Isolation and Characterization of MRSA from Locally Processed Meat Hawked in Gombe, Nigeria

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Abstract

Three types of locally processed meat products were collected from vendors across hawking points in Gombe town. Stick meat (tsire) 30 samples, Roasted meat (balangu) 30 samples and dried meat (kilishi) 15 samples making 75 samples. Samples were taken to the Microbiology Laboratory of Gombe State University and analyzed for the presence of methicillin resistant Staphylococcus aureus (MRSA) through culturing, biochemical tests and DNA analysis. The isolated Staphylococcus aureus were subjected to antimicrobial susceptibility test using standard antibiotics. The result showed 13.33% of the total isolates to be Methicillin Resistant Staphylococcus aureus as confirmed by the presence of mecA1, mecA 2 and pvl genes by polymerase chain reaction. This is of great health importance to the public.

Key words: Meat, Methicillin, resistance Antimicrobial Cefoxitin, MecA1

INTRODUCTION

Staphylococcus is a human pathogen, causing infections ranging from relatively mild skin and soft tissue infections to life threatening sepsis, pneumonia, osteomyelitis, endocarditis as well as toxin mediated syndromes such as toxic shock syndrome (TSS) and food poisoning (Shittu et al., 2011). Staphylococcus aureus is able to cause a large diversity of both benign and lethal infections in humans and animals because of a wide range of virulence factors that include various toxins and enzymes (Bal and Gould, 2005). It has emerged as one of the most important human pathogens and has become a leading cause of hospital and community acquired infections (Shittu and Lin, 2006).

Studies on the microbiological quality of some meat products such as stick meat (tsire) and dried meat (kilishi) have shown them to have organisms of public health concern (Igene, et. al., 1989). Staph. aureus is one of the more common causes of food poisoning. Commonly affected foods include processed meat, custard pastries, potato salad and ice cream that have been contaminated with the bacteria from human skin (Robert, 2004). Methicillin-resistant Staphylococcus aureus (MRSA) has become a leading cause of hospital-acquired infections worldwide accounting for more than 60% of S. aureus isolates in hospitals in the United states (Ayepola,, 2012,) Cases of MRSA infections have been documented among healthy community-dwelling persons without the established risk factors for MRSA infections. This work is aimed at determining the occurrences of MRSA in Gombe and environs.

Materials and methods

Sample collection

A total of 75 samples of three different types of roasted meat snacks were collected from meat vendors by direct buying. The samples were collected in sterile polythene bags, double wrapped in another polythene bags to avoid air contamination and brought immediately to the microbiological laboratory of Gombe state University for MRSA screening.
Isolation of S. aureus
In the laboratory, 25g of meat sample was
homogenized in 225ml peptone water
supplemented with 7% Sodium Chloride
(NaCl) were prepared. The samples were
aseptically blended with a blender, after
which the blended samples were poured into
a labeled conical flask and incubated at 37ºC
for 24hrs.

Isolation on Mannitol salt agar (MSA)
(TM Titan Biotech Ltd): This was used to
screen for S. aureus due to the organism’s
ability to ferments mannitol and to grow on
agar containing 70–100 g/l sodium chloride,
this is a selective criterion of MSA, to
observe mannitol utilisation is confirmed by
the resulting medium change to yellow from
its initial pink colour (Shamsuddeen 2016).

Isolation on Baird Parker agar (BPA)
(Biomark Laboratories. Ltd).
Baird Parker Agar Base was supplemented
with 50ml egg yolk and Potassium Tellurite
for each 63g which was dissolved in 950ml
distilled water. From the MSA, a colony was
picked using a wire loop, which was
introduced on the BPA and incubated at
37ºC for 24hrs. On BPA all colonies that
appeared black were later picked and
inoculated on Blood agar(TM Titan Biotech
Ltd) for Haemolysis observation (FAO,
1979)

Isolation on Blood agar (TM Titan
Biotech Ltd):
Colonies from the BPA were inoculated by
streaking on to Blood Agar (BA) using a
wire loop and the plates were incubated at
37ºC for 24 hrs. The S. aureus produced
yellow to cream 1–2 mm in diameter colonies
after overnight 24hrs incubation which were beta
haemolytic (Cheesebrough, 2008).

Isolation on Cysteine electrolyte
deficient (CLED) agar(TM Titan Biotech Ltd):
From the MSA plate colonies were picked
and were re-introduced on CLED using a
wireloop and the plates were incubated at
37ºC for 24hrs. Deep yellow colonies were
produced with a total change of the medium
colour from green to complete yellow
(Cheesebrough, 2008).

Antimicrobial susceptibility testing
Susceptibility of the isolates to cefoxitin
was tested using disc diffusion method as
standardized by CLSI 2014 (Clinical and
Laboratory Standards Institute, 2014).

Molecular analyses
DNA extraction (using Instagene Matrix,
Biorad®)
The DNA extraction and preparation for
Polymerase Chain Reaction and
electrophoresis was carried out at Veterinary
teaching Hospital of Ahmadu Bello
university, Zaria. The black colonies on the
BPA supplemented with cefoxitin were
inoculated on Lysogeny broth (LB) medium
prepared in the laboratory which contain
yeast extract 0.5g, NaCl 0.5g, Peptone Water
0.5g, NaOH, which was dissolved in 100ml
distilled water. The samples were inoculated
into the medium and incubated at 37oc for
24hrs 1.0ml of the organisms suspension
were pipetted each into appendorf tubes,
centrifuged at 10000rpm/2min and the
supernatant was discarded., 500ul of lyses
buffer was added and the tubes were
incubated at -37ºC for 30min in J R Selecta
5a incubator . The appendof tubes were
later vortexed and centrifuged at 10000rpm
for 2mins. Later 400ul of protease solution
was later added and incubated as
37ºC/30min.
The content of the appendof tubes were
transferred into spin column and centrifuged
at 10000rpm/10min and 400ul pre-wash
buffer solution was added and centrifuged
again at 10000rpm/1min and 200ul wash
buffer was added and centrifuged, later
10000rpm, 100ul DNAse elusion buffer was
added to elude the DNA down into the spin
tube that were inserted into the appendoef
tubes and centrifuged until a clear DNA
solution was realised which was preserved at
-20ºC.

Gel electrophoresis
From the DNA extract, 15ul was mixed with
a 6x DNA Loading dye for conventional
colour tracking in DNA migration. Agarose
gel was poured into chamber of PowerPC
HC Biorad electrophoresis machine.
Comb was removed from the solidified gel and the gel was inserted into the chamber then later 5x buffer was poured. The DNA extract mixture was pipetted into the comb holes and later the machine was set at 75°C for 40min. This was done to make sure that the DNA extract surely contains DNA.

Primers used
1. Staph756F (5'- AACTCTGTTATTAGG GAAGAACA-3')
2. mecA1 (5'- GTA GAA ATG ACT GAA CGT CCG ATA A - 3')
3. mecA2 (5’ – CCA ATT CCA CAT TGT TTC GGT CTA A - 3')
4. spa (5’ – CGC TGC ACC TAA CGC TAA TG – 3')
5. pvl-F (5’ – GCTGGACAAAAACTTCTTGGGAAT AT – 3')

These Primers were used for the amplification of the fragments of the methicillin-resistant gene (mecA).

Positive control used was S. Aureus (Staph756F). Also, negative control was used. By adding DNA of a fungi (Wichelhaus et al., 2001).

Polymerase Chain Reaction (PCR)
Master Mix 12.5ul x number of samples
Primer 1ul/sample
Water 0.5ul/sample
Template 7.0ul/sample

All the PCR tubes were centrifuged to mix and the tubes were later loaded into the PCR machine and set to 40 circles.

Each circle has five steps with its respective time. The first was the initial denaturing temperature of the DNA denoted with 95.0 which lasted 5min, the second was the denaturing temperature denoted as 94.0 which lasted for 30 seconds, the third denoted 55.0 which lasted for 30 second was the annealing temperature where the targeted gene and the primers meet, the forth was the extension temperature denoted 72.0 which lasted for 30 seconds where in the extension along the sequence occurs and finally the final extension denoted as 4.0 which marks the synthesis of the complement gene sequence can last to infinity after the final circle

After the 40th circle the contents of the PCR tubes were subjected to electrophoresis again for 45min, removed and put into gel documentation machine Biorad universal hood which was connected to a computer system, using a computer programme the result was printed on the computer screen.

RESULTS:
Of the 30 suya, 30 balangu and 15 kilishi samples tested, 9, 17 and 15 yielded Staphylococcus aureus respectively as presented in Table 1., with their respective characteristics on the different media used.

Table1: Isolation of Staphylococcus aureus on different media from the different meat products

<table>
<thead>
<tr>
<th>S/T</th>
<th>N</th>
<th>Growth</th>
<th>MSA</th>
<th>BPA</th>
<th>CLED</th>
<th>BA</th>
<th>CaT</th>
<th>CoT</th>
<th>Inference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Tsire</td>
<td>30</td>
<td>09(30%)</td>
<td>Yellow</td>
<td>Black</td>
<td>Yellow</td>
<td>Haemolysis</td>
<td>+</td>
<td>+</td>
<td>S. aureus</td>
</tr>
<tr>
<td>Balangu</td>
<td>30</td>
<td>17(56.7%)</td>
<td>Yellow</td>
<td>Black</td>
<td>Yellow</td>
<td>Haemolysis</td>
<td>+</td>
<td>+</td>
<td>S. aureus</td>
</tr>
<tr>
<td>Kilishi</td>
<td>15</td>
<td>15(100)</td>
<td>Yellow</td>
<td>Black</td>
<td>Yellow</td>
<td>Haemolysis</td>
<td>+</td>
<td>+</td>
<td>S. aureus</td>
</tr>
<tr>
<td>Total</td>
<td>75</td>
<td>75(100%)</td>
<td></td>
<td></td>
<td></td>
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<td></td>
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</tbody>
</table>

Key
S/T: Sample type
N: number of samples
MSA: Mannitol salt agar
BPA: Baird Parker Agar
CLED: Cysteine Electrolyte Deficient agar
BA: Blood agar
CaT: Catalase test
CoT: Coagulase test
Out of the *Staphylococcus aureus* isolates from the meat products, 2, 3, and 5 isolates from suya, Balangu and kilishi respectively were confirmed to be MRSA based on resistance to cefoxitin.

### Table 3: Antimicrobial susceptibility of the isolates to cefoxitin single disc

<table>
<thead>
<tr>
<th>Source</th>
<th>Number of samples</th>
<th>Susceptibility</th>
<th>MRSA</th>
</tr>
</thead>
<tbody>
<tr>
<td>Tsire</td>
<td>09</td>
<td>S: 4, I: 3, R: 2</td>
<td>2 (22.3%)</td>
</tr>
<tr>
<td>Balangu</td>
<td>17</td>
<td>S: 8, I: 6, R: 3</td>
<td>3 (17.6%)</td>
</tr>
<tr>
<td>Kilishi</td>
<td>15</td>
<td>S: 6, I: 4, R: 5</td>
<td>5 (33.34%)</td>
</tr>
<tr>
<td>Total</td>
<td>41</td>
<td></td>
<td>10 (13.33%)</td>
</tr>
</tbody>
</table>

**Key**
- **S**: Sensitive; zone diameter of $\geq 28\text{mm}$
- **I**: Intermediate; zone diameter of 24–27mm
- **R**: Resistant; zone diameter of $\leq 23\text{mm}$
- **MRSA**: Methicillin Resistant *Staph. aureus*

### DNA analysis for detection of mecA gene

Plate 1. Bands of mecA gene after separation on Agarous Gel Electophoresis

1, 10 and 16 were the ladder, 2 positive control. Band 1 was the mecA1, the second mecA2 and the third was the PVL, column 2 to 14 were samples while 15 was negative control.

**Discussion**

The results of this study have confirmed the occurrence of MRSA in *tsire*, *balangu* and *kilishi* with the highest occurrence in *Kilishi*. This may be due to the fact that antimicrobial resistance come due to exposure to conventional drug (WHO 2015) and nowadays cattle and sheep are always exposed to antimicrobial during vaccines and when infected with a disease.

The presence of MRSA on the meat products may be as a result of human contamination of the meat either during processing or in the spices used or at the point of sale in the market. This idea is in line with what was inferred by Obrien *et al.*, 2012 who showed in their studies that even the USA markets that are advanced could not protect their finished meat product from after processing contamination with MRSA especially pork products. Contamination by handlers may occur especially in the tropical regions of the world more frequently due to the rise in temperature where a seller can use the back of the hand or handkerchief to relieve his sweat and use the same hand to cut meat especially the kilishi where hands are used in cutting instead of knives. Weese *et al* (2010) has shown that, the contamination of food (meat) with sweat is possible.
The idea of passing resistant gene across species was earlier discussed by Otalu et al., (2015) where it was reported that due to surface contamination by the MRSA there may be a possibility of the organism passing the resistance gene across species.

The human population are long-term carriers of S. aureus which can be found as part of the normal skin flora and in the nostrils. S. aureus is the most common species of Staphylococcus to cause Staphylococcal infections and is a successful pathogen due to a combination of nasal carriage and bacterial immunoevasive strategies (Kluytmans et al, 1997). Staphylococcus aureus (S. aureus) has long been recognized as one of the most important bacteria that cause disease in humans. (Kluytmans et al, 1997) It is the leading cause of skin and soft tissue infections such as abscesses (boils), furuncles, and cellulitis. Although most Staphylococcal infections are not serious, S. aureus can cause serious infections such as bloodstream infections (bacteraemia), pneumonia, or bone and joint infections. (Boucher et al., 2010).

**Conclusion**

Conclusively this study has succeeded in isolating S. aureus from Suya, Balangu and Kilishi within selected areas of Gombe town in Gombe State. Also from the sample collected MRSA was isolated in all the three sources.

**Recommendation**

All meat handlers and the general public should exercise strict personal and environmental hygiene in all operations to avoid cross contamination of food products.

**References**


CLSI (2014) An informational supplement for global application developed through the Clinical and Laboratory Standards Institute consensus process


