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## Detection of Biofilm and some Enterotoxins of *Staphylococcus aureus* Isolates in Ice Cream

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#### **ARTICLE INFO** ABSTRACT Staphylococcus aureus is the most bacteria that have ability to form a biofilm and secret different types **Original Research** of enterotoxins that cause food poisoning in humans. Biofilms is a community of microorganisms encased in a matrix of extracellular polysaccharide (slime), called polysaccharide intercellular adhesion **Received:** (PIA). They have related to a diversity of chronic and persistent infections. This study aims to detect the 05 August 2021 ability of S. aureus isolated from ice cream to form biofilm by Congo red agar (CRA), microliter plate, and PCR and the ability of S. aureus to produce enterotoxins by PCR. 15 S. aureus isolates were grown on CRA and microtiter plate method then subjected for detection of icaA and icaD genes by PCR and Accepted: for the presence of enterotoxins genes (sea, seb, sec, sed, and see) which are responsible for S. aureus 26 September 2021 biofilm formation and Staphylococcus food poisoning. 73.3% of the isolates were biofilm producers on Congo red agar, 60% of the isolates were positive for biofilm production using microtiter plate method and by PCR technique, all the isolates 100% had icaD gene and 86.6% had icaA gene. The enterotoxin Keywords: seb gene was detected in 5 (33.3%) S. aureus isolates, the enterotoxin see gene was detected in 4 (26.6%) S. aureus isolates while sea, seb and sed gens were not detected in any S. aureus isolates. In conclusion all aureus isolates were positive for icaD gene and some of S. aureus isolates were positive for icaA gene Biofilm, Enterotoxins, Food, which are responsible for biofilm formation and some S. aureus isolates were positive for enterotoxin B S. aureus, PCR and enterotoxin E, which responsible for food intoxication so the ice-cream considered a potential source for food intoxication and persistent infection caused by S. aureus.

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## Introduction

Milk and dairy products are the source of nutrients required for the growth of many microorganisms, including Staphylococci (Farzana et al., 2004). Bacterial Milk contamination usually occurs throughout the milking process, and this depends on the sanitary condition of the environment and utensils used for milking and the milker's hands (Smith et al., 2007). Also, it can gain access to milk by direct excretion from udders with clinical or subclinical Staphylococcal mastitis (Peles et al. 2007). Staphylococci have been described as bacteria that may attach to the contact surfaces in both milk and meat processing industries, form biofilms and survive on them. Their attachment to food contact surfaces in food processing plants, and subsequent biofilm formation pose a risk of contamination in milk and meat products. Bacterial contamination of foodstuffs can lead to their decay or transmission of diseases (Schlegelová et al., 2008). The formation of biofilms is increasingly recognized as an important factor in the virulence of Staphylococcus (Oliveira et al., 2006). Bacteria in the biofilm are highly resistant to both innate and specific host defense mechanisms due to their extracellular polysaccharide matrix and low metabolic rate, among other things, they are not susceptible to phagocytes and antibiotic-resistant macrophages, which only attack dividing cells. These local conditions are conducive to the continued existence of bacteria for months to years, and periodic outbreaks (Potera, 1999).

The implications of biofilm formation for infections and drug resistance have triggered increased interest in the characterization of the genes involved in biofilm formation. The intercellular adhesion (*ica*) locus consists of the genes *icaADBC*, and among the *ica* genes, *icaA* and *icaD* have been reported to play a significant role in biofilm formation in *Staphylococcus aureus* (*S. aureus*) and *Staphylococcus epidermidis*) (Cramton *et al.*, 1999).

*S. aureus* is one of the major bacterial pathogens which cause food poisoning (Yu-Cheng *et al.*, 2008). Staphylococcal food poisoning is a mild intoxication occurring after the ingestion of food containing Staphylococcal enterotoxins (SEs) (Chiang *et al.*, 2008)

There were five major classical SEs types, named; SEA, SEB, SEC, SED, and SEE. However, new genes encoding enterotoxins are currently being identified, for example, from SEG to SEU.

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One or more of these genes are thought to be involved in Staphylococcal food poisoning (Afifi *et al.*, 2011).

Staphylococcal (SE) enterotoxin is part of the pyrogenic protein associated with many human diseases. These proteins are resistant to thermal inactivation and to gastrointestinal proteases, causing emesis and diarrhea, and can act as superantigens (Pinchuk *et al.*, 2010). A wide variety of enterotoxin and enterotoxin-like coding genes (more than 20 SEs) have been categorized to have a significant role in stages of host colonizing, gastroenteritis infections, and invasion of skin, mucus, and host defense mechanisms (Argudín *et al.*, 2010). Most genes coding for SEs is located on mobile elements such as plasmids, bacteriophages or pathogenicity islands (Lindsay *et al.*, 1998; Zhang *et al.*, 1998). Therefore, horizontal transmission between strains is not uncommon.

Staphylococcal enterotoxin B (*seb*) is the toxin mostly associated with typical food poisoning. It has also been shown to cause a non-menstrual toxic shock syndrome (TSS) (CDC, 2014). *Seb* has been studied as a potential biological warfare agent because it is easily dispersed; it is very stable and when inhaled at very high doses, it can cause extensive systemic damage, multiple organ failure, and even shock and death. However, *seb* is classified as disabling because in most cases, aerosol exposure does not lead to death, but a temporary but at the same time severe disabling disease that lasts up to 2 weeks. (Ulrich *et al.*, 1997). So, the purpose of this study was to detect the ability of *S. aureus* to form biofilm phenotypically and genotypically and the ability of these strains to secrete enterotoxins genetically.

## **Materials and methods**

#### Bacterial isolates

Fifteen *S. aureus* isolates were isolated from ice-cream samples and identified through culture on mannitol salt agar and biochemical identification and confirmed by PCR technique according to Samir *et al.* (2019). These isolates were subjected for biofilm formation phenotypically and genotypically and enterotoxins secretion by PCR.

## Screening of Staphylococcus aureus for biofilm production by congo red agar (CRA) plate.

Production of biofilm from all isolates was studied by the cultivation of the *S. aureus* isolates on CRA plates, CRA prepared by adding 0.8 g of congo red dye and 36 g of sucrose

Table 1. Primers used in this study

to 1L of BHI (Oxoid), then plates were incubated at 37 °C for 24 h. After incubation, black colonies with a dry crystalline consistency were established as biofilm positive and nonbiofilm producing strains produce red smooth colonies (Gundogan *et al.*, 2006; Krukowski *et al.*, 2008).

## Using the microtiter plate method to determine quantitative biofilm formation

The overnight culture was diluted 1:200 with tryptic soya broth containing 0.25% glucose, and 200  $\mu$ l of each dilution were seeded per well in a sterile 96-well polystyrene microtiter plate and incubated at 37 °C for 18 h. After washing 3 times in phosphate buffered saline (pH 7), wells are dried for 1 h at 60 °C and attached biofilm was stained with 1% crystal violet for 15 minutes. After rinsing 3 times with distilled water, drying was done at room temperature and the absorbance of the adherent biofilm was measured at 490 nm in a microplate reader (Cucarella et al., 2001). The Interpretation of biofilm production was calculated according to Stepanovic et al. (2007): The average OD values were calculated for all tested strains and negative controls since all tests were performed in triplicate and repeated three times. Second, the cut-off value (ODc) was established. It is defined as three standard deviations (SD) above the mean OD of the negative control: = average OD of negative control + 3x standard deviation (SD) of negative control. Then the average OD values of all tested strains compared with the ODc as follow; if  $OD \leq ODc =$  no biofilm producer; ODc< OD  $\leq$  2×ODc= weak biofilm producer; 2× ODc <OD≤4×ODc= moderate biofilm producer; 4×ODc <OD= strong biofilm producer.

PCR method for the identification of icaA and icaD genes and enterotoxins genes

#### Extraction of DNA

The extractions of the genomic DNA were conducted according to instruction of QIAamp DNA mini kit (Qiagen, Germany, GmbH).

#### Polymerase chain reaction (PCR)

The primers for the amplification of *icaA* and *icaD* genes and enterotoxins genes were designed as mentioned in Table 1.

Gene	Primer sequence	I anoth of amplified product	Reference		
Gene	(5'-3')	Length of amplified product	Reference		
icaA	F-CCT AAC TAA CGA AAG GTA G	1315 bp			
ICAA	R-AAG ATA TAG CGA TAA GTG C	1515 bp	Ciftci et al. (2009)		
icaD	F-AAA CGT AAG AGA GGT GG	381 bp			
	R-GGC AAT ATG ATC AAG ATA	581 Up			
sea	F-GGTTATCAATGTGCGGGTGG	102 bp			
	R- CGGCACTTTTTTCTCTTCGG	102 bp	Mehrotra et al. (2000)		
,	F-GTATGGTGGTGTAACTGAGC	164 bp			
seb	R-CCAAATAGTGACGAGTTAGG	164 bp			
	F-AGATGAAGTAGTTGATGTGTATGG	451 bp			
sec	R- CACACTTTTAGAATCAACCG	451 bp			
sed	F- CCAATAATAGGAGAAAATAAAAG	279 hr			
	R- ATTGGTATTTTTTTTTCGTTC	278 bp			
	F- AGGTTTTTTCACAGGTCATCC	200 hr			
see	R- CTTTTTTTTTTCTTCGGTCAATC	209 bp			

### Uniplex PCR for detection biofilm genes

Primers for *icaA* and *icaD* were used in 25  $\mu$ l reaction volume consisted of, 1  $\mu$ l of each primer, 12.5  $\mu$ l Emerald Amp GT PCR master mix, 4.5  $\mu$ l PCR grade water, and 6 $\mu$ l of template DNA. The reaction was done in a thermocycler (Applied Biosystem 2720) based on the conditions mentioned in Table 2.

### Preparation of Sea, Sed and See multiplex PCR reaction

Primers for *Sea*, *Sed* and *See* were used in 50  $\mu$ l reaction volume consisted of, 1 $\mu$ l of each primer (20 pml), 25  $\mu$ l Emerald Amp GT PCR master mix, 11  $\mu$ l PCR grade water, and 8  $\mu$ l of template DNA. The reaction was done in thermal cycler (Applied Biosystem 2720) based on the conditions mentioned in Table 2.

### Preparation of Seb and Sec duplex PCR reaction

Primers for *Seb* and *Sec* were used in 50  $\mu$ l reaction volume consisted of, 1  $\mu$ l of each primer (20 pml), 25  $\mu$ l Emerald Amp GT PCR master mix, 13  $\mu$ l PCR grade water, and 8  $\mu$ l of template DNA. The reaction was done in thermal cycler (Applied Biosystem 2720) based on the conditions mentioned in Table 2.

Investigation of the PCR products according to Sambrook *et al.* (1989) with modification

The products of the uniplex, duplex, and multiplex PCR were separated by electrophoresis on a 1.5% agarose gel (AppliChem, Germany, GmbH) in  $1 \times$  TBE buffer at room temperature using a gradient of 5V/cm. For gel analysis, 20 µl of each

### Table 2. Temperature and program conditions during PCR.

product was loaded in each gel well. A 100-bp DNA ladder (Qiagen, Germany) was used to find out the amplicon sizes. The gel was visualized by a gel documentation system (Alpha Innotech, Biometra).

## Results

# Detection of biofilm-producing phenotype by Congo red agar method and microtiter plate method

Based on Congo red agar plate, 11 out of 15 *S. aureus* isolates were produced biofilm and showed black colonies, while 4 out of 15 isolates were no biofilm-producing showing red colonies (Table 3 and Fig. 1). However, by microtiter plate method, 2 isolates out of 15 *S. aureus* isolates, were strong biofilm producers, 7 isolates were moderate biofilm producers, and 6 isolates were weak biofilm producers (Table 3).



Fig. 1. A) *S. aureus* isolate showing black colonies on Congo red agar, B) Two *S. aureus* isolates showing red colonies on Congo red agar.

## PCR detection of icaA and icaD

All 15 isolates were examined for the presence of *icaA* and

Gene	Primary denaturation	Secondary denaturation	Annealing	Extension	No. of cycles	Final extension
I A	94°C	94°C	49°C	72°C	25	72°C
IcaA	5 min.	30 sec.	1 min.	1 min.	35	12 min.
LD	94°C	94°C	49°C	72°C	25	72°C
IcaD	5 min.	30 sec.	30 sec.	30 sec.	35	7 min.
For Ford and For	94°C	94°C	50°C	72°C	25	72°C
Sea, Sed and See	5 min.	30 sec.	30 sec.	30 sec.	35	7 min.
C.L. and C.	94°C	94°C	50°C	72°C	25	72°C
Seb and Sec	5 min.	30 sec.	40 sec.	40 sec.	35	10 min.

#### Table 3. Results of phenotypic detection of biofilm production

				Phe	notypic detec	tion				
Method		Congo r	ed agar	l agar Microtitre plate						
Results	Black colonies		Red colonies		Strong producer		Moderate producer		Weak producer	
Results										
	No	%	No.	%	No.	%	No.	%	No.	%
-	11	73.30%	4	26.60%	2	13.3	7	46.6	6	40
Total					1	5				

### Table 4. Results of genotypic detection of biofilm production

				Genotypic	e detection			
Genes	Ica A				Ica D			
	Pos	itive	Neg	ative	Pos	itive	Neg	ative
Results	No.	%	No.	%	No.	%	No.	%
	13	86.6	2	13.3	15	100	0	0
Total				1	5			

*icaD* genes. Among the 15 isolates, 13 isolates revealed the presence of *icaA* gene as shown in Table 4, Fig. 2, and all the 15 isolates have *icaD* gene as shown in Fig. 3.



Fig. 2. PCR results of *icaA* gene among *S. aureus* isolates. Lane L: DNA ladder, Lane pos: control positive, Lane neg: control negative, lane 1,2,3,5,6,8,9,10,11,12,13 and 14 positives for *icaA*. Lane 7, 15 negatives for *icaA*.



Fig. 3. PCR results of *icaD* gene among *S. aureus* isolates. Lane L: DNA ladder, Lane pos: control positive, Lane neg: control negative, lane 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13,14,15 positive for *icaD*.

#### Occurrence of enterotoxin genes among S. aureus isolates

All the 15 *S. aureus* isolates were examined for the presence of enterotoxin genes (*sea, seb, sec, sed* and *see*). Among the 15 *S. aureus* isolates, two enterotoxin genes (*seb* and *see*) were detected. The enterotoxin *seb* gene was detected in 5 (33.3%) *S. aureus* isolates as shown in Fig. 4, However, the enterotoxin *see* gene was detected in 4 (26.6%) *S. aureus* isolates (Fig. 5).



Fig. 4. PCR results of enterotoxin genes (*sea*, *sed* and *see*) among Staph aureus isolates. Lane M: DNA marker, Lane pos: control positive, Lane neg: control negative, lane 1,4,6 and 9 positives for *see*. Lane 2,3,5,7,8,10,11,12,13,14,15 negative for presence of *sea*, *sed* or *see*.



Fig. 5. PCR results of enterotoxin genes (*seb*, *sec*) among *S. aureus* isolates. Lane M: DNA marker, Lane pos: control positive, Lane neg: control negative, lane 3,5,9,10,14 positive for *seb*. Lane 1,2,4,6,7,8,11,12,13,15 negative for *seb* or *sec*.

## Discussion

S. aureus with biofilm formation helps bacteria to survive

in the host and is responsible for persistent or chronic infection (Christensen *et al.*, 1985; Bernardi *et al.*, 2007). They exhibit resistance to antibiotics by various methods including restriction of penetration of antibiotics into biofilms, decreasing the growth rate, and expression of resistance genes (Kim, 2001).

Several studies have shown that mucus and biofilm formed in *S. aureus* strains that cause catheter-associated and nosocomial infections is associated with the presence of the *icaA* and *icaD* genes (Arciola *et al.*, 2001; 2002). In this study, the results of a PCR test for the *icaA* and *icaD* genes and phenotypic tests were important to develop diagnostic tests for biofilm-producing microorganisms.

There are various methods for biofilm detection. (Christensen *et al.*, 1985). In this study, we evaluated the 15 *S. aureus* isolates for their ability to form biofilms by three screening methods (CRA, MTP and PCR).

The obtained results showed that among the 15 isolates of S. aureus, 11 (73.3 %) are biofilm producers against 4 (26.6%) non-biofilm producers by CRA method similar results were reported by Namvar et al. (2013), who reported that 65% positive results with Congo red agar and by Gowrishankar et al. (2016), who reported that 77.8% of S. aureus isolates tested positive for slime using the CRA method. Also, this result agrees with the previous reports by Kouidhi et al. (2010); Arciola et al. (2002) and Ammendolia et al. (1999), where 88.9%, 60.8, and 50 of S. aureus were found to be positive for slime production, respectively. However, (Mathur et al., 2006; Taj et al., 2012; Ba et al., 2014) reported a smaller number of biofilm production by Staphylococci species by this method they found positive results with CRA in 1.97%, 3.47%, and 4.47% respectively. As researchers have only recently found that PIA/PNAG (polysaccharide intracellular adhesions/poly Nacetyl glucosamine) have little input in the biofilm matrix of S. aureus, so cannot be detected by the CRA method (Taj et al., 2012; Knobloch et al., 2002).

The microtiter plate test is a convenient and economical quantitative technique for the identification of critical factors and optimal culture conditions for biofilm formation. This technique is used for the direct detection of polysaccharide production because spectrophotometric measurements provide quantitative information on the ability of bacterial strains to rapidly grow while adhering to the substratum (Stepanovic *et al.*, 2000).

This study showed that the results of biofilm production by microtiter plate method were 13.3% strong biofilm producer, 46.6% moderate biofilm producer, and 40% weak biofilm producer. These results nearly agree with Mathur *et al.* (2006), who reported that 14.47 % strong and 39.4 % moderate biofilm producer, while 46.0 % of isolates were weak or no biofilm was detected. Also, the results in this study agreed with Kot *et al.* (2013), who found that weak biofilm formers were 48.6%, while 40% and 11.4% of strains were moderate and strong biofilm producers, respectively.

The data for the MTP test were not in agreement with Darwish and Asfour (2013), who observed that the results of biofilm production by MTP method were 52.5%, 27.5%, and 20% of *S. aureus* isolates that had strong, moderate, and weak biofilm producers, respectively.

The difference between the results of CRA and MTP methods can be attributed to the fact that phenotypic expression of biofilm formation is very sensitive to in vitro conditions, so various methods can be used for detection. In addition, both of these tests measure the same phenomenon, but in different ways. CRA has been used as an indirect indicator of polysaccharide production (Baselga *et al.*, 1993; Stevens *et al.*, 2009). A combination of phenotypic and genotypic methods would be recommended for identifying biofilm-producing strains, the detection of two biofilm-related genes and their incidence in *Staphylococcus* isolates were investigated using PCR reactions.

The intercellular adhesion (*ica*) locus, consisting of the genes *icaADBC*, has been reported to have a potential role of biofilm formation (Vasudevan *et al.*, 2003). Among the ica genes, *icaA* and *icaD* have been reported to play a significant role in biofilm formation in *S. aureus* and *S. epidermidis* (Gotz, 2002). The gene encoded by ica has been shown to cause the intercellular biosynthesis of PIA molecules, and It can participate in the biofilm accumulation stage. Various studies have demonstrated the key role of the ica gene as a virulence factor in staphylococcal infections (Namvar *et al.*, 2013).

In this study, the prevalence of *icaA* and *icaD* genes in *S. aureus* was 86.6% and 100%, respectively, which nearly agree with Marques *et al.*, (2017), who detected that *icaA* and *icaD* in 85% and 95% isolates, respectively. Castelani *et al.* (2015) reported that PCR detected the *icaA* and *icaD* genes in 98% and 100% of *S. aureus* isolates, respectively. Furthermore, Namvar *et al.* (2013) found that all isolates were positive for the *icaD* gene determined by PCR. In addition, results from this study are consistent with Notcovich *et al.* (2018), who stated that the PCR results showed that all but one of the isolates were positive for *icaA* and *icaD* genes, with the one exception being negative for *icaA*.

Through comparison of genotypic and phenotypic biofilm characteristics of the isolates revealed that two isolates showed a good correlation between phenotypic detection by Congo red agar producing black colonies and by microtiter plate method that showed strong adherence and also, genotypically, they have both genes responsible for biofilm formation.

It has been reported that failure of staphylococcal strains that possess the ica locus to form biofilm in vitro could be due to point mutations in the locus and/or other unidentified factors negatively regulate the synthesis of polysaccharide cell adhesion or affect the formation of biofilms (Cramton *et al.*, 1999).

There is some experimental evidence that the development of new clones, called biofilm negative, has *icaA* and *icaD* genes (Arciola *et al.*, 2001). It has been shown that the expression of the *icaADBC* operon is a highly variable factor that is regulated by phasic changes and rearrangements of the genome. It has been suggested that variable biofilm expression helps bacteria adapt to the environmental change conditions of incubation (Costerton *et al.*, 1999; Rachid *et al.*, 2000).

It has previously been demonstrated that the phenotypic expression of biofilm formation is highly sensitive to in vitro conditions (Baselga *et al.*, 1993) and hence can be detected variably by different methods. Therefore, a combination of various methods (phenotypic and genotypic) would be useful for identifying biofilm producing *S. aureus*.

The present study showed that one of the isolates was biofilm producer phenotypically but genotypically have only *icaD*, this suggesting that biofilm can be formed even when only one ica loci gene is present (De Almeida *et al.*, 2017) These results are like those obtained by Darwish and Asfour (2013) with bovine milk samples. These authors reported that the prevalence rates of *icaA* and *icaD* genes were 15.0 and 62.5%, respectively. Furthermore, Ciftci *et al.* (2009) found that 16 (27.1%) and 38 (64.4%) out of 59 strains were positive for *icaA* and *icaD* genes, respectively. The lower detection of *icaA*, and therefore the differences in the prevalence rates can be attributed to the variation in DNA sequences. This may lead to failed amplification of the genes in some isolates and consequently false negative results (Tormo *et al.*, 2005; Ferrer *et al.*, 2012; Darwish and Asfour, 2013).

In this study, the 4 isolates which did not produce slime factor on CRA plate in vitro, were positive for both *icaA* and *icaD* genes. This suggests that certain environmental conditions or the presence of other genes may affect the possibility of phenotypic behavior on the Congo red agar plate, that may show colonies that did not fully express the ica gene (Ciftci *et al.*, 2009).

One of the aims of this study is to evaluate the presence of staphylococcal enterotoxins genes in the staphylococcal isolates. The 15 S. aureus isolates were tested for the presence of sea, seb, sec, sed, see genes by PCR. The data illustrated that 60% of the isolates have enterotoxin genes. This agrees with Normanno et al. (2007), who reported a 59.8% prevalence of se genes in food samples, and with Nazari et al. (2014), who reported that the gene encoding enterotoxin was found in 53.8% of S. aureus isolates that were positive for at least one enterotoxin gene. and also, with Pereira et al. (2009), who found the prevalence of enterotoxigenic strains was 68.2%. Also, the results nearly agree with Omoe et al. (2002), who found that 77.4% S. aureus isolates were positive for one or more se genes, and with Mashouf et al. (2015), who reported that the prevalence of SEs was 77.6% among the tested isolates. According to research, genes can be located in plasmids (sed and sei), bacteriophages (sea and see), and pathogenic islands. (seb and sec), and chromosomes (seq, seh, and sei); therefore enterotoxin-producing S. aureus carry several se genes (Alibayov et al., 2014).

In this study, *seb* enterotoxin was detected in 33.3% of *S. aureus* isolates. The result agreed with Nazari *et al.* (2014), who detected *seb* in 26.9% and disagree with Kitai *et al.* (2005) and Rasoul *et al.* (2015), who observed *seb* in 64.1% and 4.1% of *S. aureus* respectively. The enterotoxin *see* was detected in 26.6% of *S. aureus* isolated in this study. This nearly agrees with Asadollahi *et al.* (2014), who reported that *see* gene found in 31%. and disagree with El-Nagar *et al.* (2017), who found 4.8% of the isolates have *see.* Some studies reported that none of the isolates were positive for *see* (Rahimi *et al.*, 2013; Nazari *et al.*, 2014), which disagree with the obtained results.

## Conclusion

According to the findings of this study, *S. aureus* isolated from ice cream were pathogenic, harbor *icaA* and *icaD* gene, which are responsible for biofilm formation and also some of *S. aureus* isolates carry *seb* and *see*, which cause food intoxication. Therefore, much more attention should be paid to hygienic measures during ice cream manufactures.

## **Conflict of interest**

The authors declare that they have no conflict of interest.

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