Molecular Typing and Drug Resistance Patterns of *Staphylococcus aureus* Isolated From Raw Beef and Chicken Meat Samples

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**ABSTRACT**

**Background:** *Staphylococcus aureus* is one of the most important food-borne pathogens. The objective of this study was to determine the prevalence, molecular types and drug resistance pattern of *S. aureus* isolated from retail meat in Tabriz city.

**Materials & Methods:** 60 raw meat samples (chicken and beef) were taken from different markets and were inoculated in selective Mueller Hinton broth media supplemented with 10% NaCl. Identification of *S. aureus* isolates was performed using conventional biochemical tests. Susceptibility to different antibiotics and genotypes of isolates were determined by disc diffusion and spa typing methods respectively.

**Results:** Fifteen *S. aureus* strains were isolated from 60 different meat samples which belonged to spa types t14870, t3802, t1814, t491, 1386, 13424 and spa type t14870 with the frequency of 33.3% was the most prevalent genotype among *S. aureus* isolates. spa types of three isolates were not found in Ridom Spa Server data base and were considered as novel types. About 46.6% of isolates were resistant to more than one antibiotic and 13.3% of isolates were identified as methicillin resistant *S. aureus* (MRSA). Tigecycline, imipenem and ceftazidime were found to be the most effective agents against *S. aureus* isolates.

**Conclusion:** Our results revealed a 25% contamination rate with *S. aureus*. Most of the molecular types of isolates were found to be linked to human infections. High rate of antibiotic resistance was observed among the isolates which poses a great threat to public health.

**Keywords:** *Staphylococcus aureus*, MRSA, spa typing, Meat, Antibiotic resistance

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**Introduction**

*Staphylococcus aureus* is one of the most important foodborne pathogens and the most common causes of food poisoning (1). This bacterium is known in many countries as the third leading cause of foodborne illnesses after *Salmonella* and *Vibrio parahaemolyticus* (2). Milk, dairy products and meat are some of the foods associated with staphylococcal food poisoning [1]. This bacterium multiplies quickly at room temperature and secretes its heat-resistant enterotoxins, causing food poisoning following consumption of foods contaminated with these toxins. *S. aureus* is also a cause of various diseases in humans such as skin and soft tissue infections, bacteremia and pneumonia and is a serious problem in hospitals and the food industry (3). The pathogenicity of
S. aureus is mediated by the bacterial specific structure and extracellular secretions such as various toxins. In recent decades, the widespread use of antibiotics has led to the emergence of multidrug-resistant (MDR) bacterial strains. S. aureus has a high adaptive capacity to varying environmental conditions and quickly becomes resistant to virtually all antibiotics (4). Recently, MDR strains of S. aureus have been frequently reported from food poisoning outbreaks and isolated from various food products (3, 5, 6). In particular, isolation of methicillin-resistant S. aureus (MRSA) from meat products raises concerns that these contaminated meats may be a means of transmitting MRSA to human communities (7). The term livestock-associated MRSA (LA-MRSA) is used to differentiate methicillin-resistant S. aureus of human origin (acquired from hospital or community) from those isolated from livestock. LA-MRSA strains have the potential to cause disease in humans and often show multidrug resistance profiles (8). Genotyping of microbial strains is important to understand how bacteria spread, to find a possible source of infection, and to identify the dominant types. There are several molecular methods for typing of S. aureus and MRSA strains. These methods include DNA fingerprinting by PFGE, SCC meC typing and sequencing-based methods such as spa-typing and MLST (3, 9). In spa typing, the polymorphism of x-region of the spa gene (encoding surface protein A) is examined by PCR and sequencing. Because x-region has high degrees of polymorphism, it can be used in genotyping studies. The discriminatory power of spa typing method is lower than PFGE and higher than MLST. This method is more cost-effective than methods such as MLST that require sequencing of at least 7 genes, or the PFGE method (10, 11).

Since meat and meat products are known as important reservoirs of S. aureus and have been involved in various outbreaks, the aim of this study was to investigate the contamination rate of meat samples collected from different parts of Tabriz city with S. aureus and to determine the drug resistance pattern and genotypes of obtained isolates.

Materials and Methods

Isolation of S. aureus from meat samples

Raw beef and chicken samples were collected from various meat shops in Tabriz from June 2019 to January 2020. For sampling, 10 grams of meat sample was taken and placed in sterile tubes containing Mueller-Hinton broth supplemented with 10% NaCl. The tubes were transferred to the laboratory at cold temperature and placed in an incubator at 37°C for 24 hours. Then, different dilutions were prepared and 10 to 20 μL of each dilution was transferred to mannitol salt agar medium and placed at 37 °C for 24 hours. Colonies with yellow halo on mannitol salt agar medium were selected and after purification on nutrient agar medium were subjected for identification by microscopic observation and conventional biochemical methods (catalase, coagulase and DNase tests).

Antimicrobial Susceptibility Testing

For this purpose, disk diffusion was performed by Kirby Bauer method and using paper disks containing the following antibiotics: ampicillin, cefartarone, imipenem, levofloxacin, ciprofloxacin, sulfamethoxazole-trimethoprim (BBL Sensi-Disc™, MD, BBL) and tigecycline (Mast Co, Merseyside, UK). Interpretation of disk diffusion results was performed according to the Clinical & Laboratory Standards Institute (CLSI) (12). Interpretation of the results for tigecycline was performed using FDA guidelines, according to which bacteria with an inhibition zone diameter of 19 mm and more were considered susceptible to tigecycline.

Identification of Methicillin-Resistant Strains of Staphylococcus aureus

Two phenotypic and genotypic methods were used to identify MRSA strains. In the phenotypic method, the susceptibility of the studied isolates to cefoxitin 30 μg (BBL Sensi-Disc™, Becton – Dickinson, Sparks, MD) was evaluated by disk diffusion method. Strains with an inhibition zone diameter of 21 mm or less were considered as cefoxitin resistant and categorized as MRSA. In the genotypic method, detection of mecA and meC genes was performed by PCR method using primers listed in Table 1.

Determination of Molecular types of S. aureus Isolates by spa Typing Method

DNA extraction was performed by boiling method as follows; a loop full of bacterial colonies grown on the nutrient agar medium was dissolved in 950 μL of PBS buffer. The tubes were centrifuged for 10 minutes at 7000 rpm. The precipitate was dissolved in 200μl of sterile TE buffer (1×) and boiled for 10 minutes. After centrifugation at 15,000 rpm for 20 minutes, the supernatant was transferred to another container and 1:10 dilution of supernatant was used as DNA template in PCR reaction (https://www.eurlar.eu/CustomerData/Files/Folders/21-protocols/278_mcr multiplex-PCR-protocol-v2-oct16.pdf).

To amplify the spa gene, PCR was performed in a final volume of 50 μL containing 25 μL of Taq DNA Polymerase Master Mix Red solution (Ampliqon, Denmark), 2.8 μL of each of the reverse and forward primers (Table 1), 17.4 μL of distilled water, 2 μL of template DNA and according to the following program:

One cycle at 95°C for 10 minutes (First denaturation), 30 cycles including 1-95°C for 30 seconds (Denaturation), 2-58 °C for 45 seconds (Annealing), 3-72°C for 45 seconds (Extension), and final extension at 72°C for 10 minutes. The sequences of PCR products were determined by Codon company and analyzed by ChromasPro software. Isolates were assigned to
particular spa types using the spa typing website (http://www.spaserver.ridom.de).

Table 1. Nucleotide sequences of primers used in PCR reaction

| Primer name | Sequence (5’ to 3’) | Size of product (bp) | Reference |
|-------------|---------------------|---------------------|-----------|
| MecA-F      | TGGCTCAGGTACTGCTATCCAC AGTTCTGCAGTACCGGATTGC | 777 | This study |
| MecA-R      | GAAAAAAAGGCTTAGAACGCCTC TGCTCTAATGCTAATGCAATG | 594 | This study |
| spa-1113f   | TAAAGACGATCCTTCGGTGAGC CAGCAGTAGTGCCGTTTGCTT | Variable | [11] |
| spa-1514r   | TAAAGACGATCCTTCGGTGAGC CAGCAGTAGTGCCGTTTGCTT | Variable | [11] |

Results

Determination of the Frequency and Drug Susceptibility of S. aureus Isolated from Meat Samples

A total of 60 raw meat samples (18 chicken and 42 beef) were collected from meat markets in Tabriz during the study period. Fifteen isolates (25%) were obtained from these samples which were identified as S. aureus being observed as Gram-positive cocci with grape-like cluster arrangement under microscopic examination and being positive for catalase, coagulase and DNase tests. The contamination rates in chicken and beef samples were 27.7% and 23.8%, respectively. All isolates were evaluated for multi-drug resistance phenotype, the results of which are shown in Table 2. According to drug susceptibility testing results, all isolates (100%) were susceptible to imipenem, tigecycline and ceftaroline. The observed resistance rate to ampicillin, cefoxitin, quinolones and sulfamethoxazole-trimethoprim were 100%, 13.3%, 33.3% and 20%, respectively.

Identification of Methicillin-resistant S. aureus Isolates

MRSA isolates were identified by disk diffusion (cefoxitin disk) and PCR methods (detection of mecA/C gene). Among 15 S. aureus isolates obtained from meat samples, two were resistant to cefoxitin (with halo diameters of 17 and 19 mm) and harbored mecA gene. The mecC gene was not detected in any of the isolates.

Determination of Molecular Types of S. aureus Isolates by spa Typing Method

For all isolates identified as S. aureus by phenotypic methods, PCR for spa gene was performed using specific primers. Types t14870 and t3802 were the most abundant spa types observed in five (33.3%) and two (13.3%) isolates respectively. spa types of three isolates were not detected in the database and were considered as new types. Also, in terms of distribution of molecular types among different meat samples, t14870, which was the most common spa type was found in 40% and 30% of chicken and beef isolates, respectively. While multidrug resistance phenotype was observed in three of five isolates belonging to t14870 type (60%), the strains belonging to t3802 type (the second most common type) were associated with single drug resistance phenotype. Methicillin-resistant strains also belonged to spa types t1814 and t386, which were isolated from beef and chicken samples, respectively (Table 2).

Table 2. Genotype and drug susceptibility pattern of Staphylococcus aureus isolated from meat samples

| Isolate | spa type | Type of meat sample | Antimicrobial resistance profile |
|---------|----------|---------------------|---------------------------------|
| SA1     | t14870   | Chicken             | AM, CIP, LVX                    |
| SA2     | New type | Beef                | AM                              |
| SA3     | t3802    | Chicken             | AM                              |
| SA4     | t1814    | Beef                | AM, FOX                         |
| SA5     | t14870   | Chicken             | AM, CIP, LVX, SXT               |
| SA6     | t14870   | Beef                | AM, CIP, LVX, SXT               |
| SA7     | t491     | Beef                | AM                              |
| SA8     | New type | Chicken             | AM                              |
| SA9     | t3802    | Beef                | AM                              |
Improper use of human antibiotics in agriculture as a growth promoter or as a prophylactic agent with a dose lower than the treatment dose causes selective pressure on the bacterial populations living in the intestines of animals and the development of resistance. These resistant bacteria can be transmitted directly or indirectly to humans through animal products and cause disease in humans, or they can be a repository for the transmission of antibiotic resistance genes to human pathogenic bacteria (13, 14).

There are evidences supporting the transmission of extended-spectrum beta-lactamase (ESBL) producing Escherichia coli clones, from livestock to human being presumably through the food chains (15). Numerous studies have described the colonization of various animals with S. aureus, and methicillin resistant isolates have also been reported from food producing animals (16). In 2017, the World Health Organization recognized MRSA as one of the 12 families of bacteria that pose a serious threat to human health (17). In the present study, a 25% contamination rate with S. aureus (27.7% chicken, 23.8% beef) was observed among meat samples collected from different parts of Tabriz city. The rate of contamination observed in this study was similar to the results of Ge et al., who reported a S. aureus contamination rate of 27.9% in meat samples studied in the United States (18). This rate of contamination is also lower than that reported by Tang et al., who described S. aureus contamination rate of 68% in meat samples from Denmark (19).

In the present study, 46.6% of the isolates were resistant to more than one antibiotic. Imipenem, tigecycline, and Ceftaroline fosamil were the most effective agents against S. aureus isolated from meat samples. In contrast, 100, 20 and 33% of isolates were resistant to ampicillin, sulfamethoxazole-trimethoprim and quinolones respectively. This amount of resistance observed against quinolones, as one of the most important antibiotics used for the treatment of upper respiratory and genitourinary tract infections, can be attributed to the widespread use of these antibiotics in farm animals.

Discussion

In a study performed by Wu et al., who studied 1,850 raw meat samples and meat products from 39 cities in China, 35% of the samples were found to be contaminated with S. aureus. Only 1.26% of S. aureus isolates obtained from meat samples were sensitive to all 26 tested antibiotics, 94.6% were non-susceptible to more than 3 antibiotics and 12% of isolates showed resistance to more than 10 antibiotics (6). Xing et al., reported that 98.4% and 58.6% of the studied S. aureus were resistant to more than one and three antibiotics respectively (20).

We found methicillin-resistant bacteria in 10 and 20% of the isolates obtained from beef and chicken samples, respectively. Isolates SA4 and SA11 (13.3%) belonging to spa types t1814 and t386 were classified as MRSA. Resistance to methicillin in these two strains was confirmed by both phenotypic and genotypic methods.

The prevalence of MRSA observed in this study was higher than the values reported by Wu et al., in which 7.14% of S. aureus strains isolated from meat samples were identified as MRSA (6).

The source of microbial contamination of meat can be endogenous originating from the animal microbiota or it can be exogenous, which is related to environmental pollutants and people involved in processing and transporting meat from slaughterhouses to meat markets. Using spa typing technique, type t14870 with a frequency of 33.3% was identified as the predominant spa type in S. aureus isolates obtained from meat samples being observed in 40% and 30% of chicken and beef isolates, respectively. In three of the five isolates belonging to this type (60%) the multidrug resistance phenotype was observed, so that 80% of quinolones resistant isolates and all isolates resistant to sulfamethoxazole-trimethoprim belonged to type t14870. This type is one of the rare types in the world and there are few studies reporting detection of this genotype in human samples (23). Also, spa types t3802,

| Isolate | spa type | Type of meat sample | Antimicrobial resistance profile |
|---------|----------|---------------------|---------------------------------|
| SA10    | New type | Beef                | AM                              |
| SA11    | t386     | Chicken             | AM,FOX                          |
| SA12    | t14870   | Beef                | AM                              |
| SA13    | Non typeable | Beef             | AM                              |
| SA14    | t3424    | Beef                | AM, CIP, LVX                     |
| SA15    | t14870   | Beef                | AM, CIP, LVX, SXT                |

CIP, ciprofloxacin; LVX, levofloxacin; SXT, trimethoprim/sulfamethoxazole; AM, ampicillin; FOX, cefoxitin;
t1814, t491 and t386 that were identified among the studied samples are common human types (24-26). Identification of common spa types of human infections among isolates obtained from meat samples in this study indicates that these contaminants are probably of human origin and therefore have the potential to be pathogenic in human. Also, 3 isolates characterized with new spa types that were not found in the Ridom spa Server database and were reported for the first time in the world. Drug susceptibility testing in these isolates revealed the single drug resistance phenotype (ampicillin resistance).

The high genetic diversity observed among the studied strains indicates that the clonal expansion was not occurred and the contaminating bacteria may have originated from various sources. Wu et al. reported ST1-t127 and ST7-t091 as the two dominant spa types in 10.7% and 10.6% of S. aureus isolates obtained from meat samples, respectively (6). Narvaez et al. examined the prevalence of MRSA in meat samples from three pork factories in Canada. According to their results, most LA-MRSA isolates belonged to spa types t034 and t011. A 10% resistance rate to tigecycline was observed and less than 3% of isolates were resistant to daptomycin, gentamicin and trimethoprim-sulfamethoxazole (22).

**Conclusion**

Overall, the results of this study showed a 25% contamination rate with S. aureus in raw meat samples and most of the identified molecular types were linked with human infections. Identification of MRSA as an important human pathogen, in meat samples is a serious threat to food safety as there is always a potential for these resistant isolates to easily spread across the country via food chain or direct contact. Reducing the agricultural use of important medical antibiotics such as quinolones and other families of antimicrobials in the farm animals can contribute to reduced resistance to these antibiotics. Therefore, proper control should be done on the consumption of antibiotics in food animals and food hygiene in different stages of their preparation (animal husbandry, slaughterhouse, packaging, etc.) to prevent the emergence and dissemination of drug resistant bacteria.

**Acknowledgment**

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**Conflict of Interest**

Authors declared no conflict of interests.
# تعبین تیپ‌های مولکولی و الگوهای مقاومت آنتی‌بیوتیک سویه‌های استافیلوکوکوس/ورتونس

## جدای شده از نمونه‌های گوسنده گوشت و مرغ خام

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## چکیده

زمینه و اهداف: استافیلوکوکوس/ورتونس یکی از باطن‌های مهم منطقه از این قبیل است. اهداف این مطالعه تعمیم دروازه‌های مولکولی و الگوحای مقاومت آنتی‌بیوتیک سویه‌های استافیلوکوکوس/ورتونس از نمونه‌های گوسنده گوشت و مرغ خام تبریز، ایران را شناسایی کردن.

مواد و روش کار: نمونه‌های گوسنده گوشت و مرغ خام از مراکز فروشگاهی محلی شناسایی و به‌عنوان نمونه گیری کردند.

پژوهشگران شناسایی جدایه‌هایی به‌عنوان گونه‌هایی مانند Bacillus sp. و الگوهای مقاومت‌پذیر را با روش نرم (spu typing) شناسایی نمودند.

نتیجه‌گیری: نتایج تحقیق تاکنون نشان داده که حداقل ۲۵٪ از نمونه‌های استافیلوکوکوس/ورتونس را باعث بیماری‌های غذایی می‌گردد.

کلمات کلیدی: استافیلوکوکوس/ورتونس، گوشت، مقاومت آنتی‌بیوتیک، spu typing, MRSA, Gostk, مقاومت آنتی‌بیوتیک

## مقدمه

استافیلوکوکوس/ورتونس یکی از باطن‌های مهم منطقه از غذا است و از شایع‌ترین علل سمومی‌های غذایی به شمار می‌آید. این بакتری در سایری از کشورها به عنوان سومین عامل بروز بیماری‌های غذایی بر سال‌ها و بیمارستان‌های این‌جنس شناخته شده است. شیر، گوشت و پنیر از جمله‌های غذایی مرتبط با سمومی استافیلوکوکوس محسوب می‌شود.

ایجاد سمومی غذایی می‌تواند باعث ایجاد سمومی غذایی در انسان مانند سمومی‌های بروز و بیماری توتامیت باشد.
جداولی استلفایلوکوکوس اورتوس مقام به متن سیلیبن (Methicillin Resistant S. aureus (MRSA))
این نگرانی را ایجاد کرده که این گوشت‌های آلوده و سیلیبن‌های برای
جو اعمال MRSA انتقال با MRSA یا MRSA (LA-MRSA) 
اختش بایر افتراق استلفایلوکوکوس اورتوس یا مقایسه به متن سیلیبن
با منشا انسانی (کسب یا از تولید که از انتخاب جدایی به
اشاره به واحد MRSA سه $\text{mm}$ در انسان را می‌توان به

تیپ‌بندی سویه‌های میکروبی برای یک پرونده نهایت
باکتری، افتان منعی عفونت‌ها و شناسایی تیپ‌های بالا
موجود بسیار اهمیت دارد. این MRSA 
تیب بندی و شناسایی سویه‌های استلفایلوکوکوس اورتوس و
نحوه تایید از جمله این روش‌ها می‌توان به آنتی‌بایر
روش و روش‌های شناسایی تولید بنیت (SCC mec typing, PFGE
این استاد در انجام گرفت (9, 10).

تشخیص استلفایلوکوکوس اورتوس مقام به

تبین حساسیت از کلیک‌های 

بدین منظور دیسک‌های کاغذی حاوی 

استفاده از دیسک‌های کاغذی حاوی آنتی‌بایر یکی 

ستافیلوکوکوس، مربوط و سیلین و با

کیفیت سولفامتو، با استفاده از دستورالعمل

(انجام شد. تفسیر نتایج

کال، کواگوال و شناسایی شدن.

تشخیص استلفایلوکوکوس اورتوس مقام به

با Kirby Bauer

میکروبی

شناسایی سویه‌های استلفایلوکوکوس اورتوس مقام به

متن سیلیبن

چه جهت شناسایی سویه‌های MRSA از دو روش فتوئیتی و

زونتیبی استفاده شد. در روش فتوئیتی حساسیت جدایی مورد

(BBL Sensi-Disc™, Becton–Dickinson, Sparks, MD)

از دیسک‌های کاغذی حاوی پتروپتی

در روش فتوئیتی حساسیت جدایی مورد

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(BBL Sensi-Disc™, Becton–Dickinson, Sparks, MD)

از دیسک‌های کاغذی حاوی پتروپتی

در R</p><p>درو از گروه سلول‌های مورد
</p><p>کیفیت سولفامتو، با استفاده از دستورالعمل
</p><p>کال، کواگوال و شناسایی شدن.

تشخیص استلفایلوکوکوس اورتوس مقام به

با Kirby Bauer

میکروبی

شناسایی سویه‌های استلفایلوکوکوس اورتوس مقام به

متن سیلیبن

چه جهت شناسایی سویه‌های MRSA از دو روش فتوئیتی و

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(BBL Sensi-Disc™, Becton–Dickinson, Sparks, MD)

از دیسک‌های کاغذی حاوی پتروپتی</p><p>در R</p>
شناسایی جدایی‌های استافیلکوکوس اوروروس مقاوم به متی سیلیم

شناختی جدایی‌های استافیلکوکوس اوروروس مقاوم به متی سیلیم (MRSA) با بد بود روش دایکس دیپس و دیسک سقوطیت و رابداری زن meca/C صورت گرفت. از ساین 15 جدایی استافیلکوکوس اوروروس به‌دست آمده از نمونه‌های گوشت دو جدایی مقاوم به سقوطیتی بوده (با فقر حاله‌های meca/C شناسایی شد و در هر جدایی زن meca/C لازم به ذکر است زن meca/C در هر کدام از جدایی‌های مورد بررسی ساختاری نشد.

تیپینگ یا نتیجه‌گیری مولکولی جدایی‌های استافیلکوکوس

در مجموع 30 نمونه گوشت خام (گوشت مرغ) و اوروروس گوشت (MrsA) به خصوصیت هوش سه‌شل برپایه در مدت زمان مقاومت جمع‌آوری شد. از تعداد 15 جدایی (15/2) به‌دست آمد که بر صفت کوکسیا های درخست و ارزیابی خشخاشی از پرسی میکروسکوپی مشاهده شدند و دارای یک‌تایی مثبت نسبت بالایی در نتایج کانال بالایی و گوشت (MrsA) 20/2 و میان مورد مشاهده شده در گوشت مرغ و گوشت به ترتیب 20/3 و 20/7. بود تعداد نمونه‌ها فاکتور گسترشی دارای مثابه داده‌های قبلی در هر 2 و 13/2.

تیپینگ یا نتیجه‌گیری اوروروس با روش spa typing

برای تمامی اوروروسی که در روش رنگ‌گذاری به‌عنوان پس پس اوروروس اوروروس تیپینگ هوش شدنتمایز از پس اوروروسی اخترین اجسام گرفته. بر اساس نتایج بدست‌آمده

| سرچشمه (bp) | اندازه محلول (μL) | نام پرایمر |
|---------------|-------------------|------------|
| این ططاطا | GGGCTCAGCTATGCTACCCAGTTGCTCCTAATGCTAATGCAATG | MecA-F |
| این ططاطا | GAAAAAGATTCGAAACGCTCCTGGCTCTCTATGCTAAATGCAATG | MecA-R |
| متغیر | TAAAGACGGATCCTGGAGTCGCACCGGTAGTTGCTT | MecC-F |
| متغیر | TAAAGACGGATCCTGGAGTCGCACCGGTAGTTGCTT | MecC-R |
| متغیر | GAAAAAGATTCGAAACGCTCCTGGCTCTCTATGCTAAATGCAATG | spa |

یافته‌ها

تیپینگ یا نتیجه‌گیری دارویی استافیلکوکوس

اوروروس یا جدایی‌های مشاهده نشان داده شده است. در تست تعیین فراوانی و حساسیت دارویی اوروروس اوروروس مقاوم در واکنش DNA Polymerase Master Mix Red (Ampliqon, 2/μL.Denmark).

جدول 1. نتایج پروموتوپی دارویی استافیلکوکوس و واکنش.
سمانه فرهمد و همکاران | تیپ‌های مولکولی استافیلوکوکوس اورتوس جدایه شده از گوشت

تیپ‌های 4870 و 13802 از فراوان‌ترین spa type های مشاهده شده در جدایه‌های استافیلوکوکوس اورتوس به دست آمده از نمونه‌های گوشت بودند که در ترتیبی در پایگاه داده‌های مورد بررسی ردقیق‌نشده و به عنوان تیپ‌های جدید در نظر گرفته شدند. همچنین از نظر توزیع تیپ‌های مولکولی در میان نمونه‌های گوشت متفاوت، نمونه‌های گوشت بودی که در پایگاه داده‌های مورد بررسی ردیابی نشدند مشاهده شدند. همچنین در میان نمونه‌های گوشت مقاوم به متی سیلین نیز به spa type های 1814 و 386 تعیق یافته و به ترتیبی در نمونه‌های گوشت گوساله و مرغ جدایی شده (جدول 2).
تشکل مشاهده ای از استافیلوکوکوس و رونس جدایی شده از گوشت به عنوان MRSA مشاهده شد. در مورد مطالعه MRSA که در نمونه‌های گوشت مورد نظر شده است، توجه باید به ملاحظه کلی روند در بالا قرار داشته باشد. این مطالعه نشان داد که با توجه به الگوی حادت در در روند و رنگ و در نمونه‌های گوشت در این مطالعه، مشاهده گردید.
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Reference

1. Kadariya J, Smith TC, Thapaliya D. Staphylococcus aureus and staphylocoocal food-borne disease: an ongoing challenge in public health. BioMed research international. 2014;2014. [DOI:10.1155/2014/827965] [PMID] [PMCID]

2. Wei-Wei L, Zhu J, Zhen S, Liang X, Jiang Y, Ning L. Analysis of foodborne disease outbreaks in China mainland in 2011. Chin J Food Hygiene. 2018;30:283-8.

3. Jackson CR, Davis JA, Barrett JB. Prevalence and characterization of methicillin-resistant Staphylococcus aureus isolates from retail meat and humans in Georgia. Journal of clinical microbiology. 2013;51:1199-207. [DOI:10.1128/JCM.03166-12] [PMID] [PMCID]

4. McCallum N, Berger-Bächi B, Senn MM. Regulation of antibiotic resistance in Staphylococcus aureus. International Journal of Medical Microbiology. 2010;300:118-29. [DOI:10.1016/j.ijmm.2009.08.015] [PMID]

5. Papadopoulou P, Papadopoulou T, Angelidis AS, Boukouvala E, Zdragas A, Papa A, et al. Prevalence of Staphylococcus aureus and of methicillin-resistant S. aureus (MRSA) along the production chain of dairy products in north-western Greece. Food microbiology. 2018;69:43-50. [DOI:10.1016/j.fm.2017.07.016] [PMID]

6. Wu S, Huang J, Wu Q, Zhang J, Zhang F, Yang X, et al. Staphylococcus aureus isolated from retail meat and meat products in China: incidence, antibiotic resistance and genetic diversity. Frontiers in microbiology. 2018;9:2767. [DOI:10.3389/fmicb.2018.02767] [PMID] [PMCID]

7. Voss A, Loeffen F, Bakker J, Klaassen C, Wulf M. Methicillin-resistant Staphylococcus aureus in pig farming. Emerging infectious diseases. 2005;11:1965. [DOI:10.3201/eid1112.050828] [PMID] [PMCID]

8. Kadlec K, Entorf M, Peters T. Occurrence and characteristics of livestock-associated methicillin-resistant Staphylococcus aureus in quarter milk samples from dairy cows in Germany. Frontiers in microbiology. 2019;10. [DOI:10.3389/fmicb.2019.01295] [PMID] [PMCID]

9. Wang X, Li G, Xia X, Yang B, Xi M, Meng J. Methicillin-susceptibility and molecular typing of methicillin-resistant Staphylococcus aureus in retail foods in Shaanxi, China. Foodborne pathogens and disease. 2014;11:281-6. [DOI:10.1089/fpd.2013.1643] [PMID]

10. Koreen L, Ramsawamy SV, Graviss EA, Naidich S, Musser JM, Kreiswirth BN. spa typing method for discriminating among Staphylococcus aureus isolates: implications for use of a single marker to detect genetic micro- and macrovariation. Journal of clinical microbiology. 2004;42:792-9. [DOI:10.1128/JCM.42.2.792-799.2004] [PMID] [PMCID]

11. Stommenger B, Braulke C, Heuck D, Schmidt C, Pasemann B, Nübel U, et al. spa typing of Staphylococcus aureus as a frontline tool in epidemiological typing. Journal of clinical microbiology. 2008;46:574-81. [DOI:10.1128/JCM.01599-07] [PMID] [PMCID]

12. Patel JB. Performance standards for antimicrobial susceptibility testing: Clinical and Laboratory Standards Institute; 2017.
13. Founou LL, Founou RC, Essack SY. Antibiotic resistance in the food chain: a developing country-perspective. Frontiers in microbiology. 2016;7:1881. [DOI:10.3389/fmicb.2016.01881] [PMID] [PMCID]

14. Chang Q, Wang W, Regev-Yochay G, Lipsitch M, Hanage WP. Antibiotics in agriculture and the risk to human health: how worried should we be? Evolutionary applications. 2015;8:240-7. [DOI:10.1111/eva.12185] [PMID] [PMCID]

15. Kluymans IA, Overdevest IT, Willemsen I, Kluymans-Van Den Bergh MF, Van Der Zwaluw K, Heck M, et al. Extended-spectrum β-lactamase-producing Escherichia coli from retail chicken meat and humans: comparison of strains, plasmids, resistance genes, and virulence factors. Clinical Infectious Diseases. 2012;56:478-87. [DOI:10.1093/cid/cis929] [PMID]

16. Gharsa H, Slama KB, Lozano C, Gómez-Sanz E, Klibi N, Sallem RB, et al. Prevalence, antibiotic resistance, virulence traits and genetic lineages of Staphylococcus aureus in healthy sheep in Tunisia. Veterinary microbiology. 2012;156:367-73. [DOI:10.1016/j.vetmic.2011.11.009] [PMID]

17. Asokan GV, Vanitha A. WHO global priority pathogens list on antibiotic resistance: why is it necessary for people to realize one health data. Perspectives in public health. 2018;138:87-8. [DOI:10.1177/1757913917743881] [PMID]

18. Ge B, Mukherjee S, Hsu C-H, Davis JA, Tran TTT, Yang Q, et al. MRSA and multidrug-resistant Staphylococcus aureus in US retail meats, 2010-2011. Food microbiology. 2017;62:289-97. [DOI:10.1016/j.fm.2016.10.029] [PMID]

19. Tang Y, Larsen J, Kjeldgaard J, Andersen PS, Skov R, Ingmer H. Methicillin-resistant and-susceptible Staphylococcus aureus from retail meat in Denmark. International journal of food microbiology. 2017;249:72-6. [DOI:10.1016/j.ijfoodmicro.2017.03.001] [PMID]

20. Xing X, Li G, Zhang W, Wang X, Xia X, Yang B, et al. Prevalence, antimicrobial susceptibility, and enterotoxin gene detection of Staphylococcus aureus isolates in ready-to-eat foods in Shaanxi, People's Republic of China. Journal of food protection. 2014;77:331-4. [DOI:10.4315/0362-028X.JFP-13-301] [PMID]

21. Kim YJ, Oh DH, Song BR, Heo EJ, Lim JS, Moon JS, et al. Molecular characterization, antibiotic resistance, and virulence profile of methicillin-resistant Staphylococcus aureus strains isolated from imported and domestic meat in Korea. Foodborne pathogens and disease. 2015;12:390-8. [DOI:10.1089/fpd.2014.1885] [PMID]

22. Narvaez-Bravo C, Toufeer M, Weese S, Diarra M, Deckert A, Reid-Smith R, et al. Prevalence of methicillin-resistant Staphylococcus aureus in Canadian commercial pork processing plants. Journal of applied microbiology. 2016;120:770-80. [DOI:10.1111/jam.13024] [PMID]

23. Alni RH, Mohammadzadeh A, Mahmoodi P. Molecular typing of Staphylococcus aureus of different origins based on the polymorphism of the spa gene: characterization of a novel spa type. 3 Biotech. 2018;8:58. [DOI:10.1007/s13205-017-1061-6] [PMID] [PMCID]

24. Abbassian S, Farahani NN, Mir Z, Alinejad F, Haeili M, Rahmardehi M, et al. Genotypic characterization of Staphylococcus aureus isolated from a burn centre by using agr, spa and SCCmec typing methods. New microbres and new infections. 2018;26:15-9. [DOI:10.1016/j.nmn.2018.08.001] [PMID] [PMCID]

25. Rijnders M, Deuverenb R, Boumans M, Hoogkamp-Korstanje J, Beisser P, Stobberingh E. Population structure of Staphylococcus aureus strains isolated from intensive care unit patients in the Netherlands over an 11-year period (1996 to 2006). Journal of clinical microbiology. 2009;47:4090-5. [DOI:10.1128/JCM.00820-09] [PMID] [PMCID]

26. Hashemizadeh Z, Hadi N, Mohebi S, Kalantar-Neyestanaki D, Bazargani A. Characterization of SCCmec, spa types and Multi Drug Resistant of methicillin-resistant Staphylococcus aureus isolates among inpatients and outpatients in a referral hospital in Shiraz, Iran. BMC research notes. 2019;12:614. [DOI:10.1186/s13104-019-4627-z] [PMID] [PMCID]