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RESEARCH ARTICLE

Evaluation of microbiological quality and safety of fresh-cut fruit products at retail levels in Korea

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Abstract The risk of foodborne illnesses caused by pathogens could be increased in fresh-cut fruit products owing to contamination during processing. Therefore, this study was conducted to investigate the microbiological quality and safety of commercial fresh-cut fruit products in Korea. Additionally, the growth of *Listeria monocytogenes* in selected fresh-cut fruits was evaluated, and their growth curves were analyzed using predictive growth modeling. The mean count of total aerobic bacteria, coliforms, and yeast/mold was 3.67±1.73 $\log_{10}$ CFU/g, 1.54±1.01 $\log_{10}$ CFU/g, and 3.81±1.51 $\log_{10}$ CFU/g, respectively. *Escherichia coli, Staphylococcus aureus, Escherichia coli* O157:H7, *L. monocytogenes*, *Salmonella* spp., and *Cyclospora* spp. were not detected in any of the tested samples. Only *Bacillus cereus* was detected in a few samples at the mean level of 1.72±0.13 $\log_{10}$ CFU/g. The growth *of L. monocytogenes* varied depending on the type of fruit; they grew well in non-acidic fresh-cut fruit products during storage at 10 °C.

Keywords Fresh-cut fruit products · Microbiological quality · Microbial safety · Low temperature storage · Predictive growth modeling

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Introduction

Consumption of fruits has been recommended by various organizations such as the World Health Organization (WHO), as they contain abundant dietary fiber, vitamins, minerals, and phytochemicals and are low in calories (Singla et al., 2020). According to the Ministry of Agriculture, Food and Rural Affairs (2020), the per capita fruit consumption in Korea was 56.6 kg in 2019 and has been steadily over 55 kg since the 2000s. Specifically, the consumption of fresh-cut fruit products has recently increased significantly owing to the development of processing technology, a busy lifestyle, and the increase in single-person households. According to the Korea Rural Economic Institute (Kim, 2019), the sales of domestic fresh-cut foods in 2018 reached 181.7 billion—an annual increase of 22.9% compared to 2008 and a 7.9-fold increase in 10 years. Between 2016 and 2017, it increased by 48.3%. The consumption of fresh-cut fruit products will continue to increase owing to the expansion of online markets, the availability of early morning delivery services, an increase in fresh produce at convenience stores, and the appearance of customized fresh-fruit products.

Pathogenic microbial contamination of fresh produce, including fruits, may occur from farm to table (Paramithiotis et al., 2017). From 2010 to 2017, 1,797 food-borne

outbreaks were caused by pathogenic microorganisms in the USA, of which 228 (12.7%) were attributed to fresh produce (CDC, 2018). Based on the incidence of foodborne outbreaks in fresh-produce historically, the pathogens of concern are *Salmonella* spp., *Escherichia coli* O157:H7, *Shigella* spp., *Listeria monocytogenes,* Norovirus, and pathogenic protozoa (Juneja and Sofos, 2009). In the USA, foodborne outbreaks associated with fresh produce were listeriosis from contaminated cantaloupe in 2011 and salmonellosis from cantaloupe, mango, tomato, and papaya in 2011–2017 (Carstens et al., 2019); *Salmonella* enterica serovar Enteritidis infection from peaches (CDC, 2020); and *E. coli* infection from berries (strawberries and raspberries) and apple juice in 2004–2012 (Callejón et al., 2015). Additionally, in the USA, during 2013–2017, intestinal infection caused by the parasite *Cyclospora cayetanensis* was linked to a salad mix that contained lettuce, romaine lettuce, red cabbage, carrot, and coleslaw (Buss et al., 2016; Fox, 2017).

In particular, the risk of foodborne illnesses caused by pathogens could be increased in fresh-cut fruit products because they could be contaminated with pathogens during processing, such as peeling, slicing, and packaging (Gombas et al., 2017). Additionally, the growth of pathogens in fresh-cut fruit products can be enhanced by nutrients in the fruit cells exposed during the peeling and cutting processes (Qadri et al., 2015). Contamination of foodborne pathogens in fresh-cut fruit products has been recently reported; for example, *L. monocytogenes* in cut apples and melons in Canada (Zhang et al., 2020) and *Bacillus cereus* in cut apples in Korea (Tango et al., 2018). Nevertheless, studies on the microbial contamination of fresh-cut fruit products are limited. Furthermore, information on microbial contamination assessment of related products should be provided to ensure the microbial safety of fresh-cut fruit products distributed in retail. Therefore, in this study, microbial contamination in a total of 100 fresh-cut fruit products in Korea was evaluated to investigate the microbiological quality and safety (general microbial contamination, pathogenic bacteria, and *Cyclospora* spp.) of these products. Further, the growth of *L. monocytogenes* as a psychrotrophic pathogen in four fresh-cut fruit—products (watermelon, orange, green kiwi, and melon) during—storage at 10 °C was investigated, and the growth curves were analyzed via predictive growth modeling using the modified Gompertz equation to determine its growth rate and lag time on fresh-cut fruits.

Materials and methods

Sampling of fresh-cut fruit products

A total 25 different types of mixed or single-packaged fresh-cut fruit product were evaluated in this study. Each product was evaluated in 5 repetitions therefore a total of 100 samples were analyzed by collecting 25 samples of 5 varieties for each season. The samples tested are shown in Table 1. All samples were purchased online as commercial products and analyzed on the day of purchase. The collected fruit samples for each season were influenced by their availability in the Korean market at the time of sampling.

Quantitative microbial risk assessments

To evaluate the microbial prevalence in fresh-cut fruit products, 25 g of fresh-cut fruit product samples were homogenized in sterile filter stomacher bags (Difco Laboratories, Detroit, MI, USA) containing 100 mL of Butterfield's phosphate-buffered dilution water (BPDW, Difco Laboratories), and each sample bag was stomachered (BagMixer 400, Interscience, Breteche, France) for 90 s.

Total aerobic bacteria (TAB), *E. coli*/coliforms (EC), and yeast/mold (YM) were analyzed using a petrifilm aerobic count plate, petrifilm EC count plate, and petrifilm YM count plate (3M, Seoul, Korea), respectively. The sample suspensions were diluted with 0.2% sterile peptone water (PW, Difco), and 1.0 mL of the aliquots was placed on three different petrifilms. The petrifilms were incubated at 37 °C overnight for TAB and EC and at 30 °C for 48 h for YM. For *B. cereus* and *S. aureus*, 0.1 mL of the aliquots was inoculated on mannitol egg yolk polymyxin agar (MYP, Difco) and Baird-Parker agar (BPA, Difco) and incubated at 30 °C for 24 h and 37 °C for 48 h, respectively. When presumptive colonies with typical shapes for each pathogen were determined, colonies were confirmed by 16S rRNA sequencing (SolGent Co., Daejeon, Korea) (Ponsawat et al., 2012).

Qualitative microbial risk assessments and identifications

Foodborne pathogenic bacteria

The microbial prevalence of *B. cereus*, *E. coli* O157:H7, *L. monocytogenes*, *Salmonella* spp., and *S. aureus* was investigated qualitatively using the methods described in the Korean Food Code with some modifications (MFDS, 2021a). Briefly, 25 g of samples were enriched in 225 mL tryptic soy broth (TSB, Difco) supplemented with 10% NaCl, modified tryptone soy broth (mTSB, Microgiene Co., Gunpo-si, Korea), BPDW, and buffered peptone water (BPW, Difco) at 37 °C for 24 h, and Listeria enrichment broth (LEB, Difco) at 30 °C for 24 h. For isolation of *B. cereus* and *L. monocytogenes*, pre-enrichment samples were inoculated on MYP and Oxford agar base (OAB, Difco), respectively, and incubated at 30 °C for 24 h. For

Table 1 Quantitative (log_{10} CFU/g) of bacterial count isolated from seasonal fresh-cut fruit products

Season	Sample	Raw material	Type of microorganism[1]					
			TAB	Coliform	*E. coli*	Y/M	*S. aureus*	*B. cereus*
Winter (February-March)	1	Cherry tomatoes, grapes, pear	3.42 ± 1.06^{2ef3}	0.76 ± 0.13^{e}	ND[4]	3.15 ± 0.64^{cd}	ND	ND^{b}
	2	Apple, cherry tomatoes, grapes	3.82 ± 1.12^{def}	3.51 ± 0.61^{a}	ND	1.56 ± 1.92^{e}	ND	ND^{b}
	3	Pineapple	ND^{g}	ND^{e}	ND	3.73 ± 0.25^{bcd}	ND	ND^{b}
	4	Apple, grapes, pear	4.67 ± 0.92^{abcd}	ND^{e}	ND	1.72 ± 0.59^{e}	ND	ND^{b}
	5	Apple, dragon fruit, grapes, green grapes, green kiwi, orange, pineapple, tomatoes	1.24 ± 0.45^{g}	0.70 ± 0.00^{e}	ND	3.16 ± 0.42^{cd}	ND	1.70 ± 0.00^{b}
Spring (April-May)	6	Pineapple	0.82 ± 0.27^{g}	ND^{e}	ND	6.77 ± 0.33^{a}	ND	ND^{b}
	7	Apple, dragon fruit, grapes, green kiwi, orange, pineapple	4.74 ± 0.70^{abcd}	0.91 ± 0.47^{e}	ND	6.22 ± 0.76^{a}	ND	ND^{b}
	8	Apple, cherry tomatoes, grapes, pineapple	4.06 ± 0.23^{cdef}	1.96 ± 1.57^{c}	ND	6.31 ± 0.77^{a}	ND	ND^{b}
	9	Cherry tomatoes, grapes, green kiwi, pineapples, sweet persimmons	2.95 ± 2.33^{f}	1.06 ± 0.37^{de}	ND	3.38 ± 0.28^{bcd}	ND	ND^{b}
	10	Apples, cherry tomatoes, grapes, green kiwi, oranges, pineapples, sweet persimmons	3.07 ± 0.56^{ef}	1.72 ± 0.55^{cd}	ND	4.23 ± 0.16^{bc}	ND	ND^{b}
Summer (June-July)	11	Apple, citrus, dragon fruit, grapes, green kiwi, orange, pineapple, tomatoes	3.52 ± 0.82^{def}	1.13 ± 0.40^{de}	ND	3.68 ± 0.36^{bcd}	ND	2.08 ± 0.47^{a}
	12	Pineapple	1.24 ± 0.48^{g}	0.70 ± 0.00^{e}	ND	4.49 ± 0.43^{b}	ND	1.70 ± 0.00^{b}
	13	Melon	5.05 ± 0.97^{abc}	2.89 ± 1.06^{ab}	ND	3.25 ± 1.11^{cd}	ND	ND^{b}
	14	Melon	5.78 ± 0.64^{a}	2.10 ± 0.33^{bc}	ND	4.00 ± 0.35^{bcd}	ND	ND^{b}
	15	Watermelon	5.46 ± 0.82^{ab}	2.54 ± 0.89^{bc}	ND	3.28 ± 0.28^{cd}	ND	ND^{b}
Fall (August-October)	16	Orange, pear	4.28 ± 0.30^{bcde}	0.98 ± 0.17^{de}	ND	2.89 ± 0.96^{d}	ND	ND^{b}
	17	Grapes, pear	3.70 ± 0.52^{def}	ND^{e}	ND	2.91 ± 0.47^{d}	ND	ND^{b}
	18	Melon, tomatoes	5.50 ± 0.61^{a}	2.36 ± 0.41^{bc}	ND	2.85 ± 1.23^{d}	ND	ND^{b}
	19	Melon, watermelon	4.26 ± 0.44^{bcde}	2.13 ± 0.62^{bc}	ND	4.48 ± 0.54^{b}	ND	ND^{b}
	20	Dragon fruit, fig, watermelon	5.13 ± 0.68^{abc}	2.51 ± 0.49^{bc}	ND	3.85 ± 0.94^{bcd}	ND	ND^{b}
Total			3.67 ± 1.73	1.54 ± 1.01	ND	3.80 ± 1.51	ND	1.72 ± 0.13

[1] Detection limit was 0.7 log_{10} CFU/g for TAB (total aerobic bacteria), coliforms, *E. coli,* and Y/M (yeast/mold) and 1.70 log_{10} CFU/g for *S. aureus*, and *B. cereus*, respectively.

[2] Means ± standard deviation (n = 5).

[3] Means with no significant difference among the same lowercase letters in the same column ($P > 0.05$).

[4] ND: not detected

E. coli and *S. aureus*, the samples were placed on Tellurite Cefixime-Sorbitol MacConkey Agar (TC-SMAC, Difco) and BPA, respectively, and incubated at 37 °C for 24 h. For *Salmonella* spp., 0.1 mL of BPDW enrichment was transferred to 10 mL of Rappaport-Vassiliadis R10 (RV, Difco) and incubated for an additional 24 h at 42 °C. Another 1.0 mL of the sample was added to 10 mL of tetrathionate broth (TB, Difco) and incubated at 37 °C for

24 h. Then, the enriched samples of RV and TB were streaked on xylose lysine deoxycholate (XLD, Difco) and incubated at 37 °C for 24 h. For *S. aureus* and *B. cereus*, presumptive colonies with typical shapes for each pathogen were confirmed by 16S rRNA sequencing (SolGent Co., Daejeon, Korea) (Ponsawat et al., 2012).

Cyclospora

The presence of *Cyclospora* was determined by real-time PCR (RT-PCR, GeneMate, Bioexpress, Kaysville, UT, USA) using the method of the Korean Food Code (MFDS, 2017, 2019, 2021a). Fifty grams of fresh-cut fruit products was placed in zipper bags (S. C. Johnson & Son, Inc., Seoul, Korea), and 100 mL of 0.1% liquinox™ (Alconox Inc., White Plains, NY, USA) and 0.01 M phosphate buffered saline (PBS, pH 7.4) were added. The samples were shaken at 160 rpm for 15 min using an orbital shaker (OFD 300, Best of Lab Equipment, Seoul, Korea) and passed through a 200–250 µm mesh sieve. Subsequently, the supernatant was discarded by centrifugation at 8,000 rpm for 20 min, and this process was repeated twice. The pellet was resuspended in 40 mL PBS and centrifuged at 2,500 rpm for 20 min and then at 5000 rpm for 10 min. The final pellet was resuspended in 200 µL PBS, and DNA was extracted according to the manufacturer's instructions using the QIAamp DNA Mini Kit 50 (Qiagen, Hilden, Germany). The method used for sample preparation and DNA extraction for detecting *Cyclospora* in this study has been tested in previous studies (Murphy et al., 2017; Shelds et al., 2013). The extracted DNA served as a template for RT-PCR, and positive DNA control of *Cyclospora* (PRA-3000SD) was purchased from ATCC (The Global Bioresource Center, Manassas, VA, USA). PCR reaction mixtures included 12.5 µL TaqMan Universal Master Mix II with UNG (2×, Applied Biosystems, Carlsbad, CA, USA), 1 µL primer (F), 1 µL primer (R), 5 µL distilled water, and 5 µL template DNA. The primer sequences were as follows: primer (F) sequence to 5′-GCA GCA TGG AAT AAT AAG ATA GGA CC-3′ and primer (R) sequence to 5′-CGC AGT AGT TCG TCT TTA ACA AAT CTA AG-3′. The RT-PCR conditions consisted of 2 min at 50 °C for UNG incubation, 10 min at 95 °C for denaturation, followed by 40 cycles at 95 °C for 15 s and 60 °C for 1 min, and extension at 72 °C for 5 min. The PCR products were confirmed by 2% agarose gel electrophoresis (Mupid-exU, Advance, Tokyo, Japan).

Growth kinetics of *L. monocytogenes* on fresh-cut fruits

Preparation of bacterial strains

L. monocytogenes was tested in this study because it is a psychrophilic pathogen therefore suitable for microbial growth prediction at cold temperature as a major foodborne pathogen although *L. monocytogenes* was not detected in any tested samples. *L. monocytogenes* has been used as the target bacteria for the growth prediction models in various foods including fruits at cold temperature in previous studies (Hong et al. 2014; Marik et al. 2020). *L. monocytogenes* ATCC 7644, 19114, and 19115 were obtained from the bacterial culture collection of Chung-Ang University (Anseong-si, Korea). All stock cultures were maintained at – 80 °C in 20% glycerol and activated by cultivation in TSB supplemented with 0.6% yeast extract (TSBY) at 37 °C for 24 h. To prepare cocktails, each culture of *L. monocytogenes* was mixed equally and harvested by centrifugation at 10,000 rpm for 10 min. The pellet was washed with 0.2% PW and diluted to a final concentration of 2–3 log CFU/mL.

Microbial growth on fresh-cut fruits

To evaluate the effect of pH values on the growth of *L. monocytogenes* at cold temperature, four types of fruits, watermelon, navel orange, green kiwi, and melon were selected and tested in this study. Watermelon (*Citrullus lanatus*), navel orange (*Citrus sinensis*), green kiwi (*Actinidia deliciosa*), and melon (*Cucumis melo var. cantalupensis*) were purchased from a local grocery store (Anseong-si, Korea) and stored at 4 °C until further use. All fresh fruits were washed with tap water for 30 s, dried in a laminar flow biosafety hood, and cut into similar sizes. Each fresh-cut fruit was inoculated with 0.1 mL of *L. monocytogenes* cocktail suspension and dried in a laminar flow biosafety hood for 30 min for attachment of the tested bacteria. Inoculated fresh-cut fruits were stored in polyethylene terephthalate (PET) containers individually at 10 °C for 8 days to observe the growth kinetics of the tested microorganism. After storage, samples were diluted (1:2) in 0.2% PW and homogenized for 90 s in a stomacher. Then, 0.1 mL of the aliquots was placed on OAB and incubated at 30 °C for 24 h.

Predictive modeling

Reliable estimates of the growth rate (GR) and lag time (LT) of *L. monocytogenes* on fresh-cut fruits were obtained using the primary model (Prism, version 4.0, GraphPad Software, San Diego, CA, USA). The growth kinetics were

fitted using the modified Gompertz equation (Gibson et al., 1998):

$$Y = N_0 + C \cdot \exp[-\exp\{(2.718 \cdot \mu/C) \cdot (lag - X) + 1\}]$$

where Y is the log cell number ($\log_{10}$ CFU/g), N_0 is the initial cell number (log CFU/g), C is the difference between initial and final cell numbers, X is the storage time (h), μ is the maximum rate of GR (log CFU/h), and lag is the delay before growth (LT, h).

Statistical analysis

The experiments were repeated thrice with duplicate plates, and the data were analyzed using the Statistical Analysis System (Version 9.1; SAS Institute, Cary, NC, USA) or Excel 2010 (Microsoft Office XP; Microsoft, Redmond, WA, USA). Significant differences ($P \leq 0.05$) among the mean values of the treatment groups were determined by analysis of variance (ANOVA) and Duncan's multiple range tests or Student's *t*-test.

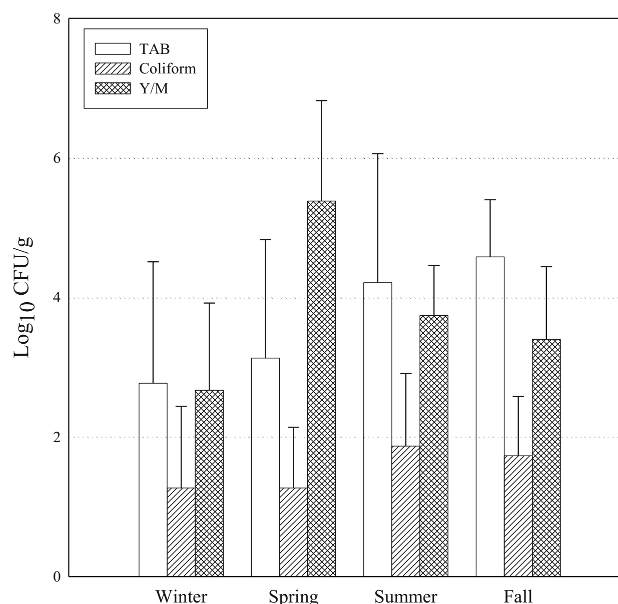

Fig. 1 Mean ($\log_{10}$ CFU/g) of microbial count isolated from seasonal fresh-cut fruit products. TAB (□), Coliform (▨), and Y/M (▩)

Results and discussion

Quantitative microbial risk assessments

A total of 100 packaged fresh-cut fruit products were collected for bacterial analysis. Of these, 30% contained a single kind of fruit, mainly grapes, pineapples, melons, and watermelons; 40% of the samples contained less than three kinds of fruits; and 30% of the samples consisted of four or more kinds of fruits. The most commonly used fruits were grapes, pineapples, apples, and cherry tomatoes. Samples containing a single fruit were most common in summer, whereas samples containing more than four kinds of fruits were common in winter and spring. Further, samples containing melons and watermelons were produced only during summer and fall. All fresh-cut fruit products were labeled according to their country of origin; 70% of the products contained imported fruits, which included grapes from Chile, Peru, the USA, and the Philippines; oranges from Australia and the USA; green kiwi from New Zealand; and dragon fruit from Vietnam. All samples were taken before the expiration date, and no visible signs of decay were observed. Nevertheless, consumption of produce with pathogens, in the absence of any signs of decay, leads to food-borne illness (Qadri et al., 2015).

Table 1 and Fig. 1 show the mean levels of TAB, coliform, *E. coli*, YM, *S. aureus*, and *B. cereus* in fresh-cut fruit products by season. The mean TAB count of the 100 samples was 3.67±1.73 $\log_{10}$ CFU/g. The mean TAB in winter samples was 2.77±1.74 $\log_{10}$ CFU/g. Similar numbers (3.13±1.70 $\log_{10}$ CFU/g) were also found in spring samples. The mean TAB counts in summer and fall samples were 4.21±1.85 $\log_{10}$ CFU/g and 4.58 ± 0.82 $\log_{10}$ CFU/g, respectively; therefore, the mean TAB in summer and fall samples was relatively higher than that in winter and spring samples but was not significantly different ($P > 0.05$). The expiration date of fresh produce is generally considered unsuitable when the TAB population reaches 7 $\log_{10}$ CFU/g (López et al., 2008). In this study, the TAB levels in all fresh-cut fruit products tested were less than 7 $\log_{10}$ CFU/g. Nevertheless, the results are not completely satisfactory, as TAB levels above 6 $\log_{10}$ CFU/g were detected in six samples (8%). In the case of sample 9, TAB was higher than 6 $\log_{10}$ CFU/g in only one out of the five replicates. Conversely, for samples 13, 14, 15, 18, and 20, high levels of TAB were detected in all five repetitions. This may be due to the presence of contaminated watermelons and melons. According to Kim et al. (2017), the levels of TAB in watermelons and melons were 6.0 ± 1.2 and 4.8 ± 1.0 $\log_{10}$ CFU/g, respectively, which are similar to the results of this study. Further, relatively high levels of TAB in watermelons and melons have also been reported in other studies (Johnston et al, 2005; Kim et al., 2014). The mean coliform count for the 100 fresh-cut fruit products tested was 1.54±1.01 $\log_{10}$ CFU/g, and there was no significant difference among seasonal products ($P > 0.05$). The mean coliform counts in winter, spring, summer, and fall samples were 1.27±1.17, 1.27±0.87, 1.87±1.04, and 1.73±0.85 $\log_{10}$ CFU/g, respectively. Among the

samples, sample 2, containing apple, cherry tomatoes, and grapes, showed the highest mean coliform counts at 3.51 ±0.61 $\log_{10}$ CFU/g. This may be due to microbial cross-contamination or microbial growth during post-harvest processes. Samples 13, 14, 15, 18, 19, and 20, containing watermelons and melons, showed relatively higher levels of coliform contamination than the other samples. The mean YM count for the 100 samples was 3.50±1.51 $\log_{10}$ CFU/g. The mean YM count in spring samples was 5.38 ±1.44 $\log_{10}$ CFU/g with a range of 2.92 to 7.11 $\log_{10}$ CFU/g, which was relatively higher than that in samples from other seasons, although significantly difference was not found ($P > 0.05$). Spring samples contained pineapples; thus, these relatively high levels of YM contamination in spring samples may be related to pineapples. Deak et al. (1993) reported that several yeasts, including *Clavispora lusitaniae, Cryptococcus laurentii, Hanseniaspora guilliamondii*, and *Saccharomyces cerevisiae*, contaminated pineapples. According to another study, strawberries, pineapples, and mango showed high levels of YM contamination at 5.2, 5.1, and 4.7 $\log_{10}$ CFU/g, respectively (Graça et al., 2017). Lloyd et al. (2005) investigated fundal infections of fresh-cut fruit using the gas chromatography-mass spectrometric method and detected various fungal contamination in fresh-cut fruit including apples, melons, oranges, and pineapples. Also, Manthou et al (2021) reported that various fungi including *Candida argentea, Candida sake,* and *Fusarium cirinatum* were found in freshly cut pineapple. In summary, the microbiological quality of fresh-cut watermelon, melon, and pineapples is more concerning than that of other fresh-cut fruits examined, especially in terms of TAB, coliform, and YM. Fresh-cut watermelon, melon, and pineapples are vulnerable to microbial contamination because, unlike the whole fruits, they are not protected by hard shells and contain more moisture than other fruits. From the results of quantitative analysis for pathogens, *B. cereus* was only detected in a few samples (5%) at a mean level of 1.72±0.13 $\log_{10}$ CFU/g. However, the levels of *B. cereus* in positive samples (5, 11, and 12) were suitable for the microbial standard of the Korea Food Code (MFDS, 2021a). Notably, *E. coli* and *S. aureus* were not detected in any of the tested samples.

Qualitative microbial risk assessments

Table 2 shows the prevalence of pathogenic bacteria for microbial quality evaluation. *S. aureus* was isolated from four samples from two different brands: one of sample 13 (only melon) and three of sample 15 (only watermelon). While colonized food handlers are the main source of *S. aureus* dissemination, equipment and environmental surfaces can also be implicated in outbreaks (Juneja and Sofos, 2009). Therefore, the presence of *S. aureus* might be due to cross-contamination during processing. *B. cereus* was isolated from five samples from three different brands: one of sample 5 (containing: apple, dragon fruit, grapes, green grapes, green kiwi, orange, pineapple, and tomato), three of sample 11 (containing: apple, citrus, dragon fruit, grape, green kiwi, orange, pineapple, and tomato), and one of sample 12 (only pineapple). *B. cereus* not only survives at extreme temperatures but can also form biofilms and spores. Therefore, it is difficult to estimate their origin. One possibility might be soil contamination because contains fruits that grow on the ground. *L. monocytogenes, Salmonella* spp., *E. coli* O157:H7, and *Cyclospora* (Fig. 2) were not detected in any fresh-cut fruit products analyzed in this study. According to the Korea Food Code, the microbiological standards of fresh-cut fruits are that *E. coli* O157:H7 and *Salmonella* spp. should be negative, *S. aureus* should be 100 CFU/g or less, and *B. cereus* should be 1,000 CFU/g or less. The results of our study indicate that all samples are in accordance with the microbiological standards of the Korea Food Code (MFDS, 2021b).

Growth kinetics of *L. monocytogenes* on fresh-cut fruit

For quantitative microbial risk assessment, a microbial growth prediction model that can predict microbial growth changes according to various environmental factors such as temperature and pH is essential. Figure 3 shows the growth curves of *L. monocytogenes* in watermelon, navel orange, green kiwi, and melon during storage at 10 °C for 8 days. Levels of *L. monocytogenes* on fresh-cut watermelon and melon with an initial load of 4.41±0.28 and 4.37±0.27 log

Table 2 Prevalence (positive sample no./total sample no. tested) of pathogenic contamination of seasonal fresh-cut fruit products

Season	*S. aureus*	*B. cereus*	*L. monocytogenes*	*Salmonella* spp.	*E. coli* O157:H7
Winter	ND[1]	4% (1/25)	ND	ND	ND
Spring	ND	ND	ND	ND	ND
Summer	16% (4/25)	16% (4/25)	ND	ND	ND
Fall	ND	ND	ND	ND	ND
Total	4% (4/100)	5% (5/100)	ND	ND	ND

[1] ND: not detected

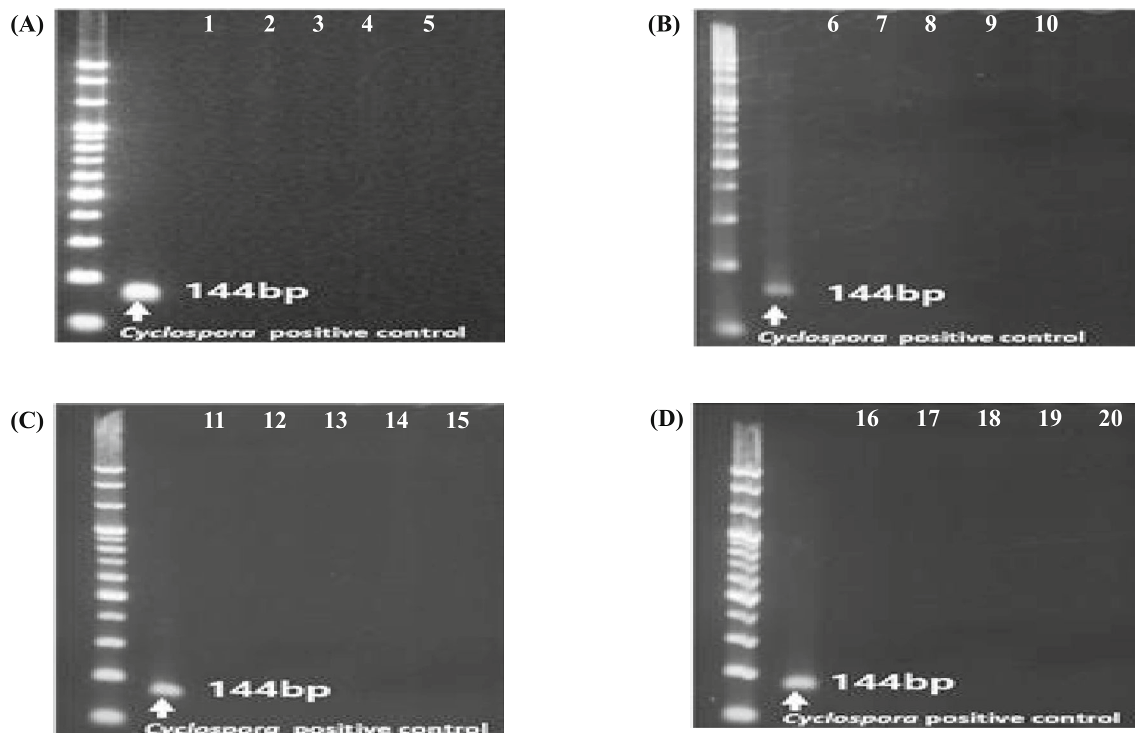

Fig. 2 PCR result of *Cyclospora* in winter (**A**), spring (**B**), summer (**C**), and fall (**D**) fresh-cut fruit products, respectively. Numbers from 1 to 20 indicate the number of samples

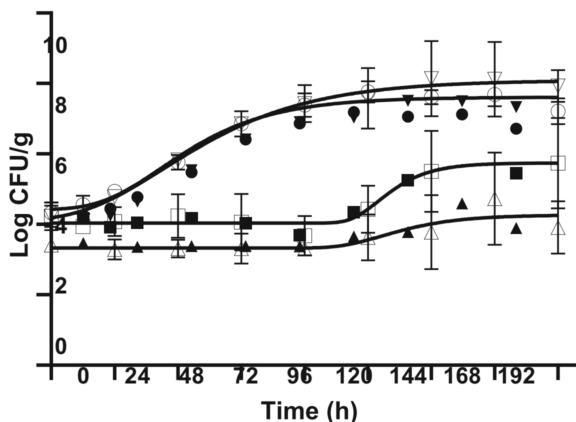

Fig. 3 Growth of *L. monocytogenes* on watermelon (●), orange (□), green kiwi (▲), and melon (▼) at 10 °C for 8 days

CFU/g reached over 7.11±0.47 and 8.00±0.61 log CFU/g, respectively, after storage. Therefore, it was confirmed that *L. monocytogenes* could grow quickly and reach high concentrations without visual signs of decay when fresh-cut watermelon and melon were stored at 10 °C. Conversely, the levels of *L. monocytogenes* were maintained or slightly increased on fresh-cut oranges and kiwis after storage. *L. monocytogenes* has a wide growth range of pH 4.4 to 9.6 (Juneja and Sofos, 2009). The pH of watermelon, orange, kiwi, and melon used in this study was 5.54±0.21, 3.72±0.33, 3.14±0.09, and 6.19±0.18, respectively. Therefore, it appears that the growth of *L. monocytogenes* on oranges and kiwis was inhibited because of their low pH.

The growth parameters determined by predictive growth modeling using the modified Gompertz model are listed in Table 3. The GR value of both watermelon and melon was 0.05 CFU/g/h, and the LT values of melon and watermelon were 11.35 and 18.39 h, respectively. According to another study using the predictive growth modeling with the modified Gompertz equation for *L. monocytogenes* growth on fresh-cut melon during storage at 10 °C, the GR and LT values were 2.22 CFU/g/h and 3.57 h, respectively (Hong et al., 2014). However, another study showed a GR value of 0.047 CFU/g/h at 10 °C for *L. innocua* growth on fresh-cut melon by predictive modeling using the Gompertz model (Guzel and Mustafa, 2015), which is similar to the results of the current study. The GR and LT levels could differ depending on the bacterial strains and testing conditions. The growth of *L. monocytogenes* on fresh-cut oranges and kiwi at 10 °C was hampered and failed to develop into full growth curves. Hence, despite storage at 10 °C, non-acidic fresh-cut fruit products such as watermelons and melons were susceptible to *L. monocytogenes* contamination and growth.

In conclusion, this study investigated the microbiological quality of fresh-cut fruit products. TAB was detected in

Table 3 Parameters obtained from the modified Gompertz equation for the growth of *L. monocytogenes* on various fresh-cut fruit products stored at 10 °C

Fresh-cut fruit products	Parameters of modified Gompertz equation[1]		
	GR	LT	R^2
Watermelon	0.05	18.39	0.9828
Orange	NA[2]	NA	NA
Green kiwi	0.02	102.30	0.6945
Melon	0.05	11.35	0.9951

[1] GR: the maximum growth rate (1/h); LT, the lag time before growth (h)

[2] NA, not available

all seasons, but samples from summer and fall had relatively higher TAB levels than those from winter and spring. Samples containing watermelon and melon had higher TAB levels than the other samples. However, the samples containing pineapple had a relatively higher level of YM than others products. Among pathogens, only *B. cereus* and *S. aureus* were detected in a few samples; *E. coli, E. coli* O157:H7, *L. monocytogenes*, *Salmonella* spp., and *Cyclospora* spp. were not detected in this study. *L. monocytogenes* inoculated in non-acidic fresh-cut fruit products, including watermelon and melon, grew well during storage at 10 °C. Although the risk of food illnesses in fresh-cut fruit products were not confirmed in this study, relatively high levels of microbial contamination have been observed in some fresh-cut fruit products. Therefore, it is necessary to continuously monitor microbiological quality and develop food safety management technologies for related products.

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Declarations

Conflict of interest The authors declare no conflict of interest.

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