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Research Article

Phenotypic and Genotypic Antibiotic Resistance of *Staphylococcus warneri* and *Staphylococcus pasteuri* Isolated from Stuffed Mussels

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ABSTRACT

This study aimed to assess the presence of Staphylococcus species in stuffed mussel samples sold in Çanakkale province and to determine the antibiotic resistance of the isolates. A total of 246 stuffed mussel samples were examined, and two different *Staphylococcus* (*S. warneri* and *S. pasteuri*) were isolated from 12.19% of the samples. Among the Staphylococcus isolates, *S. warneri* was detected at a rate of 73.33% and *S. pasteuri* at 26.67%. Bacterial isolates (N=30) were examined for their resistance to amoxicillin/clavulanic acid (30 µg), ampicillin (10 µg), erythromycin (15 µg), clindamycin (10 µg), vancomycin (30 µg), oxacillin (5 µg), tetracycline (30 µg), doxycycline hydrochloride (30 µg), chloramphenicol (30 µg), streptomycin (10 µg), gentamicin (10 µg), kanamycin (30 µg), nalidixic acid (30 µg), ciprofloxacin (5 µg), meropenem (10 µg), imipenem (10 µg), sulfamethox/ trimethoprim (25 µg), cefotaxime (30 µg), cephalothin (30 µg), ceftriaxone (30 µg), and levofloxacin (5 µg) antibiotics. Resistance to amoxicillin/clavulanic acid and erythromycin was found in all *S. warneri* isolates. In addition, all S. pasteuri isolates were found to be resistant to amoxicillin/clavulanic acid. In *S. warneri* isolates, at least three resistance genes (*BlaTEM, tetB-6, tetK-8*) and up to eight resistance genes (*BlaTEM, tetB-6, tetK-8, strA-strB, aphAI-IAB, ermC*) were identified. All *S. pasteuri* isolates exhibited blaTEM, strA-strB, and aphAI-IAB resistance genes. In conclusion, it was determined that antibiotic-resistant *S. warneri* and/or *S. pasteuri* contaminates stuffed mussel samples. This study will serve as a valuable resource for enhancing monitoring strategies in stuffed mussel production. Further studies should be conducted to determine whether the products are suitable for food safety. Therefore, it is necessary to clarify the disease effects and mechanisms of the pathogens identified in stuffed mussels.

Keywords: Stuffed mussel, *Mytilus galloprovincialis*, *S. warneri*, *S. pasteuri*, Public health, antibiotic resistance

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INTRODUCTION

Consumers directly consume ready-to-eat foods without requiring processing, such as heat treatment (WHO, 1996; Mosupye & von Holy, 1999). Those prepared by street vendors and sold especially on the streets or other public places are also defined as ready-to-eat foods and beverages (FAO, 1997). Ready-to-eat meals are encountered in various presentations and packaging in markets, restaurants, and many other areas, with street foods being the most prevalent. Street foods play a significant role in meeting a substantial part of our daily meal needs and are preferred by everyone, regardless of age or profession. Street foods can be classified as seafood, animal-derived products, pastries, sweets, fruits, and other gastronomic products (Demir et al., 2017). Stuffed mussels, especially in coastal cities, are among the most consumed street foods. Ready-to-eat foods are preferred for reasons such as easy accessibility, quick preparation, affordability, and compatibility with different taste preferences.

The most significant danger regarding street food is the uncertainty regarding its suitability for consumption in terms of food safety. The safety of foods depends on various common factors, ranging from the quality of raw materials to food processing and storage practises. Most vendors may expose the meals to conditions that are not suitable for food safety, such as "cross-contamination, unhygienic storage, and poor time-temperature" conditions (Lucca and Torres, 2006; Mepba et al., 2007). Products produced and sold without considering food safety can lead to situations that endanger human health. Bacteria that contaminate food due to various contamination sources and cause epidemic diseases in humans are among the primary concerns. In addition to causing various infections and diseases, these bacteria are becoming increasingly resistant to antibiotics, leading to challenging-to-treat illnesses. The World Health Organisation (WHO, 2017) has declared antibiotic-resistant bacteria as the "greatest and most urgent global threat" because as resistance to antibiotics increases, bacteria develop multiple antibiotic resistance. Therefore, antibiotics used for treatment do not yield successful results.

Stuffed mussels, generally prepared using *Mytilus galloprovincialis*, are ready-to-eat meals that are commonly sold on the streets in countries with coastlines along Türkiye and the Mediterranean. Throughout the processing, preparation, and cooking of stuffed mussels, they can be susceptible to human-induced contamination, and during the sales process, they may be exposed to environmental factors such as air pollution and insects. The high pH and nutrient profile of stuffed mussels create a favourable environment for microbial growth. Street vendors typically sell stuffed mussels in open-air environments on tables for 6-8 hours or even longer (Kişla and Üzgün 2008). Consumers use the mussel shell itself as a spoon, remove the stuffing, and consume it. In this case, if the mussel shell is contaminated, it becomes a source of risk when it comes into contact with the mouth. Leftover stuffed mussels at the end of the day are sometimes stored inappropriately in refrigerators (+4 °C), often at unsuitable ambient temperatures, to be put up for sale again the next day.

Studies conducted in Türkiye have reported that stuffed mussels may contain *Escherichia coli, Staphylococcus spp., Bacillus cereus, Vibrio alginolyticus, Listeria monocytogenes*, yeast, mold, and anaerobic bacteria (Bingol et al., 2008; Durgun, 2013; Üzgün, 2015; Karademir, 2018; Güngörür, 2019). However, to the best of our knowledge, there is no detailed study examining the phenotypic and genotypic antibiotic resistances of *S. warneri* and/or *S. pasteuri* species isolated from stuffed mussels. *Staphylococcus warneri* has been isolated from various sources, including fermented foods, humans, and numerous animal species (Becker et al., 2014). Studies in the literature have reported the isolation of *S. warneri* from sea cucumbers (Kim et al., 2017) and marine fish flesh (Regecova et al., 2014). *Staphylococcus pasteuri* has been reported to be present in various foods, including goat milk (Chesneau et al., 1993), Italian sausages (Rantsiou et al., 2005), and retail beef (Bhargava et al., 2014), as well as in drinking water (Faria et al., 2009). However, no literature is available regarding the isolation of *S. warneri* and *S. pasteuri* from ready-to-consume stuffed mussels.

S. pasteuri (Petti et al., 2008; Savini et al., 2008; Ramnarain et al., 2019; Morfin-Otero et al., 2012; Sánchez et al., 2013; Savini et al., 2009a; Savini et al., 2009b) and *S. warneri* (Incani et al., 2010; Dimitriadi et al., 2014; Gelman et al., 2022; Hoque et al., 2023a; Hoque et al., 2023b; Louail et al., 2023; Si et al., 2024) were appeared in reports of different diseases that could be associated with human. This study aims to investigate the presence of *S. warneri* and *S. pasteuri*, which are known to cause significant health problems in the respiratory, skin, digestive systems, etc., in humans, in stuffed mussels sold in Çanakkale and their resistance to antibiotics.

MATERIALS AND METHODS

Materials

In the scope of this study, stuffed mussels offered for sale in open and closed spaces in the market of Çanakkale Province were used as the material. Mussel samples (N=246) were collected from a total of 20 locations, with 10 from open spaces (street vendors) and 10 from closed spaces (restaurants, etc.), during the peak consumption seasons of spring (May), summer (June to August), and autumn (September-October) (Table 1). Ready-to-consume stuffed mussel samples were transported to the microbiology laboratory within 30 min in styrofoam boxes at +4°C.

Methods

Isolation and identification of bacteria

For microbiological analyses, 10 g of mussel samples were homogenised in 90 ml of peptone water for 1 min. Decimal dilutions (10^{-1} to 10^{-6}) were prepared from the homogenate. From these dilutions, inoculations were made using the spread plate and pour plate methods. Mannitol Salt Phenol Red Agar (Merck 105404) was used as the culture medium. The culture plates were incubated 35°C for 3 days in the incubator to allow for the development of microorganisms. After the bacteria were purified from the Mannitol Salt Agar medium where they grew, classical methods (colony type, morphology, gramme +/- characteristics, oxidase, catalase, H_2S, indole, etc.) were used for genus-level identification. The isolates were grown for stocks in Brain Heart Infusion (Merck 110493) liquid medium. Subsequently, they were stored at -80°C in cryogenic tubes containing 30% glycerol until further molecular identification and antibiotic susceptibility testing were performed.

Species identification of the bacterial isolates

For DNA (Deoxyribonucleic acid) isolation, the EurX GeneMATRIX Bacterial & Yeast DNA isolation kit from Poland was utilised

Table 1. Sampling plan for the study.

Seoson/ Year	Locations/ Count	Count of the Sample
Spring/2021	Street vendors/2	15
Spring/2021	Restaurants/2	15
Summer/2021	Street vendors/5	60
Summer/2021	Restaurants/5	60
Autumn/2021	Street vendors/3	48
Autumn/2021	Restaurants/3	48

(https://eurx.com.pl/docs/manuals/en/e3580.pdf). The quantity and purity of the obtained DNA after isolation were assessed using the Scientific Nanodrop 2000 device (USA) through spectrophotometric measurements conducted at Thermo.

In the PCR (Polymerase Chain Reaction) study, target gene regions for species identification were amplified using the universal primers 27F–1492R. The primer sequences used were 27F 5' AGAGTTTGATCMTGGCTCAG 3' and 1492R 5' TACGGYTACCTTGTTACGACTT 3' (Lane, 1991). The PCR mixture (35 µL) included approximately 1 PCR buffer, 1.5 mM MgCl2, 0.2 mM dNTP, 100 ng template DNA, 0.3 µM of each primer, and nuclease-free water. PCR amplification was performed using a thermal cycler (Kyratec, Geumcheon gu, Seoul Korea) with the following parameters: 95°C for 5 min (initial denaturation), 30 cycles of 95°C for 45 s (denaturation), 57°C for 45 s (annealing), 72°C for 60 s (extension), and a final step at 72°C for 5 min (final extension). Then, 10 µl of the PCR sample was loaded on a 1.5% agarose gel in 1 TAE containing ethidium bromide, and electrophoresis was performed for 90 min at 100 V. PCR products were cleaned and sequenced by BM Labosis (Ankara, Turkey) using the universal primers 27F–1492R. Sequence editing was performed using BioEdit (Bioedit v7.0.0). 16S sequences were compared against all GenBank *S. warneri* and *S. pasteuri* sequences using the BLASTN search at http://blast.ncbi.nlm.nih.gov/.

Antibiogram tests for *Staphylococcus* isolates

The Kirby-Bauer disc diffusion test was employed to determine the antibiotic resistance of the bacteria (Bauer et al., 1966). The analysis execution and interpretation of test results adhered to the standards set by the Clinical and Laboratory Standards Institute (CLSI, 2015; CLSI, 2017). The bacterial strains stored in the freezer were initially cultured at least twice in tryptic soy (TS) medium. Subsequently, the bacterial isolates were transferred to Mueller-Hinton (MH) solid medium. After successful growth, colonies displaying the best development were selected, and their density was adjusted to 0.5 McFarland in liquid medium (MH). From the adjusted-density liquid medium (0.5 McF), bacterial transfers were made to an appropriate solid culture medium using a sterile cotton swab. After bacterial inoculation on solid culture media, antibiotic discs [amoxicillin/clavulanic acid (30 µg), ampicillin (10 µg), erythromycin (15 µg), clindamycin (10 µg), vancomycin (30 µg), oxacillin (5 µg), tetracycline (30 µg), doxycycline hydrochloride (30 µg), chloramphenicol (30 µg), streptomycin (10 µg), gentamicin (10 µg), kanamycin (30 µg), nalidixic acid (30 µg), ciprofloxacin (5 µg), meropenem (10 µg), imipenem (10 µg), sulfamethox/ trimethoprim (25 µg), cefotaxime (30 µg), cephalothin (30 µg), ceftriaxone (30 µg), and levofloxacin (5 µg) were placed on the culture medium for the disc diffusion test. The plates were then incubated at 35°C for 24 h. The resulting zone diameters were measured using a ruler and interpreted according to the CLSI standards (CLSI, 2015; CLSI, 2017).

Identification of antibiotic resistance genes in bacterial isolates

For the analysis of bacterial antibiotic resistance genes, the EurX GeneMATRIX DNA Isolation Kit from Poland was used to isolate DNA from 30 samples. After DNA isolation, the quantity and purity of the obtained DNA were assessed through spectrophotometric measurements using a Thermo Scientific Nanodrop 2000 device (USA). The contents of the PCR cocktail were adjusted to 20 µL as 1 PCR buffer, 2 mM $MgCl_2$, 0.2 mM dNTP mix, 0.5 µM of each forward and reverse primer, 2 U Taq polymerase, DNA template, and PCR grade distilled water. Amplification results obtained through PCR (kyratec thermocycler) were run on a 1.0% agarose gel prepared in 1 TAE buffer and subjected to electrophoresis at 100 V for 60 min. The gel was then visualised under UV light using an ethidium bromide dye. The size of the amplicons was estimated using 50- and 100-pb DNA size markers. The primer sequences used are presented in Table 2.

RESULTS

Identification of the bacterial species

From 246 mussel samples obtained under different selling conditions, 30 *Staphylococcus* isolates were obtained through culture. Through 16S rRNA analysis, it was determined that the 30 bacterial isolates had a high similarity (≥99.12 - 100%) with species registered in the GenBank database. Eight of the isolated species were identified as *Staphylococcus pasteuri*, and 22 were identified as *Staphylococcus warneri*. In this study, Other staphylococcus members were not isolated, except *S. pasteuri* and *S. warneri*.

Antibiotic resistance findings

The phenotypic and genotypic antibiotic resistance results of the 30 isolates obtained from stuffed mussel samples are presented in Table 3. All *S. warneri* isolates demonstrated resistance to amoxicillin/clavulanic acid and erythromycin among the tested antibiotics. Additionally, seven *S. warneri* isolates exhibited intermediate sensitivity to tetracycline and streptomycin, whereas eight were found to have intermediate sensitivity to tetracycline antibiotics. In *S. warneri* isolates, at least three resistance genes (*BlaTEM, tetB-6, tetK-8*), and up to eight resistance genes (*BlaTEM, tetB-6, tetK-8, strA-strB, aphAI-IAB, ermC*) were identified (Table 3).

In this study, it was found that all *S. pasteuri* isolates were resistant to amoxicillin/clavulanic acid. Eight isolates of S. *pasteuri* were determined to have intermediate sensitivity to ampicillin and streptomycin antibiotics. Resistance genes *blaTEM, strA-strB, and aphAI-IAB* were identified in all *S. pasteuri* isolates.

DISCUSSION

In the present study, it was determined that antibiotic-resistant *S. warneri* and *S. pasteuri* contaminate stuffed mussel samples. Similarly, In Italy, samples taken from the preparation counters of ready-to-eat meal companies revealed the isolation of *S. pasteuri* and *S. warneri*. These isolates were reported to be resistant to antibiotics at rates of 83.3% and 42.9%, respectively, among Staphylococcus species (Marino et al., 2011). In Türkiye, *S. warneri* was isolated from fish gills sold at counters, whereas *S. pasteuri* was isolated from the skin and gills (Çoban & Yaman, 2023).

Similar to the present study, antibiotic resistance of *S. warneri* isolated from seafood was reported in a previous study. Isolates of *S. warneri* from sea fish meat have been reported to be resistant to penicillin, ampicillin, tetracycline, erythromycin, and/or

Table 2. List of primers for the detection of antimicrobial resistance genes.

Targeted gene			Sequence (5'-3')	Amplicon (pb)	References
β-lactamases	bla_{TEM}	F	CATTTCCGTGTCGCCCTTATTC	800	Dallenne et al. 2010
		R	CGTTCATCCATAGTTGCCTGAC		
	$bla_{S}Hv$	F	AGCCGCTTGAGCAAATTAAAC	710	
		R	ATCCCGCAGATAAATCACCAC		
	$bla_{C}rx$-*M*	F	CGCTTTGCGATGTGCAG	550	Paterson et al. 2003
		R	ACCGCGATATCGTTGGT		
	mecA	F	GTGAAGATATACCAAGTGATT	150	Alfatemi et al. 2014
		R	ATGCGCTATAGATTGAAAGGAT		
Tetracycline	*tetA*	F	GTAATTCTGAGCACTGTCGC	950	Sengeløv et al. 2003
		R	CTGCCTGGACAACATTGCTT		
	tetB	F	CTCAGTATTCCAAGCCTTTG	400	Sunde and Sørum, 2001
		R	CTAAGCACTTGTCTCCTGTT		
	tetE	F	GTGATGATGGCACTGGTCAT	1100	Sengeløv et al. 2003
		R	CTCTGCTGTACATCGCTCTT		
	tetK	F	TATTTTGGCTTTGTATTCTTTCAT	1150	Trzcinski et al. 2000
		R	GCTATACCTGTTCCCTCTGATAA		
	tetM	F	ACAGAAAGCTTATTATATAAC	171	Aminov et al. 2001
		R	TGGCGTGTCTATGATGTTCAC		
Aminoglycoside resistance	*strA-strB*	F	TATCTGCGATTGGACCCTCTG	540	Sunde and Sørum 2001
		R	CATTGCTCATCATTTGATCGGCT		
	aphAI-IAB	F	AAACGTCTTGCTCGAGGC	460	Frana et al. 2001
		R	CAAACCGTTATTCATTCGTGA		
	aac(3)-IIa	F	ATGGGCATCATTCGCACA	750	Dai et al. 2010
		R	TCTCGGCTTGAACGAATTGT		
	aac(6')-Ib	F	TTGCGATGCTCTATGAGTGGCTA	480	Katalin, 2000
		R	CTCGAATGCCTGGCGTGTTT		
Macrolides	*ermA*	F	GTTCAAGAACAATCAATACAGAG	420	Lina et al. 1999
		R	GGATCAGGAAAAGGACATTTTAC		
	ermB	F	CCGTTTACGAAATTGGAACAGGTAAAGGGC	360	
		R	GAATCGAGACTTGAGTGTGC		
	ermC	F	GCTAATATTGTTTAAATCGTCAATTCC	570	
		R	GGATCAGGAAAAGGACATTTTAC		

oxacillin, whereas *S. pasteuri* isolates have been reported to be resistant to penicillin, oxacillin, ampicillin, and/or erythromycin antibiotics (Regecová et al., 2014). Moreover, isolates of *S. warneri* from fermented sausage products on the market were reported to be resistant to ampicillin, erythromycin, kanamycin, penicillin G, cefalotin, and cefoxitin antibiotics, whereas *S. pasteuri* was reported to be resistant only to erythromycin (Geniş & Tuncer, 2018). In a study conducted by Çavdar et al. in 2022, *S. warneri* was isolated from hospital water tanks, showers, and taps, whereas *S. pasteuri* was isolated only from the water tank.

S. warneri causes disease in rainbow trout in Türkiye and shows resistance to gentamicin, oxacillin, colistin, oxytetracycline, tylosin, spectinomycin, ampicillin, clindamycin, and erythromycin antibiotics (Diler et al., 2023).

To date, there is limited information regarding the presence of antibiotic resistance genes in isolated species of *S. pasteuri* and *S. warneri* from aquatic products. For example, *S. pasteuri* isolated from Jeotgal has been reported to be resistant to linezolid, penicillin, and trimethoprim antibiotics, with trimethoprim resistance associated with carrying the dfrA gene (Jeong and Lee, 2015).

CONCLUSION

In this study, resistance to amoxicillin/clavulanic acid and erythromycin was observed in all *S. warneri* isolates. In addition, all *S. pasteuri* isolates were found to be resistant to amoxicillin/clavulanic acid. In *S. warneri* isolates, the identified resistance genes include *BlaTEM, tetB-6, tetK-8, strA-strB, aphAI-IAB,* and *ermC*, whereas in *S. pasteuri* isolates, the identified resistance genes are *blaTEM, strA-strB,* and *aphAI-IAB*. Consequently, this study will provide a valuable reference for enhancing monitoring strategies in stuffed mussel production. In further studies, the level of public health risk posed by the product should be determined. Therefore, it is necessary to clarify the pathogenic potential and mechanisms of the pathogens identified in stuffed mussels.

Table 3. *Staphylococcus* isolates identification results and phenotypic/genotypic antibiotic resistance profiles.

No	Species	Similarity*	Antibiotics	Resistance Gene					
1	*Staphylococcus warneri*	MK737139 (99.78%)	E, AMC, TE*, S*	bla_{TEM}	*tetB-6*	*tetK-8*	*strA-strB*	*aphAI-IAB*	*ermC*
2	*Staphylococcus warneri*	MT453899 (99.93%)	E, AMC, TE*	bla_{TEM}	*tetB-6*	*tetK-8*			
3	*Staphylococcus warneri*	MW527395 (100%)	E, AMC, TE	bla_{TEM}	*tetB-6*	*tetK-8*	*ermC*		
4	*Staphylococcus pasteuri*	MT539733 (99.92%)	AMC, AMP*, S*	bla_{TEM}	*strA-strB*	*aphAI-IAB*			
5	*Staphylococcus pasteuri*	MF429378 (99.72%)	AMC, AMP*, S*	bla_{TEM}	*strA-strB*	*aphAI-IAB*			
6	*Staphylococcus warneri*	MT328647 (100%)	E, AMC, TE	bla_{TEM}	*tetB-6*	*tetK-8*	*ermC*		
7	*Staphylococcus pasteuri*	OR976013 (99.12%)	AMC, AMP*, S*	bla_{TEM}	*strA-strB*	*aphAI-IAB*			
8	*Staphylococcus warneri*	MF681861 (99.14%)	E, AMC, TE*, S*	bla_{TEM}	*tetB-6*	*tetK-8*	*strA-strB*	*aphAI-IAB*	*ermC*
9	*Staphylococcus warneri*	KY218866 (99.13%)	E, AMC, TE*	bla_{TEM}	*tetB-6*	*tetK-8*			
10	*Staphylococcus warneri*	KR809427 (99.14%)	E, AMC, TE*, S*	bla_{TEM}	*tetB-6*	*tetK-8*	*strA-strB*	*aphAI-IAB*	*ermC*
11	*Staphylococcus warneri*	ON386170 (99.14%)	E, AMC, TE*, S*	bla_{TEM}	*tetB-6*	*tetK-8*	*strA-strB*	*aphAI-IAB*	*ermC*
12	*Staphylococcus warneri*	KT906680 (99.95%)	E, AMC, TE	bla_{TEM}	*tetB-6*	*tetK-8*	*ermC*		
13	*Staphylococcus warneri*	MW148447 (99.55%)	E, AMC, TE	bla_{TEM}	*tetB-6*	*tetK-8*	*ermC*		
14	*Staphylococcus warneri*	MN512291 (99.15%)	E, AMC, TE*	bla_{TEM}	*tetB-6*	*tetK-8*			
15	*Staphylococcus warneri*	KX826983 (99.15%)	E, AMC, TE*	bla_{TEM}	*tetB-6*	*tetK-8*			
16	*Staphylococcus warneri*	MZ043864 (99.14%)	E, AMC, TE	bla_{TEM}	*tetB-6*	*tetK-8*	*ermC*		
17	*Staphylococcus warneri*	LN794823 (99.15%)	E, AMC, TE	bla_{TEM}	*tetB-6*	*tetK-8*	*ermC*		
18	*Staphylococcus pasteuri*	KJ486553 (99.15%)	AMC, AMP*, S*	bla_{TEM}	*strA-strB*	*aphAI-IAB*			
19	*Staphylococcus warneri*	MF681861 (99.20%)	E, AMC, TE*, S*	bla_{TEM}	*tetB-6*	*tetK-8*	*strA-strB*	*aphAI-IAB*	*ermC*
20	*Staphylococcus pasteuri*	KR809418 (99.70%)	AMC, AMP*, S*	bla_{TEM}	*strA-strB*	*aphAI-IAB*			
21	*Staphylococcus warneri*	MG800691 (99.20%)	E, AMC, TE*, S*	bla_{TEM}	*tetB-6*	*tetK-8*	*strA-strB*	*aphAI-IAB*	*ermC*
22	*Staphylococcus warneri*	MZ043864 (99.20%)	E, AMC, TE	bla_{TEM}	*tetB-6*	*tetK-8*	*ermC*		
23	*Staphylococcus warneri*	MK737139 (99.15%)	E, AMC, TE*	bla_{TEM}	*tetB-6*	*tetK-8*			
24	*Staphylococcus warneri*	MW527395 (99.98%)	E, AMC, TE*, S*	bla_{TEM}	*tetB-6*	*tetK-8*	*strA-strB*	*aphAI-IAB*	*ermC*
25	*Staphylococcus warneri*	MT328647 (99.82%)	E, AMC, TE*	bla_{TEM}	*tetB-6*	*tetK-8*			
26	*Staphylococcus pasteuri*	OR517214 (99.73%)	AMC, AMP*, S*	bla_{TEM}	*strA-strB*	*aphAI-IAB*			
27	*Staphylococcus pasteuri*	KP261074 (99.56%)	AMC, AMP*, S*	bla_{TEM}	*strA-strB*	*aphAI-IAB*			
28	*Staphylococcus warneri*	KP860608 (99.13%)	E, AMC, TE*	bla_{TEM}	*tetB-6*	*tetK-8*			
29	*Staphylococcus warneri*	KP261060 (99.13%)	E, AMC, TE*	bla_{TEM}	*tetB-6*	*tetK-8*			
30	*Staphylococcus pasteuri*	KT582293 (99.37%)	AMC, AMP*, S*	bla_{TEM}	*strA-strB*	*aphAI-IAB*			

*Intermediate, **Accession numbers and Sequence result (similarity with 16S rRNA), AMC: amoxicillin/clavulanic acid, AMP: ampisilin, E: erythromycin, TE: tetracycline, S: streptomycin

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