RESEARCH ARTICLE

Characterization of Panton–Valentine leukocidin-positive
Staphylococcus aureus from skin and soft tissue infections and
wounds in Nigeria: a cross-sectional study [version 1; referees: 2
approved]

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Abstract

Background: Staphylococcus aureus is a significant pathogen implicated in
numerous nosocomial and community-acquired infections. The
Panton–Valentine leukocidin (PVL) can be associated with severe necrotizing
diseases such as pneumonia, skin and soft tissue infection (SSTI).

Methods: In total, 96 S. aureus isolates were obtained from patients presenting
with wounds (n=48) and soft tissue infections (SSTIs, n=48). These were
characterized based on their antimicrobial susceptibility profile, the possession
of virulence genes (e.g. capsular type, PVL), accessory gene regulator (agr)
type, and the staphylococcal protein A (spa) type. The production of the PVL
protein was assessed by western blotting.

Results: All isolates were susceptible to methicillin. The resistance was highest
to penicillin (97.9%), followed by trimethoprim/sulfamethoxazole (85.4%) and
tetracycline (10.4%). The PVL gene was found in 83.3% of isolates from SSTIs
and in 79.2% of isolates from wound. Of these, 53 (68%) produced PVL as
assessed by western blotting. The most prevalent spa type was the t084
(78.1%, n=75) and, majority of the isolates carried agr2 (82.3%, n=79).

Conclusions: Prevalence of antibiotic resistant PVL-positive methicillin
susceptible S. aureus strains has severe implications on PVL mediated
infections.

Keywords
Staphylococcus aureus, PVL
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Author roles: Ayepola OO: Conceptualization, Writing – Original Draft Preparation, Writing – Review & Editing; Olasupo NA: Supervision; Egwari LO: Resources, Supervision; Schaumburg F: Resources, Writing – Review & Editing

Competing interests: No competing interests were disclosed.

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**Introduction**

*Staphylococcus aureus* is an important human pathogen that causes significant hospital and community acquired infections\(^1\). *S. aureus* producing Panton-Valentine leukocidin (PVL) is linked to a broad array of necrotizing diseases such as pneumonia and skin and soft tissue infections (SSTIs)\(^2\). PVL is more frequently associated with community isolates\(^3\). PVL is a pore-forming toxin that can kill myeloid cells by forming channels in the plasma membrane, leading to loss of osmotic balance that ultimately lyses the cell\(^4\). Earlier reports have shown PVL to be one of the most important virulence determinants in *S. aureus* from sub Saharan Africa\(^5\). This study was conducted to investigate the presence of virulence genes including *lukS-PV/lukF-PV*, the production of the PVL protein and the antibiotic resistance in methicillin-susceptible *S. aureus* strains isolated from wounds and SSTIs between 2010 and 2011.

**Methods**

**Ethical statement**

Ethical approval for this study was obtained from the Ethics Committee of the Department of Biological Sciences, Covenant University, Ota, Ogun State, Nigeria (CUNG-2010-035). All participants signed a written informed consent before the commencement of the study.

**Characterization of isolates**

In this study we made use of an already existing database which has been published\(^6\). The study was conducted in four health facilities in Ogun and Lagos States of Nigeria between June 2010 and May 2011. Samples were collected from patients presenting with SSTIs and wound infections. The isolation and identification of the isolates were done by culture and genotyping. A total of 96 *S. aureus* isolates were obtained from wounds (n=48) and SSTIs (n=48). The Vittek automated systems (bioMérieux, Marcy L’Étoile, France) was employed to determine the antibiotic susceptibility profile. The PVL gene (*lukS-PV/lukF-PV*), capsular polysaccharides (*cap 5, cap 8*), exfoliative toxins (*eta, etb*), the toxic shock syndrome toxin (*tst*) and the *agr* type were detected by PCR. All amplifications was done in a thermocycler (Bio-Rad, Munich, Germany). The cycling conditions and primers used are as earlier published. Detection of the *lukS-PV/lukF-PV* gene was carried out using primer sequences: *luk-PV* (5'-ATCATTAGTTAAATGTCTGGACATGATCC A-3') and *luk-PV* (5'-GCATCAASTGTATTGGGATAAGCAA AAGC- 3'). The negative control was *S. aureus* ATCC 49230 (MSSA) and the positive control was sta 635/636 (a PVL-positive CA-MRSA strain). Primers specific for the variable segment of the *cap* locus. Cap5-f: (5'-GAAAGTGAACGATTAGT 84 bp repeats, was amplified by PCR. *spa* types were determined with the Ridom StaphType software version 1.5 beta (Ridom GmbH, Würzburg, Germany). All statistical computations were performed in SPSS Version 25. Data is explored using relevant descriptive analysis alongside chi\(^2\) to measure any association between antibiotic resistance, virulence genes and *lukS-PV/lukF-PV*. \(P<0.05\) is deemed to be statistically significant.

**Results and discussion**

We analyzed the characteristics of the PVL-positive *S. aureus* isolates as well as the relationship between antibiotic resistance, virulence genes and PVL gene (Table 1). Antibiotic resistance was highest to penicillin (100% in SSTI isolates and 94% in wound isolates), followed by trimethoprim/sulfamethoxazole (84% in SSTI isolates and 83% in wound isolates) and tetracycline (8% in SSTI isolates and 10% in wound isolates (Table 1). This is consistent with an earlier study which showed similar resistance rates for penicillin (98%), trimethoprim/sulfamethoxazole (80%) and tetracycline (18%) in Nigeria\(^6\). All isolates were methicillin-susceptible. The *lukS-PV/lukF-PV* gene was detected in 83.3% (n=40) of SSTI isolates and 79.2% (n=38) of wound isolates. Reports from other African countries have shown high rates of PVL positive MSSA ranging from 17% to 74%\(^7\). For example, a study in Alger hospital reported a prevalence of 72% among clinical isolates\(^8\). A multi-center study reported that deep-seated SSTIs associated with the PVL gene resulted in more hospitalizations of patients and this led more often to incision and drainage\(^9\). A meta-analysis showed PVL to be consistently associated with SSTIs than invasive diseases\(^10\). In a study
carried out in Gabon, PVL-positive isolates were found to occur more in SSTIs, and PVL was also associated with resistance to trimethoprim/sulfamethoxazole.\textsuperscript{6}

The presence of the PVL gene does not necessarily guarantee that the protein will be expressed and, if it is, toxin levels could vary widely from strain to strain. The production of PVL (in contrast to the sole presence of \textit{lukS-PV/lukF-PV}) was observed in 75\% of \textit{lukS-PV/lukF-PV} SSTI isolates and 60.5\% of \textit{lukS-PV/lukF-PV} wound isolates. \textit{In vitro} variation in the production of PVL by different strains of \textit{S. aureus} has been reported and this suggests important differences in transcriptional and/or translational control of gene expression.\textsuperscript{17} In this study, the level of PVL produced by \textit{lukS-PV/lukF-PV} positive \textit{S. aureus} isolates varied from strain to strain (Figure 1). It was observed in that none of the PVL-positive strains harboured other toxin genes such as \textit{eta}, \textit{etb} and \textit{tst}. Seven different \textit{spa} types were identified (Table 1). The most prevalent \textit{spa} type was \textit{t084} (78.1\%, \textit{n}=75). An earlier study revealed a significant association of \textit{spa-CC 084} PVL-positive isolates with PVL-positive isolates.\textsuperscript{6} Typing of the \textit{agr} locus, which controls the expression of many \textit{S. aureus} virulence factors, showed that most isolates (82.3\%, \textit{n}=79) possessed the \textit{agr2}, while none carried \textit{agr3}. Other studies have linked isolates carrying an \textit{agr4} allele to exfoliatin-related diseases and usually carry \textit{eta} and/or \textit{etb}.\textsuperscript{18,19} These were absent in this study.

In conclusion, this study showed that many \textit{S. aureus} isolates in Nigeria carry the PVL genes but few produced PVL \textit{in vitro}. Antibiotic resistance combined with the presence of the PVL genes,

<table>
<thead>
<tr>
<th>Antimicrobial resistance</th>
<th>PVL Gene</th>
<th>OR (95%CI)</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Absent</td>
<td>Present</td>
<td></td>
</tr>
<tr>
<td>Penicillin</td>
<td>R</td>
<td>16 (17.0)</td>
<td>78 (83.0)</td>
</tr>
<tr>
<td></td>
<td>S</td>
<td>2 (100.0)</td>
<td>0</td>
</tr>
<tr>
<td>Oxacillin</td>
<td>R</td>
<td>2 (100.0)</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>S</td>
<td>16 (17.0)</td>
<td>78 (83.0)</td>
</tr>
<tr>
<td>Gentamicin</td>
<td>R</td>
<td>4 (100.0)</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>S</td>
<td>14 (15.2)</td>
<td>78 (84.8)</td>
</tr>
<tr>
<td>Levofloxacin</td>
<td>R</td>
<td>4 (100.0)</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>S</td>
<td>14 (15.2)</td>
<td>78 (84.8)</td>
</tr>
<tr>
<td>Tetracycline</td>
<td>R</td>
<td>5 (50.0)</td>
<td>5 (50.0)</td>
</tr>
<tr>
<td></td>
<td>S</td>
<td>13 (15.1)</td>
<td>73 (84.9)</td>
</tr>
<tr>
<td>Trimethoprim/ sulfamethoxazole</td>
<td>R</td>
<td>12 (14.6)</td>
<td>70 (85.4)</td>
</tr>
<tr>
<td>cap 8</td>
<td>Absent</td>
<td>5 (100.0)</td>
<td>0</td>
</tr>
<tr>
<td>cap 5</td>
<td>Absent</td>
<td>13 (14.3)</td>
<td>78 (85.7)</td>
</tr>
<tr>
<td>spa type</td>
<td>t064</td>
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<td>0</td>
</tr>
<tr>
<td></td>
<td>t084</td>
<td>11 (14.7)</td>
<td>64 (85.3)</td>
</tr>
<tr>
<td></td>
<td>t159</td>
<td>1 (100.0)</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>t194</td>
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<td>0</td>
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<tr>
<td></td>
<td>t2304</td>
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<td></td>
<td>t8435</td>
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<tr>
<td></td>
<td>t8441</td>
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<td>agr</td>
<td>agr1</td>
<td>5 (100.0)</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>agr2</td>
<td>12 (15.2)</td>
<td>67 (84.8)</td>
</tr>
<tr>
<td></td>
<td>agr4</td>
<td>1 (8.3)</td>
<td>11 (91.7)</td>
</tr>
</tbody>
</table>

Note: R=resistant, S=susceptible
has serious implications in the treatment of *S. aureus* infections. This study is limited by the few study locations. A larger study population is needed to provide a better understanding of the clones of *S. aureus* in Nigeria. The results is however significant for regional surveillance.

**Data availability**

Dataset 1: Results of Vitek assay, PCR results for virulence genes, *agr* typing and *spa* typing. 10.5256/f1000research.15484.d21182720

Dataset 2: Results of PCR experiments. Gel photo for amplification of *lukS-pv* and *lukF-pv* gene. 10.5256/f1000research.15484.d21182821

Dataset 3: Results of PCR experiments. Gel photo for amplification of *agr* group. 10.5256/f1000research.15484.d21182922


**Competing interests**

No competing interests were disclosed.

**Grant information**

This study was supported by the European Molecular Biology Organization (EMBO) [ASTF 18–2011].

The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

**Acknowledgments**

The authors thank Mr Bode Onile-Ere for assistance with the statistical analysis.

**References**


Overview
The authors characterised PVL phenotypically and also investigate the presence of gene coding for PVL production, antibiotic susceptibility and agr production. The study is interesting as it goes further from detection of PVL gene to semi quantify the product.

Introduction
Line 3, remove first `and` or recast in `such as pneumonia and skin and soft tissue infections``
Spa typing is not part of the stated objectives.

Method
Characterization of isolates
``In this study we made use of an already existing database which has been published6.`` It should be clearly stated the data used from the referenced study above. The Method section should be rewritten so that all previously described method in Ayepola et al (2015) should not be rewritten in the present article but only referred to.

Results and discussion
It will be interesting to also expatiate on the proportion of isolates that are PVL positive molecularly and phenotypically i.e. the isolates with the genes and also producing PVL and those with the genes without PVL.
Spa typing reported in this study should be discussed too in relation to its epidemiological significance.

Is the work clearly and accurately presented and does it cite the current literature?
Partly

Is the study design appropriate and is the work technically sound?
Yes

Are sufficient details of methods and analysis provided to allow replication by others?
Yes

If applicable, is the statistical analysis and its interpretation appropriate?
Yes
Are all the source data underlying the results available to ensure full reproducibility?
Yes

Are the conclusions drawn adequately supported by the results?
Yes

**Competing Interests:** No competing interests were disclosed.

I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

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**Referee Report 13 September 2018**

https://doi.org/10.5256/f1000research.16878.r37150

**Solayide Abosede Adesida**
Department of Microbiology, Faculty of Science, University of Lagos, Lagos, Nigeria

**Title**
The *PVL production* did not appear to correlate with the presence of the gene. Therefore, the title should be modified to reflect the variability concerning the production of *pvl*, its detectable level, presence of the *pvl* genes and resistance rates.

**Abstract**
The authors investigated 96 *S. aureus* isolates were obtained from patients presenting with wounds and soft tissue infections in four health facilities in two States in Nigeria. Resistance to penicillin, trimethoprim/sulfamethoxazole was more than 80% and all isolates were susceptible to methicillin. The *PVL* gene was found in 83.3% and 79.2% of isolates from SSTIs and wound respectively. 53 (68%) produced *PVL* by western blotting. The most prevalent *spa* type was the t084 (78.1%, n=75) and, majority of the isolates carried *agr*2 (82.3%, n=79). The objective(s) of the study was not stated.

**Introduction**
Change "cel" to "cell"

**Methods**
1. There should be comma after the statement “In this study”
2. Since the isolates have been described as part of a larger study, in my opinion, extensive presentation of the previous methods used for characterising the isolates is not required. The current emphasis should be on the core findings which have not been presented in the existing or published database (ref.6). I suggest, you present a table summarizing the characteristics of the 96 isolates as obtained in the database.

**Results and discussion**
Information on *pvl* production and the presence of the genes is limited for the region under surveillance. In my opinion, this aspect of the work is relatively novel. Therefore, kindly, reconcile your findings on level of *pvl* production and the presence of the genes. You may also correlate these with the antibiotic resistance and perhaps the other results in the database. However, there is a lot more reports on *S. aureus* from skin and soft skin infection (wounds) with reference to *pvl* genes/production than you have cited. Please, see Sharma-Kuinkel et al1, Zhang et al, 2018, www.nature.com/scientific reports, Hamilton et al. Clinical
Infectious Diseases, 2007, 45 (2007). Other studies in Nigeria should also be considered to enrich the discussion. Overall, the discussion should be revised appropriately. However, I approve subject to the corrections suggested.

**References**

**Is the work clearly and accurately presented and does it cite the current literature?**
Partly

**Is the study design appropriate and is the work technically sound?**
Yes

**Are sufficient details of methods and analysis provided to allow replication by others?**
Yes

**If applicable, is the statistical analysis and its interpretation appropriate?**
Yes

**Are all the source data underlying the results available to ensure full reproducibility?**
Yes

**Are the conclusions drawn adequately supported by the results?**
Yes

**Competing Interests:** No competing interests were disclosed.

I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.
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