencing technologies then have the power to rapidly reveal important genetic detail for the LAB involved in these fermentations; to date, however, there has been limited output of such research. Nonetheless, in the few instances where NGS/omics have been applied, the data obtained clearly reveal the limitations of traditional metabolic and
physiological studies to fully describe complexity of LAB metabolic processes taking place during the fermentations used to produce plant-based beverages. This is clearly exemplified within the fields of brewing and oenology, wherein application of genomic and transcriptomic techniques has demonstrated benefit for increasing the ability to not only rapidly screen for spoilage LAB organisms, but importantly to also provide genetic information that can be used for product innovation through LAB fermentation. NGS/omics data obtained for brewing and enological LAB thus has the potential to not only assist in increasing the functional attributes of beer and wine, but also the expanding assortment of plant-based beverages in general. Through increased application of currently available genomics, transcriptomics, and metagenomics technologies to the LAB used in the production of diverse plant-based beverages, better product outcomes for LAB fermentation can be achieved, regardless of the raw plant substrate involved.

Conflict of Interest

All authors declare no conflicts of interest in this study.

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