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Metagenomic Comparison of Homemade and Commercial Kimchi Prepared in Korea and the United States

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ABSTRACT

It is well known that there is a myriad of factors that determine the kimchi microbial composition during fermentation, including but not limited to, salt concentrations, temperature, raw ingredients, and even manufacturing processes. Because different environments breed different species of microorganisms, the location of where raw ingredients were cultivated can also affect the kimchi microbiota. Previous studies have shown that there is a significant difference in microbial composition between kimchi from different countries, but none has been made between homemade kimchi. Seven samples of homemade kimchi from the US and South Korea (equally made under the same fermentation conditions) and commercial kimchi were used in the study. High differences in genera relative abundances between Korean and the US homemade kimchi could be concluded. The results also exhibited differences in microbial composition and diversity levels between Korean and the US commercial kimchi. This study provides further insight into understanding the complexity of how kimchi microbiome is developed by having the results support the idea that the environment where raw ingredients originate from affect the kimchi quality and taste.

Introduction

One of the most consumed side dishes in Korea is kimchi. Not only is kimchi affordable and a famous trademark representing Korean traditional food, but it also boasts numerous health benefits including, but not limited to, anti-cancer, anti-oxidative, and anti-obesity effects, and can treat constipation and forestall growth of food poisoning bacteria (Lee, S.H. et al., 2020; Park et al., 2014). Although these effects are a result of fermentation, over-fermentation can, in reverse, degrade the nutritional quality of kimchi, so it is recommended to consume kimchi within the first 3 months of storage where its nutritional content is at its best (Thilakarathna et al., 2021).

The intricate interactions between the fermentation process, lactic acid bacteria (LAB) strains, and the ingredients used to make kimchi (e.g., garlic, salt, ginger) are highly responsible for the health benefits that kimchi proudly possesses (Lee et al., 2011). During fermentation, LAB strains undergo metabolism to produce organic acids, H_2O_2, and bacteriocins that prevent the proliferation of pathogenic bacteria such as *Enterotoxigenic Escherichia coli* (ETEC) (Lee et al., 2021; Park et al., 2014). LAB strains have previously shown the ability to enrich the immune system, produce bioactive substances, and even lower cholesterol levels (Lee et al., 2011). Additionally, to name a few in terms of ingredients, alline and allicin in garlic have antibacterial and antiviral effects (Borlinghaus et al.,2014), capsaicin in chili powder prevents obesity (Jiraungkoorskul et al., 2017), sitosterol available in kimchi cabbage (*baechu)* lowers blood cholesterol (Miettinen & Vanhanen, 1994), and diallyl sulfide in onions exhibit anti-aging effects (Bastaki et al., 2021). In fact, kimchi probiotic effects can be even more enhanced by slightly manipulating ingredient concentrations as well as fermentation conditions (e.g., temperature, starters) (Park et al., 2014). For example, it is recommended to use 2.5%-3.0% salt in kimchi for anticancer and antimutagenic effects (Park et al., 2014).

Additionally, acidity levels, which help eliminate pathogenic bacteria, tend to increase more rapidly at higher fermentation temperatures (Lee et al., 2021).

Because kimchi fermentation is catalyzed by a complex system of microbiota (Lee, S.H. et al., 2020), the composition of the microbiome community changes at various fermentation stages (Kim et al., 2022) and is heavily influenced by kimchi raw ingredients (Zhang et al., 2021). It is interesting to note that microbiota from different habitats evolve distinctly at various rates, leading to significant differences in species diversities between habitats; hence, environmental conditions affect evolutionary patterns (Li et al., 2014). Therefore, the geographical region where kimchi cabbage, or any other raw ingredient, was cultivated may impact the microbiota in kimchi. This will affect the presence of LAB strains which will then ultimately determine the taste of kimchi (Lee et al., 2011). This may explain the differences in taste between kimchi fermented in the US (Florida) and in Korea. Although the comparison of microbial communities in commercial kimchi manufactured in Korea, China, and the United States has been reported before (Yun et al., 2021), there is no report yet on the comparison of microbial composition between homemade kimchi prepared in Korea and other countries. In this study, metagenomic analysis was performed to determine differences in the microbial composition with 7 samples of kimchi prepared in two countries (Korea and US) and/or with different raw ingredients: 4 samples in Korea (2 homemade, 2 commercial) and 3 samples in Florida (1 homemade, 2 commercial).

Methods

Preparation of Kimchi Samples

Homemade kimchi in Korea (KH1 & KH2) and Florida, USA (UH1) were prepared in private houses with local materials. KH1 and UH1 were prepared using the same amounts of raw ingredients, but KH2 was prepared with a greater amount of onion, chili powder, ginger, and mashed garlic and a lesser amount of green onion than KH1 (Table 1). All kimchi cabbages used for homemade kimchi were salted for 1 hour and 45 minutes before adding the rest of the ingredients. All homemade kimchi was refrigerated (2~4.5℃) for 3 days, stored at room temperature for 1 day, and refrigerated again for 1 day. Afterwards, approximately 20 to 100mL of kimchi liquid was extracted from each sample and stored in the freezer. A final ten mL of thawed kimchi liquid from each sample was used for the metagenomic analysis of the bacterial community.

Two kinds of commercial kimchi manufactured at the local factory were purchased from a local store each from the USA and Korea: Woo Sung Oriental Food Mart in Orlando, Florida and iCoop Nature Dream in Daejeon, South Korea. Kimchi from Woo Sung Mart was kept at room temperature for 1 day before being refrigerated for another 3 days. Approximately 100mL of kimchi liquid was extracted and stored in the freezer until transported to the laboratory in South Korea. Kimchi from Nature Dream was stored in the refrigerator until 5 days after its production. Approximately 20mL of kimchi liquid was then extracted from each sample and stored in the freezer until usage. Same as the homemade kimchi, a final 10mL of kimchi liquid from each commercial kimchi sample was used for the metagenomic analysis of the bacterial community.

In total, 7 samples of kimchi were used for this experiment: 2 Korean commercials (KC1 and KC2), 2 Korean homemade (KH1 and KH2), 2 US commercials (UC1 and UC2), and 1 US homemade (UH1).-All kimchi samples used for this study were naturally fermented and not inoculated with starter cultures.

Table 1. Amount of the raw ingredients used for homemade kimchi preparation.

Samples	USA Homemade (UH1)	Korea Homemade #1 (KH1)	Korea Homemade #2 (KH2)
Onion	34.0 g	34.0 g	51.5 g
Green Onion	7.7 g	7.7 g	1.7 g
Chili Powder	1.5 tbsp*	1.5 tbsp	4.5 tbsp
Glutinous Rice Porridge	2.0 tbsp	2.0 tbsp	2.0 tbsp
Kimchi Cabbage	187.0 g	187.0 g	187.0 g
Mashed Garlic	0.5 tbsp	0.5 tbsp	1.5 tbsp
Anchovy Fish Sauce	1.0 tbsp	1.0 tbsp	1.0 tbsp
Mashed Ginger	0.5 tsp**	0.5 tsp	0.5 tbsp
Salt-fermented Shrimp	0.5 tbsp	0.5 tbsp	0.5 tbsp

* tbsp = 1 US tablespoon (= 3 US teaspoon)
**tsp = 1 US teaspoon

DNA Extraction

Before extracting DNA from the kimchi samples, 10mL of each sample was centrifuged at 190xg for 20 minutes at room temperature. The supernatants were decanted into new conical tubes to discard the precipitated kimchi debris and were centrifuged again at 8000xg to obtain microbial pellets. The conical tubes were vortexed to resuspend the microbial pellets. DNA extraction was executed using the DNeasy PowerSoil Pro Kit (USA) according to the manufacturer's instructions.

Amplicon PCR Amplification and Purification

The DNA extracts from each kimchi liquid were used as the template for amplicon-PCR with reaction mixture containing a barcoded primer set: 341F (5'-TCG TCG GCA GCG TCA GAT GTG TAT AAG AGA CAG [CCT ACG GGN GGC WGC AG]-3') and 805R (5'-GTC TCG TGG GCT CGG AGA TGT GTA TAA GAG ACA G[GA CTA CHV GGG TAT CTA ATC C]-3'), specific to the V3-V4 regions of 16s ribosomal RNA gene and the EF-Taq PCR Smart mix 1 (SolGent, Korea). PCR was performed using the following conditions. First, the sample DNAs were denatured by heating at 95°C for 3 minutes in a thermal cycler, MyGenie96 Thermal Block (Bioneer, Korea). Subsequently, the solutions were heated at 95℃ for 30 seconds, 55℃ for 30seconds, 72℃ for 30 seconds for 25-30 cycles and finally held at 72℃ for 5 minutes before being stayed at 4℃. The amplified PCR products were purified using the QIAquick PCR Purification Kit (USA) according to the manufacturer's instructions.

Metagenome Amplicon Sequencing and Taxonomic Analysis

Amplified DNA fragments were analyzed by agarose gel electrophoresis and purified with the QIAquick PCR Purification Kit (Quiagen, USA) according to the manufacturer's instructions. Purified PCR products were sent to Macrogen, South Korea for metagenomic amplicon sequencing (MAS). For taxonomic analysis of the MAS results, rRNA gene sequences from the mitochondria, chloroplast, eukaryote, and archaea were removed by using Mothur pipeline v.1.43.0 (Ref K1) and the rest of the pairs were assembled and aligned. Cleaned high-quality reads were taxonomically assigned using the classify.seqs function in Mothur pipeline with SILVA database (Ref K2).

Statistical Analysis

Statistical analysis of microbial composition was performed using R software (ver. 4.2.0) to assess R values by using ANOSIM (999 Permutations) (Lee et al., 2017).

Results

Metagenome Amplicon Sequencing and Taxonomic Analysis

Agarose gel electrophoresis of the PCR products from each kimchi sample revealed the expected size of ca. 550 bp (data not shown) and gave 67 ~ 98 ng/ul of DNAs after purification. Total amplicon sequencing read pairs were aligned and assembled with paired reads sequenced from each amplicon fragment. As shown in Table 2, the numbers of finally used reads at profiling analysis were ca. 65,000 ~ 171,000.

Table 2. Number of sequencing and preprocessed reads.

Samples	Total sequencing read pairs	Number of assembled reads*	Number of used reads at profiling analysis
KC1	**234,320**	**128,275**	**65,018**
KC2	210,545	123,652	67,815
KH1	155,458	107,113	66,180
KH2	239,628	144,695	78,928
UC1	266,459	174,019	171,346
UC2	250,649	170,801	168,107
UH1	242,846	137,664	90,830

* Assembled reads: The reads were aligned and assembled with paired reads sequenced from each amplicon fragment.

Profiling analysis of the amplicon sequences from kimchi samples revealed bacterial community with various levels of taxonomic groups (Table 3): 6 phyla (with 1 unclassified phylum), 7 classes (with 1 unclassified class), 30 families (with 5 unclassified ones), and 50 genera (with 16 unclassified ones and 1 uncultured one). The genera of relatively abundant bacteria, which showed more than 10% of relative abundances at least once, were *Bacillus*, *Lactobacillus*, *Leuconostoc*, *Pantoea*, and *Weissella*. Interestingly these abundant genera except *Pantoea belonged* to the

**_un: unclassified.

class Bacilli in phylum Firmicutes, while genus *Pantoea belonged* to family Enterobacteriaceae of class gamma-proteobacteria in phylum Proteobacteria. The genus *Lactobacillus* was detected as a relatively abundant genus in all cases regardless of localization and method of kimchi manufacturing. The genus *Leuconostoc* was detected in 3 samples (KC1, KC2, and UH1). The genus *Weissella* was detected in 2 samples (KH1 and KH2). The genus *Bacillus* and *Pantoea* were detected in one sample each (KC1 and UH1, respectively).

Microbial Composition of Commercial Kimchi

The genera with the highest level of abundances for KC1 and KC2 were *Leuconostoc* (KC1: 52.24%, KC2: 56.64%) and *Lactobacillus* (KC1: 23.07%, KC2: 33.87%). *Weissella* and *Bacillus* marked up 3.54% and 15.76% respectively in KC1. As for KC2, the relative abundances for *Weissella* and *Bacillus* were 3.47% and 1.36%, respectively. Again, these two and *Leuconostoc* and *Lactobacillus* had the highest relative abundances in KC2. For commercial kimchi

samples from the US, the *Lactobacillus* genus was the highest relatively abundant (UC1: 98.37%, UC2: 98.38%) for both UC1 and UC2. The microbial community for US commercial kimchi was primarily composed of *Lactobacillus*. Other genera that made their appearances to the surface are *Weissella* (UC1: 0.11%, UC2: 0.22%) and *Leuconostoc* (UC1: 0.30%, UC2: 0.33%). Overall, there was a strong difference (R=1, ANOSIM) in microbial composition between commercial kimchi from both countries, and results showed that US commercial kimchi had very narrowed diversity in kimchi microbiota compared to that of Korea.

Microbial compositions of commercial kimchi samples were similar to each other within the same regions yet different between regions as can be seen in **Figure 1**. KC1 and KC2 exhibited heavily similar percentage distributions between *Weissella*, *Leuconostoc*, and *Lactobacillus*, with the only noticeable difference in *Bacillus*. UC1 and UC2 also revealed particularly similar percentage distributions in their microbial compositions for *Lactobacillus*, *Weissella*, and *Leuconostoc*. Interestingly, *Lactobacillus* weighed over 98% for both samples, which were also the greatest percentages out of the seven samples. However, other genera that were noticeably present in KC1 and KC2, such as *Weissella*, *Leuconostoc*, and *Bacillus*, were barely present in the US commercial kimchi samples. In short, relative abundances were spread amongst multiple genera in Korean commercial kimchi samples while it was spiked chiefly at the *Lactobacillus* genus in US commercial kimchi samples. Although further statistical analysis for microbial diversity is required, the results shown here reveal the high contrast in diversity between Korean and US commercial kimchi, with the latter displaying less diversity than Korean commercial kimchi.

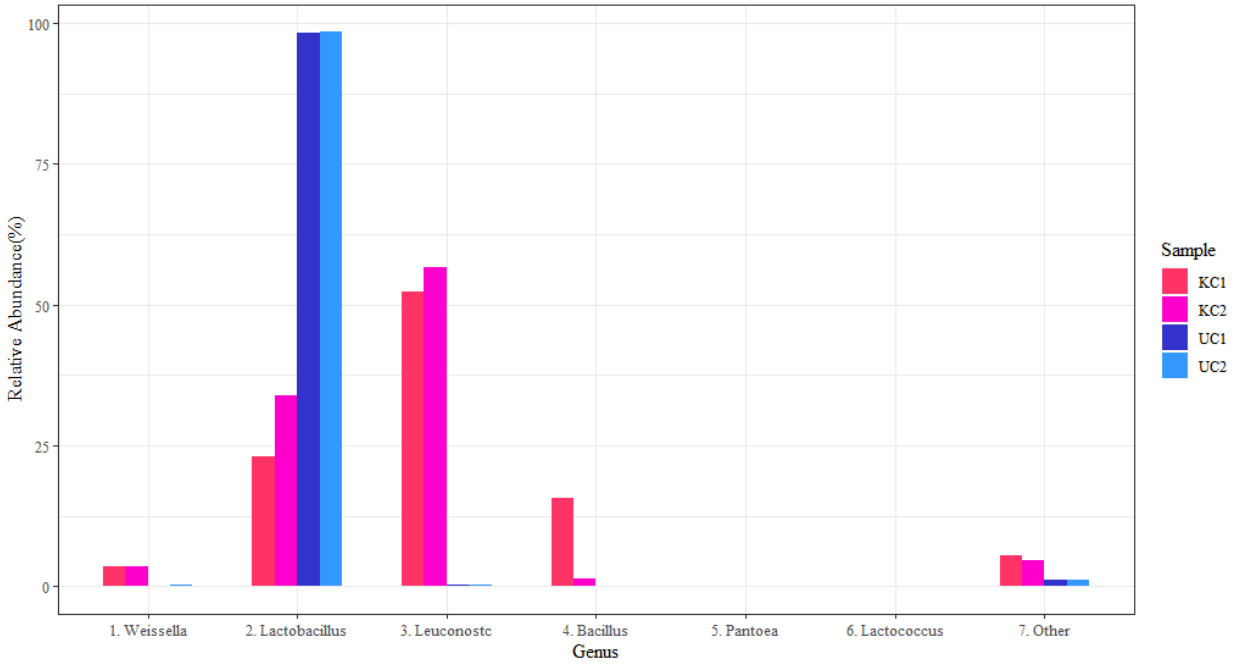

Figure 1. Comparison between Korean and US commercial kimchi genera relative abundances. Samples of the same association (e.g., KC1 and KC2 are both Korean commercial kimchi) were used with similar colors.

Table 3. Relative abundances of genus group in kimchi samples

Phylum	Class	Family	Genus	Relative Abundance (%)*						
				KC 1	KC 2	KH 1	KH 2	UC 1	UC 2	UH 1
Actino-bacteria	Actino-bacte-ria	Micrococcaceae	*Kocuria*	0.07	0.00	0.00	0.00	0.01	0.00	0.00
			Micrococcaceae_un	0.00	0.00	0.00	0.00	0.00	0.00	0.00
		Sanguibacteraceae	*Sanguibacter*	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria _un**	Bacteria _un	Bacteria_un	Bacteria_un	0.00	0.00	0.00	0.00	0.04	0.06	0.03
Bactero-idetes	Bacteroidia	Flavobacteriaceae	*Flavobacterium*	0.02	0.00	0.00	0.00	0.00	0.00	0.00
		Weeksellaceae	*Chryseobacterium*	0.05	0.00	0.00	0.00	0.00	0.00	0.00
		Sphingobacteriaceae	*Pedobacter*	0.01	0.01	0.00	0.00	0.00	0.00	0.00
			Sphingobacterium	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Cyano-bacteria	Oxyphoto-bacteria	Cyanobiaceae	*Synechococcus* _CC9902	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes	Bacilli	Bacillaceae	Bacillaceae_un	2.17	0.06	0.00	0.00	0.00	0.00	0.01
			Bacillus	**15.76**	1.36	0.05	0.00	0.00	0.00	0.12
			uncultured _Bacillaceae	0.00	0.00	0.00	0.00	0.00	0.00	0.00
		Bacillales_un	Bacillales_un	0.12	0.00	0.00	0.00	0.00	0.00	0.00
		Paenibacillaceae	Paenibacillaceae_un	0.00	0.04	0.00	0.00	0.00	0.00	0.00
		Staphylococcaceae	*Staphylococcus*	0.00	0.00	0.03	0.00	0.00	0.00	0.07
		Bacilli_un	Bacilli_un	0.55	3.03	0.00	0.00	0.00	0.00	0.32
		Enterococcaceae	Enterococcaceae_un	0.02	0.01	0.00	0.00	0.00	0.00	0.00
			Tetragenococcus	0.00	0.09	0.00	0.00	0.00	0.00	0.00
		Lactobacillaceae	Lactobacillaceae_un	0.00	0.00	0.01	0.02	0.00	0.01	0.00
			Lactobacillus	**23.07**	**33.87**	**17.22**	**34.50**	**98.37**	**98.38**	**20.07**
		Lactobacillales_un	Lacto-bacillales_un	1.26	0.56	1.01	1.81	0.89	0.77	0.22
		Leuconostocaceae	***Leuconostoc***	**52.24**	**56.64**	0.68	2.23	0.30	0.33	**62.68**
			Leuconos-toca-ceae_un	0.48	0.55	2.64	6.14	0.03	0.00	0.20
			Weissella	3.54	3.47	**74.95**	**55.05**	0.11	0.22	0.06
		Streptococcaceae	*Lactococcus*	0.00	0.00	3.28	0.14	0.01	0.02	0.00
			Streptococcaceae_un	0.00	0.00	0.00	0.03	0.02	0.00	0.00
Proteo-bacteria	Alpha-proteobacteria	Caulobacteraceae	*Brevundimonas*	0.13	0.02	0.00	0.00	0.00	0.00	0.00
		Beijerinckiaceae	*Methylobacterium*	0.02	0.00	0.00	0.00	0.03	0.02	0.00
		Rhizobiaceae	*Aureimonas*	0.12	0.00	0.00	0.00	0.03	0.03	0.00

			Rhizobiaceae_un	0.09	0.02	0.00	0.00	0.03	0.02	0.00
		Rhizobiales_un	Rhizobiales_un	0.00	0.00	0.00	0.00	0.02	0.00	0.00
		Xanthobacteraceae	Xantho-bacteraceae_un	0.02	0.00	0.00	0.00	0.00	0.00	0.00
		Sphingomonadaceae	*Sphingomonas*	0.00	0.00	0.00	0.00	0.01	0.01	0.00
	Gamma-proteobacteria	Burkholderiaceae	Burkholderiaceae_un	0.09	0.00	0.00	0.00	0.00	0.00	0.00
			Herbaspirillum	0.02	0.00	0.00	0.00	0.00	0.00	0.00
		Methylophilaceae	*Methylophilus*	0.01	0.00	0.00	0.00	0.00	0.00	0.00
		Enterobacteriaceae	*Enterobacillus*	0.00	0.00	0.00	0.00	0.00	0.00	0.00
			Enterobacter	0.00	0.04	0.00	0.00	0.00	0.00	0.00
			Entero-bacteri-aceae_un	0.04	0.08	0.02	0.07	0.00	0.01	3.50
			Klebsiella	0.00	0.00	0.10	0.00	0.00	0.00	0.00
			Lelliottia	0.00	0.00	0.00	0.00	0.03	0.02	0.00
			Nissabacter	0.00	0.00	0.00	0.03	0.00	0.00	0.00
			Pantoea	0.00	0.00	0.00	0.00	0.00	0.00	**12.72**
			Pectobacterium	0.03	0.00	0.00	0.00	0.00	0.00	0.00
			Rahnella	0.00	0.03	0.00	0.00	0.00	0.00	0.00
		Moraxellaceae	*Acinetobacter*	0.00	0.00	0.00	0.00	0.00	0.01	0.00
			Psychrobacter	0.00	0.00	0.00	0.00	0.00	0.00	0.00
		Pseudomonadaceae	*Pseudomonas*	0.04	0.11	0.00	0.00	0.00	0.00	0.00
		Vibrionaceae	*Vibrio*	0.00	0.00	0.00	0.00	0.07	0.09	0.00
		Xanthomonadaceae	*Stenotrophomonas*	0.01	0.00	0.00	0.00	0.00	0.00	0.00

* Fractions lesser than 0.01% were denoted as 0.00, bigger than 1% were marked with blue gray background, greater than 10% were emboldened, and the greatest were underlined.

Microbial Composition of Homemade Kimchi

Effect of Localization on Microbial Composition

Both KH1 and KH2 exhibited *Weissella* (KH1: 74.95%, KH2: 55.05%) and *Lactobacillus* (KH1: 17.22%, KH2: 34.50%) to be the most abundant genera. *Lactococcus* and *Leuconostoc* had the third highest relative abundances in KH1 (3.28%) and KH2 (2.23%), respectively. UH1 presented results unique to the other samples in that it was the only sample with *Pantoea* that constituted the kimchi microbiome at least 1.00%. The *Leuconostoc* genus was the most prevalent in UH1 with a relative abundance of 62.68%, the second being *Lactobacillus* with an abundance of 20.07%, and the third being *Pantoea* with an abundance of 12.72%.

The distributions of relative abundances between Korean and US homemade kimchi were different (R=1, ANOSIM). The comparison and variances are depicted by **Figure 2**. The most abundant genus in KH1 and KH2 (*Weissella*) was barely found at all in UH1, and the most abundant genus in UH1 (*Leuconostoc*) was either the third or fourth most abundant in the two Korean homemade kimchi samples. In short, genera that were abundant in KH1

and KH2 did not take up as many proportions in UH1 and *vice versa*. Overall, the distribution of genera relative abundances was different based on homemade kimchi samples from the US and in Korea.

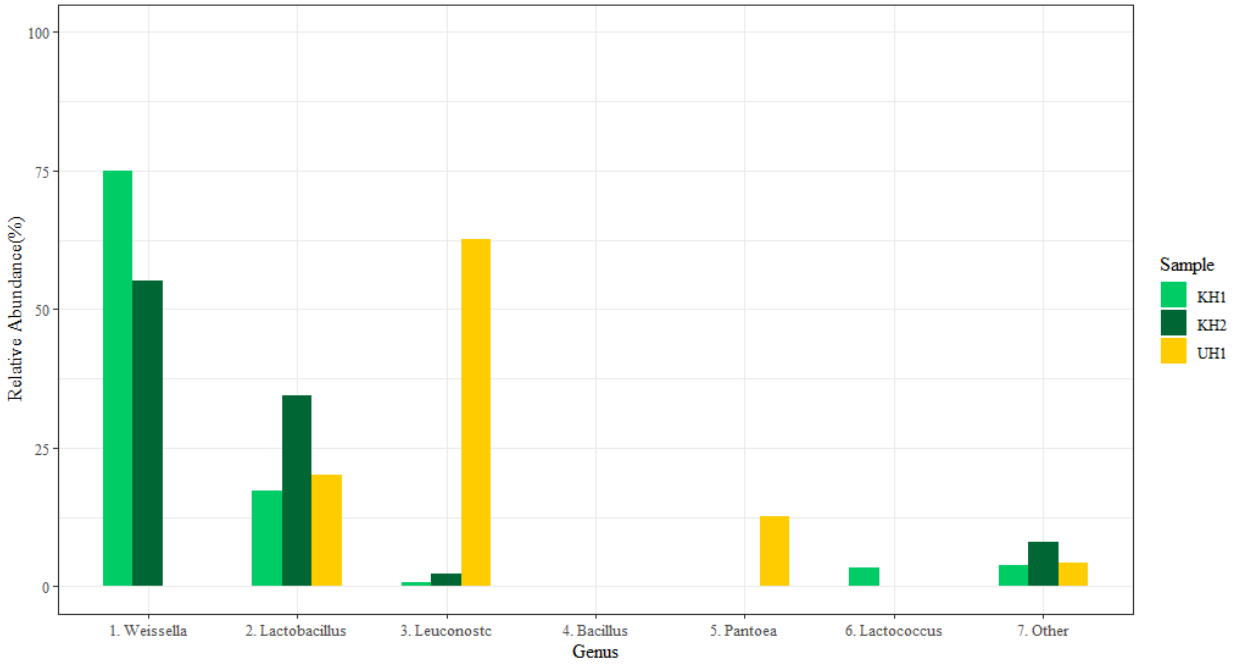

Figure 2. Comparison between Korean and US homemade kimchi genera relative abundances

Effect of Raw Ingredients on Microbial Composition

The distribution of genera relative abundances in KH1 and KH2 noticeably resembled each other (**Figure 2**). *Weissella* was the highest relatively abundant genus for both samples, with *Lactobacillus* coming as second. KH1 displayed a higher relative abundance in *Weissella* and *Lactococcus* than KH2, but a lower relative abundance in *Lactobacillus* and *Leuconostoc*. The exceptionally similar relative abundance distributions between KH1 and KH2 indicate similar diversity levels within the microbial communities. Although the highest relatively abundant genera were consistent with each other in both samples, there were slight differences within the proportions that may explain the effects of different concentrations of raw ingredients on the kimchi microbial community.

Discussion

Our results show significant differences in microbial composition between Korean and US commercial kimchi. The same goes as well for US and Korean homemade kimchi. While the significant difference in microbial composition between US and Korea commercial kimchi could be attributed to different manufacturing processes and types of raw ingredients as well as each amount used, the contrast between Korean and US homemade kimchi (KH1 and UH1) microbiota supports the idea that the environment where raw ingredients were cultivated does impact the kimchi microbiome and hence, the quality and taste of it. Evolution and evolution rates happen distinctly and independently between different environments (Li et al., 2014), indicating that the same types of raw ingredients from completely different environments will have unequal microbial compositions, supporting these results. The differences in microbial composition in kimchi depending on the location where it was manufactured are consistent with previous studies (Lee, H.-W. et al., 2020; Yun et al., 2021).

Furthermore, the differences in relative abundances for certain genera between KH1 and KH2 can be explained by the different amounts of specific raw ingredients used. KH2, which used more ginger and chili powder, revealed a higher proportion of *Leuconostoc* than KH1, consistent to the previous study that ginger and red chili powder prompts growth of *Leuconostoc* bacteria (Yi et al., 1995). However, our result that KH2 had a lower proportion of *Weissella* despite using more red chili powder is inconsistent with another previous study that the amount of red chili powder used positively correlates with the relative abundance of *Weissella* (Jeong et al., 2013). Although there may be differences in terms of genera relative abundances between our results and previous studies and additional studies are necessary, the idea that different concentrations of raw ingredients affect the metabolic activity of microorganisms and presence of LAB strains is supported.

Generally, our results were consistent with the previous study that *Lactobacillus*, *Leuconostoc*, and *Weissella* are the most found lactic acid bacteria strains in kimchi (Lee, S.H. et al., 2020). Compiling the results and information from above, the amount of raw ingredients used did affect the kimchi microbiota, but the environment where kimchi was fermented had an even greater impact. This can be used to evaluate and assess unique health qualities for kimchi produced all around the world in different environments. Previous studies state that Korean commercial kimchi is highly antioxidant and shows more diversity in microbial composition compared to kimchi made in China and the US (Yun et al., 2021). Chinese kimchi had a relative abundance of *Lactobacillus* up to 70%, higher than that of the United States and Korea, while US kimchi had a lower relative abundance level for *Weissella* than the other two countries (Yun et al., 2021). *Lactobacillus* is known for having traits such as antioxidant and anticancer effects (Choi et al., 2006), and *Weissell*a is known for its anti-obesity and anti-inflammatory effects (Kwak et al., 2014), meaning that kimchi fermented in the US, Korea, and China have healthy characteristics unique to their country's kimchi. Kimchi, whether commercial or homemade, breeds various microbial communities depending on where it was fermented and as a result can have varying health benefits. Although further studies are necessary, the insights achieved from this study help support the idea that the environment where raw ingredients come from, and the amount used play an important role in developing the kimchi microbiota.

Conclusion

In this study we compared genera relative abundances between 7 kimchi samples to assess any differences in microbial composition between kimchi that were made in different environments. There were high differences amongst Korean and the US kimchi microbiota, regardless of if it was commercial and homemade. The amount of raw ingredients used also influenced kimchi microbiome though not to the extent of the location where the raw ingredients were cultivated. This study provides further insight into the complexity in how kimchi microbial composition is developed by multiple variables during fermentation.

Limitations

This study has some limitations in that more samples of each group of kimchi (e.g., Korean homemade) could have been experimented for improved statistical analysis and better precision.

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