Detection of a Novel G2603T Mutation in cfr Harboring Linezolid-Resistant *Staphylococcus haemolyticus*: First Report from India

Rhea Michelle J. Khodabux¹ Shanthi Mariappan¹ Uma Sekar¹

¹Department of Microbiology, Sri Ramachandra Institute of Higher Education and Research (SRIHER), Porur, Chennai, Tamil Nadu, India

J Lab Physicians

Introduction

*Staphylococcus haemolyticus* is an opportunistic bacterial pathogen that colonizes human skin and mucous membrane. It is the second most common coagulase-negative *Staphylo-
cocci* (CONS) isolated from clinical specimens and is associated with bloodstream infections related to intravascular catheters, skin and soft tissue infection, meningitis, endocarditis, and a variety of device-associated infections.¹ It has an inherent ability to acquire and maintain exogenous

Abstract

**Background** *Staphylococcus haemolyticus* has emerged as an important multidrug-resistant nosocomial pathogen. Linezolid is useful in the treatment of severe infections caused by methicillin-resistant *Staphylococci*. Resistance to linezolid in *Staphylococci* is due to one or more of the following mechanisms: acquisition of the *cfr* (chloramphenicol florfenicol resistance) gene, mutation in the central loop of domain V of the 23S rRNA, and mutation in the *rplC* and *rplD* genes. This study was carried out to detect and characterize resistance to linezolid among the clinical isolates of *Staphylococcus haemolyticus*.

**Materials and Methods** The study included 84 clinical isolates of *Staphylococcus haemolyticus*. Susceptibility to various antibiotics was determined by disc diffusion method. Minimum inhibitory concentration (MIC) was determined by agar dilution method. Methicillin resistance was screened using oxacillin and cefoxitin disc. Methicillin resistance was screened using oxacillin and cefoxitin disc. Polymerase chain reaction was done to detect *mecA*, *cfr* and mutations in the V domain of the 23S rRNA gene.

**Results** Resistance to linezolid was exhibited by 3 of the 84 study isolates with MIC more than 128 µg/mL. The *cfr* gene was detected in all the three isolates. The G2603T mutation was observed in the domain V of the 23S rRNA among two isolates, whereas one isolate lacked any mutation.

**Conclusion** The emergence and spread of linezolid-resistant *Staphylococcus haemolyticus* isolates carrying G2603T mutation in the domain V of the 23S rRNA and harboring the *cfr* gene pose a threat in clinical practice.
genetic material or mobile genetic elements that encode for antimicrobial resistance. Hence, they are often multidrug resistant exhibiting resistance to antimicrobial classes such as beta lactams, macrolides, lincosamides, and streptogramins and more recently displayed reduced susceptibility to glycopeptides and oxazolidinones.

Linezolid is a synthetic bacteriostatic drug, belonging to oxazolidinone class of antibiotics and is active against various multidrug-resistant gram-positive pathogens, such as methicillin-resistant Staphylococci and vancomycin-resistant Enterococci. Linezolid inhibits protein synthesis by interacting with the 23S rRNA in the 50S ribosomal subunit. It is effective in the treatment of bacteremia, nosocomial pneumonia, and severe skin and soft tissue infections.

A year after its introduction, the first clinical linezolid-resistant Staphylococcus aureus strain appeared in 2001 and thereafter few reports were published from the United States and Europe. The first linezolid-resistant Staphylococcus haemolyticus (LRSH) was reported in 2009, since then a few strains have been reported from countries such as India, China, Brazil, Italy, and Spain. More recently due to its extensive use, linezolid resistance is on the rise. This resistance is mediated by the mutations in the domain V of 23S rRNA, presence of the cfr gene, or the mutations in the ribosomal proteins. There are only very few Indian studies describing the mechanism of resistance to linezolid in Staphylococcus haemolyticus. Resistance mediated by cfr and mutation in 23S rRNA have been reported with G2603T mutation as the most common.

This study was undertaken to detect and characterize resistance to linezolid among clinical isolates of Staphylococcus haemolyticus.

Materials and Methods

Bacterial Isolates

The study was conducted in a 1,600-bedded, university teaching hospital in South India. A total of 84 clinically significant, consecutive, nonrepetitive Staphylococcus haemolyticus isolated during the period 2019 to 2021 were included in the study. The study was approved by Institutional Ethics Committee (REF: IEC-NI/19/FEB/68/12).

The source of the isolates was blood (n = 36), exudative specimens (n = 38), and urine (n = 10). The isolates were identified up to species level by standard biochemical tests and automated systems: VITEK2 GP-card (bioMerieux, Marcy l’Etoile, France) and MALDI-TOF MS (bioMerieux, Marcy l’Etoile, France).

Antimicrobial Susceptibility Testing

Antibiotic susceptibility testing was done by Kirby Bauer disc diffusion method for different classes of antimicrobial agents such as ampicillin (10 µg), cefuroxime (30 µg), erythromycin (30 µg), clindamycin (2 µg), amikacin (30 µg), ciprofloxacin (5 µg), linezolid (30 µg), and teicoplanin (30 µg). Methicillin resistance was detected by cefoxitin (30µg) and oxacillin (1µg) disc (Himedia, Mumbai, Maharashtra, India) as per Clinical and Laboratory Standards Institute (CLSI 2019) guidelines (CLSI-M100-S29). Minimum inhibitory concentration (MICs) of linezolid (MicroExpress, Goa, India) and vancomycin were determined by agar dilution method in accordance to CLSI 2019 guidelines.

Molecular Methods

DNA Extraction

Colonies of clinical strains were transferred to sterile distilled water. The samples were then boiled to prepare the DNA template. This was used as template for polymerase chain reaction (PCR).

Polymerase Chain Reaction

All the isolates were subjected to molecular confirmation using the specific nuc gene. MecA gene was amplified to detect methicillin resistance. PCR was done to detect cfr gene and the amplification of 23S rRNA gene was done to determine mutations in the V domain. All the PCR reactions were carried out with a final volume of 25 µL reaction. Each reaction contained 10 pmol of each primer (Eurofins, India) and 23 µL of master mix (Takara, India) and 2 µL of template DNA. The amplicons were separated in a 1% agarose gel containing ethidium bromide.

The primers used are described in Table 1. Previously, characterized strains were used as positive controls. Sterile Mili Q water was used as negative controls.

The obtained sequences were compared to the reference 23S rRNA gene sequences of Staphylococcus haemolyticus (JCSC1435). The sequences were submitted to GenBank database with the following accession numbers OL691912, OL691913, OL743221, OL743222, ON249039, ON249040.

The medical records were perused to collect the clinical details of the patients from whom the LRSH was isolated.

Results

Among the 84 isolates, the nuc gene was present in all the isolates, confirming the identification as Staphylococcus haemolyticus. The resistance exhibited to various classes of antimicrobials is as follows: ampicillin 95.2% (80/84), cefuroxime 79% (66/84), cefoxitin 79% (66/84), cefotaxime 79% (66/84), erythromycin 88% (74/84), clindamycin 57% (48/84), ciprofloxacin 72.6% (61/84), and linezolid 3.5% (3/84). All isolates were susceptible to vancomycin and teicoplanin.

Methicillin resistance was detected by oxacillin and cefoxitin disc diffusion method. Resistance to oxacillin was observed in 67/84 and resistance to cefoxitin was detected in 66/84 of the study isolates. The mecA gene was present in 98.5% (66/67) of the oxacillin-resistant isolates.

The linezolid-resistant isolates (n = 3) had MIC of greater than 128 µg/mL. Cfr gene was detected in all the three linezolid-resistant isolates. The domain V of the 23S rRNA gene was amplified by PCR. The obtained sequences were compared to the reference 23S rRNA gene sequences of Staphylococcus haemolyticus (JCSC1435). The BLAST alignment revealed G2603T point mutation in the domain V of 23S rRNA gene in two of the linezolid-resistant isolates.
The clinical details of the patient from whom LRSH was isolated are tabulated in Table 2.

Table 1 Primers and PCR conditions used for resistance genes

<table>
<thead>
<tr>
<th>Gene</th>
<th>Primer</th>
<th>PCR conditions</th>
<th>Amplicon</th>
<th>References</th>
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</table>
| 23s rRNA | F- CGCGGGCGTAATATAACG  
R- CAGCATTATACCGTCCATAC | Initial denaturation: 95°C for 3 min  
Denaturation: 95°C for 30 s  
Annealing: 55°C for 30 s  
Extension: 72°C for 30 s for 30 cycles  
Final extension: 5 min at 72°C | 846    | 2          |
| nuc    | F- TAGTGGTAGGGCTATTAGCC  
R- ACGATATTTGCCATTGGTG  | Initial denaturation: 94°C for 3 min  
Denaturation: 95°C for 30 s  
Annealing: 50°C for 30 s  
Extension: 72°C for 45 s for 30 cycles  
Final extension: 7 min at 72°C | 434    | 10         |
| meA    | F- GTAGAATGACTGAAGTCGGATA  
R- CCAATTCCACATTTGCCGGTCTAA | Initial denaturation: 94°C for 3 min  
Denaturation: 94°C for 30 s  
Annealing: 50°C for 30 s  
Extension: 72°C for 45 s for 30 cycles  
Final extension: 7 min at 72°C | 310    | 11         |
| cfr    | F-TGAAGTATAAAGCAGGTTGGAGT  
R- ACCATATAATTGACCAAGCAGC | Initial denaturation: 94°C for 2 min  
Denaturation: 94°C for 10 s  
Annealing: 55°C for 30 s  
Extension: 72°C for 30 s for 30 cycles  
Final extension: 7 min at 72°C | 746    | 12         |

Abbreviation: PCR, polymerase chain reaction.

Discussion

Staphylococcus haemolyticus is increasingly recognized as an important pathogen due to its ability to develop multiple drug resistance, its adaptability and ability to survive in the hospital environment, especially on medical devices. Linezolid, an oxazolidinone, is indicated for the treatment for a variety of Gram-positive infections; it is often the last-resort antibiotic for the treatment of infections caused by methicillin-resistant Staphylococcus aureus.

Resistance to linezolid in Staphylococcus is due to one or more of the following mechanisms: acquisition of the cfr (chloramphenicol florfenicol resistance) gene, mutation in the central loop of domain V of the 23S rRNA, and mutation in the rplC and rplD genes, which encodes for the 50S ribosomal proteins L3 and L4, respectively.

Following its first detection in 2001, sporadic cases of linezolid resistance have been reported globally. In India, the first case report on LRSH from North India was published in 2011 followed by another report in 2012 and later from South India. In the former, mechanism of resistance was not studied, while the latter described the mechanism of resistance was due to the presence of cfr and mutation in domain V of 23S rRNA. A recent study published from South India reported linezolid resistance in 3.7% (13/356) of Staphylococcus aureus with 12 isolates harboring the cfr gene. Mutation in domain V of 23S rRNA was not looked for in their study. In a hospital from Delhi, nine LRSH isolates were characterized and it was found that all of them carried the cfr gene along with mutation G2614T in domain V of 23S rRNA.

A study from Vietnam carried out whole genome sequencing and demonstrated the transferability of the plasmid carrying the cfr gene. However, in this study gene transfer experiments were not carried out.
This study reports dual mechanisms of resistance to linezolid. Although the mutational resistance to linezolid poses a threat in clinical practice, the acquisition of the \( \textit{cfr} \) gene is threatening because of its potency for horizontal transmission between species. Only one isolate carried the \( \textit{cfr} \) gene alone and lacked any mutations, which is similar to the observations made in previous studies.\(^2\),\(^3\)

In this study, of the three patients who had infection with LRSH, two patients underwent wound debridement and ray amputation for removal of nidus of infection and source control. Though these patients were treated with beta lactam antibiotics and fluoroquinolone, they recovered and were discharged from the hospital. It may be reasonably assumed that \( \textit{Staphylococcus haemolyticus} \) could have been a colonizer in the wound and the recovery may be attributed to source control. Follow-up was lost in one patient.

Since many CONS are usually considered as part of normal skin flora, most clinical laboratories do not test for antimicrobial susceptibility unless from a sterile site such as blood. These organisms have relatively low virulence but are now increasingly recognized as clinically significant. As the pathogenic significance becomes apparent, it becomes necessary to characterize them and study their antimicrobial susceptibility profile.\(^4\)

### Conclusion

The presence of \( \textit{cfr} \) gene along with mutations is alarming. Prudent use of linezolid and strengthening implementation of infection control measures and screening of patients with
linezolid resistant-CONS should be mandated to curtail the spread of resistance and preserve the drug.

Funding
This study was supported by the Founder chancellor Shri N.P.V. Ramasamy Udayar fellowship, provided by Sri Ramachandra Institute of Higher Education and Research, Porur, Chennai, Tamil Nadu, India.

Conflict of Interest
None declared.

References

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