Tracking Linezolid Antimicrobial Activity and Resistance in North America: Results from the LEADER Program for 2013

REVISED ABSTRACT

Background: The LEADER Program has monitored the activity of linezolid (LZD) and comparator agents in USA medical centers since 2004. The percent of non-susceptible (NS) Gram-positive (GP) monitored isolates has remained below 1% (range, 0.14-0.45%; 0.17% in 2012).

Methods: In 2013, a total of 7,183 GP pathogens were sampled from 60 medical centers across the USA. Isolates were susceptibility (S) tested by CLSI reference broth microdilution methods. LZD NS isolates were confirmed by repeated reference S testing, with the LZD Etest (bioMerieux, Hazelwood, Missouri, USA) and CLSI disk diffusion methods.

Results: A total of 3,035 S. aureus strains were submitted. Methicillin-resistant S. aureus (MRSA; 47.9%) varied from 35.1% (Middle Atlantic) to 58.7% (East South Central). Resistance rates among MRSA for many antimicrobial agents were much higher than in MSSA. Examples included the β -lactam agents, levofloxacin (MRSA, 64.2%, MSSA, 11.2%), clindamycin (26.7%, 5.3%), and erythromycin (87.8%, 31.9%). The LZD MIC_{50/90} for S. aureus was 1/1 µg/ml (S, 99.9%). There were two LZD NS isolates (MRSA from California and Michigan); both contained *cfr*. The MIC₅₀ and modal MIC for MRSA and MSSA were the same. A total of 580 CoNS isolates exhibited a LZD MIC_{50/90} at 0.5/1 μ g/ml (S, 99.5%). The three LZD NS CoNS isolates contained mutations at 23S rRNA and L3 and/or L4. LZD was active against Enterococci with a MIC_{50/90} at 1/1 μ g/ml and 99.4% S. All LZD NS enterococci had a G2476T mutation and one also contained a *cfr*. S to LZD for 399 viridans group streptococci (VGS) and 964 β-hemolytic streptococci was 99.7 and 100.0%, respectively. There was one S. sanguinis isolate (LZD NS [MIC, 4 µg/ml]), which demonstrated a mutation at the G2576 nucleotide of the 23S rRNA. LZD S for all organisms tested (7,183) was 99.83% with only 12 isolates (6 enterococci, 2 S. aureus, 3 S. epidermidis, 1 VGS) testing NS.

Conclusions: LZD among USA medical centers demonstrated excellent activity and a sustained S rate of 99.83%. LZD MIC population distributions remain stable without evidence of "MIC creep" among monitored species. These data show no evidence of widespread dissemination of the *cfr* resistance determinant in LEADER Program monitored USA medical centers.

INTRODUCTION

Linezolid, approved by the Food and Drug Administration (FDA) in 2000, is an important therapeutic agent used to treat uncomplicated and complicated skin and skin structure infections (cSSSI) and nosocomial pneumonia caused by commonly occurring Grampositive pathogens. Linezolid is also indicated for the treatment of vancomycin-resistant *Enterococcus faecium* (VRE) infections (including cases with concurrent bacteremia). This compound has emerged as a valuable treatment option against Gram-positive, such as methicillin-resistant Staphylococcus aureus (MRSA), drugresistant Streptococcus pneumoniae (DRSP) and VRE isolates that are resistant to conventional drugs.

Oxazolidinone resistance has been detected, mainly among Enterococcus species and coagulase-negative staphylococci (CoNS), but the occurrence rates remain rare for S. aureus and streptococci The oxazolidinone mechanism of action has been described as selective binding to the 50S ribosomal subunit of the 23S rRNA molecule with resultant inhibition of protein synthesis. Target site mutations and a mobile *cfr*-mediated resistance mechanism to linezolid have been detected among Staphylococcus spp. isolates

The Linezolid Experience and Accurate Determination of Resistance (LEADER) surveillance program has monitored linezolid activity, spectrum and resistance rates in the United States (USA) since 2004. This program serves to generate national in vitro data for linezolid and comparator agents to provide benchmark data to which local susceptibility patterns may be compared. In addition, molecular testing of isolates with decreased linezolid susceptibility allows detection of emerging resistance that would not be possible in routine clinical laboratory practice.

MATERIALS AND METHODS

Bacterial strain collection. A total of 7,183 Gram-positive pathogens were submitted to JMI Laboratories and distributed among the following organism groups: S. aureus (3,035 strains), S. *pneumoniae* (1281), β-hemolytic streptococci (964), enterococci (924), CoNS (580), and viridans group streptococci (399). The nine USA Census Bureau Regions were represented by sixty medical centers. Each recruited medical center was instructed to forward \geq 100 organisms with the following species or genus distribution: S. aureus (50 strains), coagulase-negative staphylococci (CoNS; 15 strains), enterococci (15 strains), S. pneumoniae (10 strains), β-hemolytic streptococci (5 strains) and viridans group streptococci (5 strains). The strains were predominantly from bacteremias, although isolates from pneumonia (respiratory tract), cutaneous wound infections or cSSSI, and urinary tract infections were acceptable.

Antimicrobial susceptibility test methods. All susceptibility tests were performed in a CLIA-certified and GLP-compliant reference laboratory (JMI Laboratories) using Clinical and Laboratory Standards Institute (CLSI) broth microdilution methods (frozen- and dry-form 96-well plates; CLSI M07-A9, 2012) and published interpretive criteria (CLSI M100-S24, 2014). Frozen-form reference broth microdilution testing, with the linezolid Etest (bioMerieux, Hazelwood, Missouri, USA) and CLSI disk diffusion susceptibility testing methods (CLSI M02-A11, 2012) were used to confirm isolates exhibiting a linezolid MIC value of $\geq 4 \mu g/ml$.

Staphylococcal isolates (*S. aureus*, CoNS) found to be resistant to erythromycin, but susceptible to clindamycin (ERCS) were screened by the CLSI broth dilution inducible clindamycin screening test as outlined in the M100-S24 (2014) document.

Molecular screening was performed on isolates displaying confirmed linezolid MIC results of $\geq 4 \mu g/ml$ to identify the presence of *cfr*, target site mutations (23S rRNA and ribosomal proteins L3 and/or L4) and possible epidemic clonality using pulsed field gel electrophoresis (PFGE).

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RESULTS

- A total of 3,035 S. aureus strains were submitted for testing by the reference broth microdilution method. The MRSA rates, determined via a prevalence mode of sample testing, varied by region from 35.1% (Mid-Atlantic) to 58.7% (East South Central) with the overall rate at 47.9% (data not shown). The overall LEADER MRSA rate has decreased 10.3% since 2007 (Figure 1).
- Resistance rates, in particular, for MRSA in 2013 were much higher than in MSSA including levofloxacin (MRSA, 64.2%, MSSA, 11.2%), clindamycin (26.7%, 5.3%), and erythromycin (87.8%, 31.9%; Table 1). However, linezolid, daptomycin, and vancomycin retained 99.9-100.0% activity against both MRSA and MSSA with linezolid exhibiting a MIC_{50/90} at $1/1 \mu g/ml$ (Tables 1 and 2).
- CLSI interpretive criteria indicated that clindamycin resistance in S. aureus was 15.6%, MRSA (26.7%), and MSSA (5.3%). Screening for inducible clindamycin resistance indicated an overall resistance induction rate of 27.1% among ERCS S. aureus and 17.1% among MRSA. The results indicated the true clindamycin resistance rate for all S. aureus strains was 27.2% and for MRSA was 37.1% (data not shown).
- A total of 580 CoNS isolates exhibited a linezolid MIC_{50/90} at 0.5/1 µg/ml (99.5% susceptible) and was unaffected by oxacillin resistance (Table 1). Resistance rates for other comparator agents ranged from 16.0% for gentamicin to 68.6% for oxacillin. Linezolid, daptomycin and vancomycin exhibited very high susceptibility rates (99.5-100%; **Table 1**).
- Linezolid was very active against all enterococci with a MIC_{50/90} at 1/1 µg/ml and 99.4% susceptible and highly active against VRE (98.0% susceptible) exhibiting MIC_{50/90} at 1/1 μ g/ml also.
- Linezolid was active against all *S. pneumoniae* (MIC₅₀, and MIC₉₀ at 1 µg/ml). A total of 43.6% of *S. pneumoniae* isolates were nonsusceptible to penicillin (MIC, $\geq 0.12 \mu g/ml$), a rate that has increased 5.6% since 2010 (38.0%). Erythromycin and clindamycin resistance were high among all S. pneumoniae (46.5 and 18.3%, respectively; Table 1).
- Susceptibility to linezolid for 399 viridans group streptococci and 964 β -hemolytic streptococci was 99.7 and 100.0%, respectively. Linezolid, daptomycin, and vancomycin (>99.0% susceptible), were highly active against all viridans group streptococci and β hemolytic streptococci tested (**Table 1**).
- Two linezolid-resistant MRSA were detected. They both contained cfr (one strain each from California [linezolid MIC, 32 µg/ml] and Michigan [linezolid MIC, 8 µg/ml]). The three non-susceptible CoNS isolates all identified as S. epidermidis and originated from Michigan, North Carolina and Texas. The North Carolina isolate matched the PFGE profile noted from two isolates surveyed last year (SEPI454E). All linezolid non-susceptible enterococci had a G2476T mutation and one also contained a *cfr*. There was one non-susceptible S. sanguinis isolate (MIC, 4 µg/ml), which demonstrated a mutation at the G2576 nucleotide of the 23S rRNA (**Table 3**).

Table 1. Linezolid activity compared to other agents when tested in the LEADER Program (USA, 2013), 7,183 strains.

Organism/antimicrobia (no. tested) S. aureus, methicillin-Linezolid Ciprofloxacin Clindamycin Daptomycin Erythromycin Gentamicin TMP/SMX^b Vancomycin aureus, methicillin-Linezolid Ciprofloxacin Clindamycin Daptomycin Erythromycin Gentamicin TMP/SMX Vancomycin bagulase-negative Linezolid Ciprofloxacin Clindamycin Daptomycin Erythromycin Gentamicin Oxacillin TMP/SMX Vancomycin nterococci (924)^d Linezolid Ampicillin Ciprofloxacin Piperacillin/tazobac Teicoplanin Vancomycin S. pneumoniae (1,281 Linezolid Amoxicillin/clavula Ceftriaxone Ciprofloxacin Clindamycin Erythromycin Levofloxacin Penicillin^e Vancomycin iridans group strepto Linezolid Ceftriaxone Ciprofloxacin Clindamycin Erythromycin Levofloxacin Penicillin Vancomycin B-hemolytic streptoco Linezolid Ceftriaxone Ciprofloxacin Clindamycin Erythromycin Levofloxacin Penicillin Vancomycin Criteria as published Trimethoprim/sulfam Includes 15 species. Includes seven species. Criteria as published by the CLSI [2014] for 'Penicillin oral penicillin V' (S ≤0.06, I=0.121, R≥2 µg/mľ Includes 27 species Includes: Streptococcus agalactiae (523 strains), Streptococcus dysgalactiae (78 strains), and Streptococcus pyogenes (363 strains).

| al agent | | MIC (µg/ | ′ml) | CLSI ^a |
|------------------------|------------------------|-------------------|----------------------------|--|
| - | MIC_{50} | MIC ₉₀ | Range | %S / %I / %R |
| esistant (* | 1,454) | | | |
| | 1 | 1 | ≤0.12->8 | 99.9 / 0.0 / 0.1 |
| | >4 ≤0.25 | >4 | 0.12->4 | 31.8 / 1.4 / 66.8 |
| | ≤0.25 0.25 | >2 0.5 | ≤0.25->2 0.06-2 | 73.0 / 0.3 / 26.7 99.9 / - / - |
| | >16 | >16 | ≤0.12->16 | 9.9 / 2.3 / 87.8 |
| | ≤1 | ≤1 | ≤1->8 | 97.3 / 0.0 / 2.7 |
| | ≤0.5 | ≤0.5 | ≤0.5->4 | 97.9 / 0.0 / 2.1 |
| | 1 | 1 | 0.25-2 | 100.0 / 0.0 / 0.0 |
| susceptible | e (1,581) | | | |
| | 1 | 1 | ≤0.12-2 | 100.0 / 0.0 / 0.0 |
| | 0.25 ≤0.25 | >4 ≤0.25 | 0.06->4 | 86.6 / 1.5 / 11.9 94.4 / 0.3 / 5.3 |
| | ≤0.25 0.25 | ≤0.25 0.25 | ≤0.25->2 ≤0.06-1 | 94.4 / 0.3 / 5.3 |
| | 0.25 | >16 | ≤0.12->16 | 64.9 / 3.2 / 31.9 |
| | ≤1 | ≤1 | ≤1->8 | 99.2 / 0.2 / 0.6 |
| | ≤0.5 | ≤0.5 | ≤0.5->4 | 99.4 / 0.0 / 0.6 |
| | 1 | 1 | 0.25-2 | 100.0 / 0.0 / 0.0 |
| aphylocod | cci (580) ^c | | | |
| | 0.5 | 1 | 0.25->8 | 99.5 / 0.0 / 0.5 |
| | 0.5 | >4 | ≤0.03->4 | 58.8 / 0.3 / 40.9 |
| | ≤0.25 | >2 | ≤0.25->2 | 67.9 / 1.8 / 30.3 100.0 / - / - |
| | 0.25 >16 | 0.5 >16 | ≤0.06-1 ≤0.12->16 | 38.4 / 1.9 / 59.7 |
| | ≤1 | >8 | <u>≤</u> 0.12->10 ≤1->8 | 78.1 / 5.9 / 16.0 |
| | 1 | >2 | ≤0.25->2 | 31.4 / 0.0 / 68.6 |
| | ≤0.5 | >4 | ≤0.5->4 | 67.1 / 0.0 / 32.9 |
| | 1 | 2 | 0.25-2 | 100.0 / 0.0 / 0.0 |
| | | | | |
| | 1 | 1 | 0.25->8 | 99.4 / 0.0 / 0.6 |
| | 1 1 | >8 | ≤0.25->8 | 75.2 / 0.0 / 24.8 |
| tam | 4 | >4 >64 | 0.25->4 ≤0.5->64 | 51.4 / 7.5 / 41.1 75.2 / - / - |
| am | - ≤2 | >16 | ≟0.0 >04 ≤2->16 | 79.8 / 0.9 / 19.3 |
| | 1 | >16 | 0.25->16 | 78.5 / 0.6 / 20.9 |
|) | | | | |
| | 1 | 1 | ≤0.12-2 | 100.0 / - / - |
| ic acid | ≤1 | 4 | ≤1->8 | 86.0 / 4.2 / 9.8 |
| | ≤0.06 | 1 | ≤0.06-8 | 91.6 / 8.1 / 0.3 |
| | 1 | 2 | 0.12->4 | -/-/- |
| | ≤0.25 ≤0.12 | >2 >16 | ≤0.25->2 ≤0.12->16 | 81.1 / 0.6 / 18.3 52.5 / 1.0 / 46.5 |
| | _0.12 1 | 1 | 0.25->4 | 98.6 / 0.3 / 1.1 |
| | ≤0.06 | 2 | ≤0.06-8 | 56.4 / 26.0 / 17.6 |
| | 0.25 | 0.5 | ≤0.12-0.5 | 100.0 / - / - |
| cocci (399 | 9) ^f | | | |
| | 0.5 | 1 | ≤0.12-4 | 99.7 / - / - |
| | 0.25 | 0.5 | ≤0.06-8 | 95.2 / 2.5 / 2.3 |
| | 1 ≤0.25 | 4 >2 | 0.06->4 ≤0.25->2 | - / - / - 87.6 / 0.5 / 11.9 |
| | <u>≤</u> 0.25 0.25 | >2 16 | ≤0.25->2 ≤0.12->16 | 50.6 / 3.3 / 46.1 |
| | 1 | 2 | ≤0.12->4 | 95.0 / 0.5 / 4.5 |
| | ≤0.06 | 0.5 | ≤0.06->8 | 76.7 / 20.8 / 2.5 |
| | 0.5 | 0.5 | ≤0.12-1 | 100.0 / - / - |
| cci (964) ^g | | | | |
| | 1 | 1 | ≤0.12–1 | 100.0 / - / - |
| | ≤0.06 | 0.12 | ≤0.06-0.12 | 100.0 / - / - |
| | 0.5 ≤0.25 | 1 | ≤0.03->4 ≤0.25->2 | - / - / - 79.3 / 0.2 / 20.5 |
| | ≤0.25 ≤0.12 | >2 >16 | ≤0.25->2 ≤0.12->16 | 79.370.2720.5 61.071.1737.9 |
| | 0.5 | 1 | ≤0.12->4 | 99.2 / 0.3 / 0.5 |
| | ≤0.06 | ≤0.06 | ≤0.06-0.12 | 100.0 / - / - |
| | 0.25 | 0.5 | ≤0.12-0.5 | 100.0 / - / - |
| d by the CL | | | | |
| nethoxazole | σ. | | | |

 Table 2.
 Number of isolates inhibited at each linezolid MIC when testing six
 different groups of Gram-positive cocci isolated from all USA census regions (LEADER Program, 2013); 7,183 total strains.

| Number of isolates inhibited at linezolid MIC (μ g/mI): | | | | | | | |
|--|---|---|--|--|--|--|---|
| ≤0.12 | 0.25 | 0.5 | 1 | 2 | 4 | 8 | >8 |
| 1 | 2 | 473 | <u>488</u> a | - | - | - | - |
| 3 | 23 | 458 | <u>484</u> | 13 | - | - | - |
| 0 | 7 | 151 | <u>719</u> | 41 | 0 | 3 | 3 |
| 4 | 12 | 585 | <u>2335</u> | 97 | 0 | 1 | 1 |
| 3 | 5 | 332 | <u>1076</u> | 36 | 0 | 1 | 1 |
| 1 | 7 | 253 | <u>1259</u> | 61 | 0 | 0 | 0 |
| 5 | 17 | 222 | <u>154</u> | 0 | 1 | - | - |
| 0 | 84 | 424 | <u>68</u> | 1 | 0 | 0 | 3 |
| 0 | 59 | 287 | <u>48</u> | 1 | 0 | 0 | 3 |
| 0 | 25 | 137 | <u>20</u> | 0 | 0 | 0 | 0 |
| | 1 3 0 4 3 1 5 0 0 | ≤0.12 0.25 1 2 3 23 0 7 4 12 3 5 1 7 5 17 0 84 0 59 | ≤0.12 0.25 0.5 12 473 3 23 458 07 151 4 12 585 3 5 332 17 253 5 17 222 0 84 424 0 59 287 | ≤0.120.250.5112473 488^a 323458 484 07151 719 412585 2335 35332107617253 1259 517222 154 084424 68 059287 48 | ≤0.120.250.51212473 488^a -323458 484 1307151 719 41412585 2335 9735332107636172531259615172221540084424681059287481 | ≤0.120.250.512412473 488^a 323458 484 13-07151 719 410412585 2335 9703533210763601725312596105172221540108442468100592874810 | ≤0.120.250.5124812473 488^a 323458 484 1307151 719 4103412585 2335 9701353321076360117253 1259 6100517222 154 01-084424 68 100059287 48 100 |

a. Underlined value represents MIC

Table 3. Isolates with elevated or resistant-level linezolid MIC values (≥4 µg/m in the 2013 LEADER Program.

| | | | | | Linezol | | | |
|----------------------|----------------|------------------|-------------------|-----------------|-----------------|--------------|--|-----------------------|
| | | | | A == = (| (µg/ | | - Desistance | |
| Isolate ID number | Organism | City | State | Age/ Sex | Frozen -form | Dry- form | Resistance mechanisms | PFGE |
| 146-371 | S. aureus | Long Beach | California | 21/M | 32 | >8 | <i>cfr</i> , G2576T, L3 (D159E, G152D) | SA146A ^a |
| 003-21572 | S. aureus | Detroit | Michigan | 59/M | 8 | 8 | cfr | |
| 454-10665 | S. epidermidis | Winston Salem | North Carolina | 20/M | 32 | >8 | G2576T, L3 (H146P, M156T) | SEPI454E ^b |
| 116-11612 | S. epidermidis | Houston | Texas | 21/M | 64 | >8 | G2576T, L3 (H146R, M156T), L4 (71G72 ins) | SEPI116F ^c |
| 003-29089 | S. epidermidis | Detroit | Michigan | 53/F | 128 | >8 | G2576T, L3 (G137S, H146P, M156T), L4 (71G72 ins) | SEPI3K ^d |
| 422-26617 | S. sanguinis | Aurora | Colorado | 21/M | 4 | 4 | G2576T | NA |
| 116-11589 | E. faecium | Houston | Texas | 54/F | 16 | >8 | G2576T (+) | EFM116C ^e |
| 004-14445 | E. faecium | Akron | Ohio | 64/F | 32 | >8 | G2576T (+) | NA |
| 467-18556 | E. faecium | Los Angeles | California | 36/F | 32 | >8 | G2576T (+) | NA |
| 448-18961 | E. faecium | New Orleans | Louisiana | 63/M | 8 | 8 | <i>cfr</i> , G2576T (+) | EFM448B ^f |
| 464-24785 | E. faecium | Maywood | Illinois | 55/F | 8 | 8 | G2576T (+) | |
| 453-23688 | E. faecalis | Hershey | Pennsylvania | 44/F | 8 | 8 | G2576T (+) | |

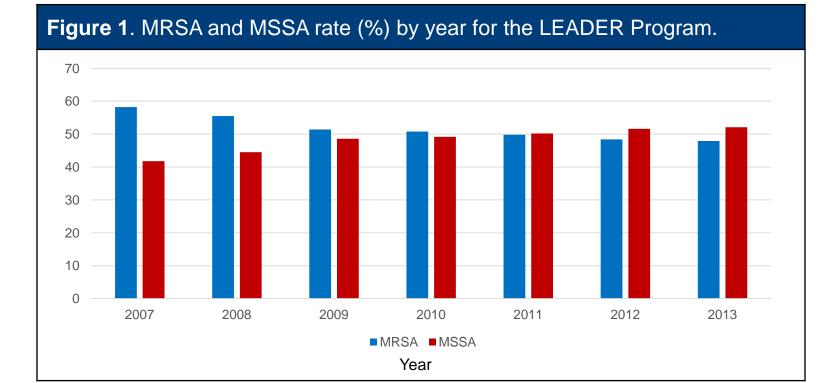
One cfr-positive SA detected in 2011 from this site displayed the same PFGE profile.

Two linezolid-resistant SEPI displaying the same PFGE profile were detected during the 2012 Program. Linezolid-resistant SEPI isolates originating from this site during previous years (2006 – 2011) had distinct PFGE profiles.

PFGE profile identical to that from isolate (LZD MIC 128 µg/ml) detected in 2012.

PFGE profile distinct from those noted for non-S isolates detected from this site during the 2011 (EFM 116A) and 2012 (EFM116B)

Two non-S EFM showing distinct PFGE profiles were detected from site number 448 during the 2012 Program. One isolate (from 2012) displayed the same EFM448B pattern as the isolate from 2013.



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CONCLUSIONS

- Susceptibility to linezolid was 99.83% for 7,183 organisms tested from 60 USA medical centers with only 12 isolates (six Enterococci, two S. aureus, three S. epidermidis, and one S. sanguinis) testing non-susceptible.
- Linezolid resistant isolates included mutations in rRNA, L3. L4, L22 and *cfr* (Table 3). The majority of resistant isolates harbored ribosomal mutations and not *cfr*.
- Linezolid continues to demonstrate excellent in vitro activity against targeted Gram-positive pathogens with no evidence of "MIC creep" among monitored species. Although no increasing resistance trends have been observed, continued monitoring of linezolid activity through the LEADER Program should be continued to detect future trends in resistance and geographic variance.

ACKNOWLEDGEMENT

The authors would like to thank all participating centers for contributing isolates to this surveillance protocol. This study was sponsored by Pfizer

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