Methicillin resistant *Staphylococcus aureus* isolated from meat raw in Cartagena, Colombia

*Staphylococcus aureus* resistente a meticilina aislado de productos cárnicos crudos en Cartagena, Colombia

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**ABSTRACT**

Key words:  
MRSA  
MSSA  
PCR  
Panton Valentine  
Leukocidin toxin (PVL)  
Meat products  
Bacterial resistance

To determine the prevalence of Methicillin Resistant *Staphylococcus aureus* (MRSA) isolated in establishments that commercialize raw ground beef and pork chops in Cartagena- Colombia. 160 samples were analyzed through microbiological cultures in Baire Parcker agar, and it was determined the presence of mecA gen that codifies the methicillin resistance and the pvl that codifies the Panton- Valentine leukocidin toxin (PVL) by the multiplex PCR technique. The antibiotic susceptibility profile for MRSA strains was realized by automatized methods and for MSSA strains it was used Kirby Bauer. 66 samples were confirmed as *S. aureus* by PCR. The prevalence of MRSA was 7.5% and 33.8% of MSSA. The 66% of the strains were isolated from raw ground beef and the 34% of pork chop meat. The isolations presented about 2 – 12% of multi-resistance to the antibiotics used. The MRSA showed resistance to amoxicillin- clavulanate (57%), ampicillin- sulbactam and cefazolin (85%), erythromycin and clindamycin (7%), tetracycline (35%). The 10% of the isolated strains had the gen of PVL toxin and the 71% of those were identified in samples of raw pork meat and the 28% in raw ground beef. This study reports for the first time, how meat raw products commercialized in the city of Cartagena could build a dissemination source of MRSA carrier of PVL toxin that could generate a public health disease.

**RESUMEN**

Palabras claves:  
SARM  
SASM  
PCR  
Toxina Panton Valentin  
Leucocidina (PVL)  
Productos cárnicos  
Resistencia bacteriana

Se determinó la prevalencia de *Staphylococcus aureus* resistente a Meticilina (SARM) aislado en expendios que comercializaban carne cruda molida de res y chuleta de cerdo en Cartagena - Colombia. Fueron analizadas 160 muestras a través de cultivo microbiológico en agar Baire Parcker y se determinó la presencia del gen mecA que codifica la resistencia a la meticilina y de pvl que codifica la toxina leucocidina de Panton-Valentine (PVL) mediante la técnica de PCR múltiple. El perfil de susceptibilidad antibiótica para las cepas SARM fue realizado por métodos automatizados y para cepas SASM se utilizó Kirby Bauer. 66 muestras fueron confirmadas como *S. aureus* por PCR, la prevalencia de SARM fue de 7.5% y 33.8% de SASM. El 66% de las cepas fueron aisladas de carne molida de res y 34% de carne de chuleta de cerdo. Los aislamientos presentaron entre 2 a 12% de multirresistencia a los antibióticos utilizados. Los SARM mostraron resistencia a amoxicilina-clavulonato (57%), ampicilina – sulbactam y cefazolina (85%), eritromicina y clindamicina (7%), tetraciclin (35%). El 10% de las cepas aisladas tenían el gen de la toxina PVL y el 71% de estos fue identificado en muestras de carne cruda de cerdo y el 28% en carne cruda molida de res. Este estudio reporta por primera vez, como productos cárnicos crudos comercializados en la ciudad de Cartagena pueden constituir una fuente de diseminación de cepas SARM portadoras de la toxina PVL, lo cual podría generar un problema de salud pública.

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Since its isolation in 1961 until now, methicillin resistant *Staphylococcus aureus* (MRSA) has been considered one of the main pathogens in healthcare-associated infections at hospitals, nevertheless, in the last two decades the scene of infections caused by this bacteria has been changing due to the emergency and dissemination of productive strains of community acquired infections, known as CA-MRSA (Bustos et al., 2006). This strains defer from the traditional hospitalarie ones, not only in their epidemiological behaviour but also in their susceptibility to antibiotics and virulence (Zetola et al., 2005). The CA-MRSA strains has been showed virulent features, and have caused serious outbreaks in gated communities as family, military groups, recluses, kindergartners and athletes (Ho et al., 2007). Most of these strains produce the toxin Panton-Valentine leukocidin (PVL), which has been associated with necrotizing pneumonia in all age groups; containing the chromosomal cassette SCCmec type IV or V, which confers methicillin resistance which is encoded in the *mecA* gene that is located in this cassette (McClure et al., 2006; Hiramatsu et al., 2001). This genetic vehicle can carry other genes as Tn554 gene that confers macrolid, clindamycin and streptogramins resistance, the pT181 gene, confers tetracycline resistance. The same SSCmec can carry virulence genes enterotoxin B and C and toxic shock toxin (Barbara-Wysockib et al., 2010; Zuo et al., 2008). Additionally, MRSA strains have the ability to produce intermittent colonizations (children, 10-40% and adults, 30%) being the most common site, the nasal cavity, which can lead to infections with severity varying degrees as infections of the skin and tissues through osteomyelitis and rapidly evolving and high mortality necrotizing pneumonia (Quiroga et al., 2013).

Regarding to multi-resistant *Staphylococcus aureus* strains related with food industry it has been shown that these has predominantly colonized people who works in the production of animal origin food. It also has been reported high prevalence of *S. aureus* on pigs of different parts of the world (Smith and Pearson, 2010; Rijen et al., 2007). By the way, studies such as Gilchrist et al. (2007), have shown contamination of meat with multiresistant *S. aureus* to clinically important antibiotics as Ciprofloxacin, quinupristin / dalfopristin, clindamycin, erythromycin, oxacillin, and daptomycin. Also in a study made in Colombia, they found that the prevalence of resistance to erythromycin and clindamycin in *S. aureus*, was around 57 and 58%, respectively (Reyes et al., 2007). In the city of Cartagena they have been studies that report the presence of CA-MRSA in individuals with no clinical antecedents. Álvarez et al. (2006), in patients with nasal pathology treated in the Otolaryngology service at the Universitary Hospital of the Carribean in Cartagena, reported a prevalence of *S. aureus* 22.8% and 5.26% for MRSA; another investigation by Bettin et al. (2012), reported that the 16% of the Medical students carry at least one of the MRSA strains in their nostrils for one or two years of their stay in clinics, where they perform their professional practices. The purpose of this study was to determine the prevalence of *S. aureus* CA-MRSA and antimicrobial susceptibility profile from samples of ground beef and raw pork meat sold in the city of Cartagena, in order to meet potential sources of spread of such pathogenic microorganisms.

**MATERIALS AND METHODS**

**Obtaining the samples**

An observational descriptive study was conducted in 40 establishments which commercialize beef and raw pork, distributed in three locations in the city of Cartagena: 19 (47.5%) in the localidad histórica y del Caribe (LHC); 16 (40%) in the localidad industrial de la bahía (LIB) and 5 (12.5%) in the localidad turistica (LT), where the statistical criteria for the selection of the shops that marketed the two types of meat was: estimated variance of 0.19 according to preliminary investigation; a 5% of error and a minimum probability of 75%. The establishments (sampling units) were randomly selected and in each one dispensing samples between 100-300 g of ground beef (CM) and raw pork chop meat (CC) were taken. The sampling was conducted from July 2012 to May 2013, taking into account the guidelines set out in the Norma Técnica Colombiana NTC 4491-2 (2004).

**Microbiological analysis**

Once the samples were taken, these were labeled, refrigerated to 4 °C and transported to the science laboratory of food at the Universidad del Sinú- Seccional Cartagena. Microbiological cultures were performed for the count of *S. aureus* through the count in Baird Parcker® agar plate technique. The procedure consisted on performing three samples of serial dilutions (10⁻¹, 10⁻² and 10⁻³), and plated in duplicates, incubated it for 48 hours at 35 °C,
Methicillin resistant *Staphylococcus aureus* isolated from meat raw in Cartagena, Colombia

According to INVIMA (1998), and the NTC 4779 (2007). The sample reading was realized according to the NTC 1325 (2008) that establishes as an acceptable microbiological requirement for *S. aureus* 100-300 CFU g\(^{-1}\) of meat raw processed, cool and/or frozen products. Samples were the growth was not showed, were reported as <100 CFU g\(^{-1}\). The specificity and sensibility controls of the culture medium realized with the *S. aureus* sample ATCC 25923.

**Molecular Identification**

The genomic DNA in each isolation was reached according to the protocol described by Bettin *et al.* (2012). Were each presumptive isolation was cultured on a Plate Count\(^{\circledR}\) agar and incubated for 24 h at 37 °C. Five colonies were suspended in 0.5 mL of TE buffer and centrifugated at 13,000 rpm x 5 min, heated for 30 min and finally centrifuged at 13,000 rpm for 15 min. The supernatant that contains the bacterial DNA was stored at -20 °C until a subsequent amplification through the multiplex polymerase chain reaction (M-PCR).

**Polymerase chain reaction (PCR) test**

Every isolated MRSA were tipifyed using a multiple PCR essay according with the protocol described by (Zhang *et al.*, 2005). The recollected DNA was subjected to a M-PCR to amplify the *mecA* gene (who determine the methicillin resistance), that amplifies a 147 pb fragment, the *nuc* gene of the specific *S. aureus* thermostable nuclease that amplifies a 300 pb fragment and the 437 pb of the *Luk-PVL* of the PVL toxin. The control strains were *S. aureus* ATCC 33591 (*mecA* +; *nuc* +; PVL -) and ATCC 25923 (*mecA* -; *nuc* +; PVL +) and water for negative control of the PCR assays. The DNA was amplified in a reaction volume of 25uL containing 12.5 uL of PCR mix (PCR master Mix; Promega), 0.2 uM of each primer and 5 uL of template DNA. The reaction was conducted in an Axigen\(^{\circledR}\) thermal cycler under the following conditions: an initial cycle of denaturation at 94 °C for 5 min, followed by 30 cycles of 94 °C for 1 min, 50 °C for 1 min, and 72 °C 2 min with a final extension cycle at 72 °C for 10 min. All products were visualized on agarose gel 1.5% with ethidium bromide (0.5 ug mL\(^{-1}\)), using a UV transilluminator.

**Antibiotic susceptibility profile.** The method used to identify MRSA strains was the MicroScan automated system, Siemens\(^{\circledR}\), using panels for dehydrated Gram positive, supplied by Siemens. For the MSSA strains was used the diffusion method on Kirby Bauver disc. The MSSA strains were determined the following antimicrobials susceptibility: gentamicin 10 mg, 15 mg erythromycin, trimethoprim / sulfamethoxazole 23.75 mg and 1.25 mg, 2 mg clindamycin and rifampin 5mg, those antibiotics were supplied by DIFCO. For oxacillin resistance mediated by the *mecA* gene, was performed as a screening test the microdilution agar technique and a disk diffusion with 30 ng cefoxitin (DIFCO) in a Mueller-Hinton agar. The plates were incubated at 35 °C between 16 to 20 hours. Reading and interpretation was performed according to the guide lines of CLSI, (2013). The positive *mecA* control strain was *S. aureus* ATCC 43300.

**RESULTS AND DISCUSSION**

Emergence of methicillin resistant *Staphylococcus aureus* strains in the community with different characteristics from MRSA hospital strains, has caused an alert among health centers and organizations dedicated to the study and control of this microorganism. CA-MRSA infections are an emerging problem in many parts of the world. The injury level yet known, the epidemiological change, clinical manifestations and control can become into a significant public health problem in the near future. Establishing health measures it’s neccesary to control the re-emergence of this pathogen and, as possible, to eliminate it in time for preventing it to become a serious threat to the community. In total 160 samples were taken in 40 establishment that comercialized raw meat products, 80 samples of ground beef and 80 samples of pork chop meat. 47.5% (76/160) of the samples was taken in the LHC, 40% in the industrial bay place (LIB) and 12.5% in the tourist place (LT).

From the 160 samples analyzed, in 46% of the samples (75/160) were obtained presumptive counts os *S. aureus* greater than 100 CFU g\(^{-1}\) in 54% (85/160) no microbial growth was obtained, which is reported as counts <100 CFU g\(^{-1}\). At the 75th samples counted > 100 CFU g\(^{-1}\) were subjected to the technique of polymerase chain reaction (PCR) to confirm the identification of the bacterial genus and in 66 samples (88%) the presence of *S. aureus* was confirmed and in 9 (12%) was not possible to determine the genus. From the 66 samples confirmed by PCR, 18% (12/66) were positive for the *mecA* gene indicating that they were MRSA strains, and 54 (82%) did not have the gene, confirming them as methicillin sensitive or MSSA strains. As for its origin, 66% were isolated from ground
beef meat and 34% pork chop, regardless if they were MRSA or MSSA. Regarding to it provinance, the 66% were isolated from ground beef and 34% from pork chop meat regardless if they were MSRA or MSSA.

From the 66 confirmed samples, 23 (35%) had acceptable microbiological counts of food quality (100-300 CFU g⁻¹) according to the Norma Técnica Colombiana NTC 1325 (2008); and 43 samples (65%) presented higher counts than 300 CFU g⁻¹. From the 12 positive samples for MRAS, just 4 of them had acceptable quality counts, while 8 had counts above the accepted standard. The results of the isolated global prevalence of MRAS and MSSA are presented in the Table 1. Furthermore, in Figure 1 the results of PCR amplified products for the presence of meca in positive samples are shown.

<table>
<thead>
<tr>
<th>Count (FCU g⁻¹)</th>
<th>Samples (n)</th>
<th>MRSA (%)</th>
<th>MSSA (%)</th>
<th>Other Genus (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>&lt; 100</td>
<td>85*</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>100 – 300</td>
<td>32</td>
<td>4 (125)</td>
<td>19 (594)</td>
<td>9 (281)</td>
</tr>
<tr>
<td>&gt; 300</td>
<td>43</td>
<td>8 (186)</td>
<td>35 (814)</td>
<td>0</td>
</tr>
<tr>
<td>Total</td>
<td>160</td>
<td>12 (75)</td>
<td>54 (338)</td>
<td>9 (56)</td>
</tr>
</tbody>
</table>

* Number of samples detected was not microbial growth.

Most animals can be colonized by S. aureus, various researches reports isolated MRSA strains from pigs, cows, chicken and others (De Neeling et al., 2007; Huijsdens et al., 2006), especially reported colonization cases by this strain in pigs, farmers and their families. In Netherland people who are in contact with pigs it’s recognized as a risk factor for MRSA (Van Duijkeren et al., 2007), according to this, it has been suggested the relation to the emergence of MRSA strains in pigs and the antibiotic use in agriculture (Wulf and Voss, 2008). Results of this research reports the evidence of MRSA in meat products comercialized in the city of Cartagena, and the increase of this organism in relation to the virulence and pathogenicity, coinciding with other researches were the identification and development of new cases in different geographical locations has been confirmed by the implications on public health in both developed and developing countries (Lim et al., 2012; Deurenberg et al., 2006).

Figure 1. Electrophoresis in Agarose gel of the products of multiplex PCR, indicating positive detection from the nuc gene (MSSA) and meca (MRSA) in the analyzed strains. Lanes 1, 4-13, 15 and 16 indicate confirmation MSSA strains. Lanes 3, 14 and 18 indicate that there was not nuc detection, they do not belong to the Staphylococcus genus. Lanes 2 and 17 indicate the presence of MRSA and additionally to the presence of PVL gene in strain of the lane 17. C (-) negative control.

For the distribution of MRSA strains it was observed that there was the presence of these strains in the three locations, being LIB and LT the localities that contributed with four isolates each one, and the localidad del caribe...
norte contributed with two. There were 10 establishments in total which the presence of the mecA gene in the analyzed samples was there. The presence of the PVL gene was found in 7 (10.6%) of the 66 strains confirmed as S. aureus by PCR, of which six samples, two of ground beef and 4 pork meat were identified as MRSA and only one of the pork meat as MSSA. This gene was isolated in the (71%) of the pork chop meat samples and in the (28%) of the ground beef samples, one of the pork isolated strains was identified as MSSA. Studies show the prevalence of MRSA in ground raw meat (Fontes et al., 2013; Boer et al., 2009; Hanson et al., 2011) in agreement with our results. The presence of this strain in food may be due to the contamination of the slaughterhouse ducts or by the deficient hygiene practice of the operator, inasmuch as nasal area is considered the primary colonized site by S. aureus, who is also found in the intestinal tract (Bhalla et al., 2007).

Two of the samples presented the encoding gene for the PVL toxin, they were isolated from meat samples with colony counts that were between the reference parameters: 100-300 CFU g⁻¹ (Table 2) which is considered suitable for human consumption, five of the samples with the presence of this gene were rejected by showing higher counts than 300 CFU g⁻¹, according to the Norma Técnica Colombiana NTC 1325 (2008). The establishments where the toxin genes were found were distributed in the three localities, and corresponds to two establishments per locality. Presence of MRSA strains that carriers PVL toxin in establishments in the three localities in the city Cartagena constitutes a risk to the population because it could be presented pathologies associated to this toxin that has the ability of destroying white blood cells and also necrotizing injuries in lungs and soft tissues (Rossney et al., 2007). Because of the invasive and virulent ability of this toxin, it has reached a great importance and concern in society, which currently conducted numerous studies in different countries about the isolation of MRSA’s capable of producing the toxin (Witte et al., 2005). According to this Hanson et al. (2011) reported two isolated strains from pork meat, with a global prevalence of 1.2%; instead just one isolated MRSA was positive to the PVL gene. A recent study in Japan identified MSSA t034 in pigs (Asai et al., 2012). Another study in China described T189, associated with ST188, as one of the more common clones responsible for bacteremia (Yu et al., 2012). Therefore, food handlers carrying S. aureus T189 may present higher risk of infection and food transmission.

<table>
<thead>
<tr>
<th>Code Samples</th>
<th>Type of sample</th>
<th>count FCU g⁻¹</th>
<th>present / absent MRSA</th>
<th>gen PVL</th>
</tr>
</thead>
<tbody>
<tr>
<td>5CM1</td>
<td>Beef</td>
<td>1500</td>
<td>positive</td>
<td>positive</td>
</tr>
<tr>
<td>27CM1</td>
<td></td>
<td>600</td>
<td>positive</td>
<td>positive</td>
</tr>
<tr>
<td>5CC1</td>
<td>Pork chop</td>
<td>500</td>
<td>positive</td>
<td>positive</td>
</tr>
<tr>
<td>27CC1</td>
<td></td>
<td>600</td>
<td>positive</td>
<td>positive</td>
</tr>
<tr>
<td>31CC1</td>
<td></td>
<td>200</td>
<td>positive</td>
<td>positive</td>
</tr>
<tr>
<td>55CC1</td>
<td></td>
<td>1700</td>
<td>positive</td>
<td>positive</td>
</tr>
<tr>
<td>23CC2</td>
<td></td>
<td>200</td>
<td>negative</td>
<td>positive</td>
</tr>
</tbody>
</table>

Table 2. Colony count (CFU g⁻¹) vs presence of the encoding gene for the PVL toxin.

Figure 2 shows the percentage results of multiresistant strains of S. aureus isolated from meat products. Antibiotic multidrug-resistance were observed in the 66 isolated strains. One of the isolated strain showed resistance to 8 antibiotics (Amoxicillin-clavulanate, erythromycin, clindamycin, tetracyclines and cefazolin, penicillin, rifampin and ampicillin sulbatam), but even so it was identified as MSSA. MRSA strains were resistant to the following antibiotics: 57% amoxacillin-clavulanate, ampicillin - sulbactam and cefazolin, 85% penicillin, 7% erythromycin and clindamycin, 35% to tetracycline.
Regarding the antibiotic susceptibility of *S. aureus* isolated in food, the study of Gilchrist et al. (2007) where 5136 samples of meat and poultry were analyzed, found that 47% of the samples were contaminated with *S. aureus*, which 52% of isolates showed multidrug resistance to antibiotics, which allows to state that the widespread use of antimicrobials in food production of animal origin, could be one of the causes of the emergence of multidrug resistance. A study by Ho et al. (2014) in food handlers made in six food companies, showed that people exposed to raw meat have higher risk of being colonized with *S. aureus* strains, it was also reported strains resistant to tetracycline (20%) and erythromycin (16%). So it is possible that multidrug-resistant strains come from food handlers.

Another study conducted in five cities of USA, founding in beef and poultry, multiple resistance to clinically important antibiotics like ciprofloxacin, quinupristin / dalfopristin, clindamycin, erythromycin, oxacillin, and daptomycin (Marty et al., 2012). This study is consistent with our results, as it was found highly resistant to antibiotics commonly used to treat infections caused by this bacterium. MRSA has apparently responded well to therapies based on clindamycin and even with trimethoprim sulfametazol in communities with high prevalence of Methicillin Resistant Staphylococcus for handling soft tissues minor infections (Jorgensen, 2000; Agnoletti et al., 2014). In the present study it was found 7% of MRSA strains resistant to clindamycin, indicating the risk of acquiring these strains through food.

**CONCLUSIONS**

7.5% of *Staphylococcus aureus* reported were MRSA and 33.8% were MSSA, in a total of 25% of the sampled establishments. The type of analyzed meat that obtained the highest percentage of MRSA was ground beef with 66%. MRSA strains are distribute in the three locations in the city of Cartagena, 40% in the localidad Virgen y Turística, 40% in the localidad Industrial de la Bahía and 20% in the localidad Histórica y del Caribe. It was found a marked antibiotic resistance in the methicillin resistant *Staphylococcus aureus* strains and in strains that carried the PVL toxin, obtaining a antibiotic multidrug resistance. It was confirmed circulation and possible spread of MRSA strains capable of producing genes encoding PVL toxin in meat products, which represents a risk to meat consumers in the city of Cartagena.
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