#### AMENDED ABSTRACT

Background: The LEADER Program has completed an expanded fourth year of LZD surveillance in the USA, monitoring Gram-positive (GP) isolates in 60 medical centers. LZD has emerged as a viable therapeutic alternative for infections caused by R GP organisms such as methicillin-R S. aureus (MRSA) and vancomycin-resistant enterococci (VRE).

Methods: 6,305 GP isolates from 60 sites were sent to the monitor for identification confirmation and CLSI broth microdilution susceptibility (S) testing. Sites were distributed across the 9 USA census regions and each participant submitted 100 isolates in the following organism groups (no.): S. aureus (SA; 3,318), coagulase-negative staphylococci (CoNS; 1,020), enterococci (ENT, 705), S. pneumoniae (SPN; 622), viridans group (VGS; 249) and B-haemolytic streptococci (BHS; 391). Molecular studies (PCR, PFGE) were performed to identify R mechanisms and possible clonality within or between hospitals.

**Results:** LZD-R rates remained very low (<1%) and consistent with previous results.

Table. LZD activity in the USA by year

	% non-susceptible or resistant					
Organisms (no., all years)	2004	2005	2006	2007		
<i>S. aureus</i> (12,124)	0.00	0.03	0.03	0.06		
CoNS (2,854)	0.20	1.13	1.61	1.76		
Enterococci (2,659)	0.80	0.64	1.83	1.13		
All streptococci <sup>a</sup> (3,241)	0.00	0.00	0.00	0.00		
All organisms (20,878)	0.14	0.24	0.45	0.44		
a. Includes: SPN (2,041), VGS (438) and BHS (762).						

Two SA isolates (Texas and Ohio) were detected as non-S to LZD; One isolate was PCR-positive for the rare *cfr* gene. Inducible clindamycin (CC)-R was 38.1% among erythromycin-R, CC-S SA strains. In CoNS, 18 isolates were LZD-R (6 species; 8 states). Only 3 CoNS isolates were negative for the common G2576T mutation, with one (Arizona) PCR-positive for *cfr*. Eight LZD-R ENT strains were positive for the G2576T mutation and represented a slight decrease in R rate compared to 2006 results. VRE rates increased by 1.4% in 2007, against which LZD and daptomycin were most active. The LZD  $MIC_{50}$  for all organism groups was unchanged from 2006 except for SA and VGS which increased slightly (two-fold). The LZD  $MIC_{90}$  for all organism groups was stable.

**Conclusion:** LZD resistance rates were generally lower in 2007, even with the addition of 10 medical centers. The discovery of the multi-R cfr determinant in staphylococci has not been previously reported in the USA and proves the effectiveness of LEADER in detecting novel R. It is therefore critical to monitor for emerging LZD-R in the context of this new, mobile genetic threat.

### INTRODUCTION

The LEADER Program has provided linezolid resistance surveillance data for four years in the United States (USA). Linezolid, the first oxazolidinone class agent to be licensed for use in clinical practice, has been used to treat Grampositive pathogens in complicated skin and soft tissue infections (cSSTI) and nosocomial pneumonias, after its USA-Food and Drug Administration (FDA) approval in early 2000. Linezolid has emerged as a viable treatment alternative for infections caused by Gram-positive organisms that are resistant to conventional drugs, such as methicillin-resistant Staphylococcus aureus (MRSA), drug-resistant Streptococcus pneumoniae (DRSP) and vancomycinresistant enterococci (VRE). Therefore, it is prudent and required via regulatory agencies to monitor the potency and possible emerging resistances to linezolid as the use of this agent increases, both in volume and geographic distribution.

The linezolid 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. Among the documented uncommon occurrences of linezolid resistance reported to date for staphylococci and enterococci, G2576 or T2500 target site mutations have been the typical mechanism. For the first time (2007) in the LEADER Program, a *cfr*-mediated resistance mechanism to linezolid has emerged among staphylococci.

#### MATERIALS AND METHODS

The 60 medical centers were selected to represent all nine USA Bureau of Census geographic zones or regions (5-8 sites/region) as follows: Pacific (California [2], Hawaii [1], Oregon [1], Washington [3]), Mountain (Arizona [2], Colorado [1], Montana [1], Utah [1]), West North Central (Iowa [1], Kansas [3], Missouri [2], Nebraska [1]), West South Central (Arkansas [1], Texas [4]), East North Central (Indiana [1], Michigan [2], Ohio [3], Wisconsin [2]), East South Central (Kentucky [2], Mississippi [1], Tennessee [4]), New England (Connecticut [1], Maine [1], Massachusetts [3], Vermont [1]), Middle Atlantic (Pennsylvania [1], New York [3], New Jersey [3]), and South Atlantic (Florida [3], Maryland [1], North Carolina [1], Virginia [1], Washington DC [2]).

Each medical center was instructed to forward 100 organisms with the following species distribution: S. aureus (50 strains), coagulase-negative staphylococci (CoNS; 20 strains), enterococci (10 strains), S. pneumoniae (10 strains), and B-haemolytic streptococci and viridans group streptococci (five strains each). The strains should be dominantly from bacteremias although isolates from documented pneumonia, cutaneous wound infections and urinary tract infections were acceptable. The forwarded clinical isolates (6,305 total strains) were distributed among the following organism groups: S. aureus (3,318), CoNS (1,020), enterococci (705), S. pneumoniae (622), viridans group streptococci (249) and *B*-haemolytic streptococci (391).

All susceptibility tests were performed by a GLP-compliant reference laboratory using Clinical and Laboratory Standards Institute (CLSI; formerly the NCCLS) broth microdilution methods and published interpretive criteria (CLSI M100-S18, 2008). Linezolid-resistant isolates were confirmed by repeated reference broth microdilution testing and with the linezolid Etest (AB BIODISK, Solna, Sweden) and disk diffusion susceptibility testing. Molecular (PCR) testing was performed on linezolid-resistant isolates to identify recognized target site mutations and potential clonality using pulsed field gel electrophoresis (PFGE), automated ribotyping and various PCR procedures. Staphylococci that were negative for the common G2576T or U mutation were also screened for the phenicol resistance mediating gene, *cfr*. Furthermore, S. aureus strains found to be resistant to erythromycin and susceptible to clindamycin were screened by the CLSI D-test to detect inducible clindamycin resistance per M100-S18 recommended methods.

- isolates per region. MRSA rates were determined via a 52.6% (Mountain) to 67.1% (ES Central).
- 62% (Table 1).

# Linezolid Experience and Accurate Determination of Resistance (LEADER) Program 2007: **Assessing Oxazolidinone and Inducible Clindamycin Resistance** JE ROSS, LM DESHPANDE, M CASTANHEIRA, RE MENDES JMI Laboratories, North Liberty, IA, USA

#### RESULTS

• A total of 3,318 S. aureus strains were tested by the reference broth microdilution method (CLSI, M7-A7, 2006) with collected samples varying from 263 (WS Central) to 469 (EN Central) prevalence mode of testing, overall rate at 58.2%. Participant sites complied with the request and the MRSA rate varied from

• The CLSI D-test detected an overall resistance induction rate of 38.1% among erythromycin-resistant, clindamycin-susceptible (ERCS) phenotypic S. aureus; 39.4% in 2006. The distribution of rates by Census region and year varied widely between 17 and

- Linezolid demonstrated excellent comparative activity across all S. aureus tested (Tables 2 and 3). The linezolid  $MIC_{90}$  for S. aureus was 2  $\mu$ g/ml and when the MRSA and MSSA were examined separately, the  $MIC_{50}$  and modal MIC for both groups was 1  $\mu$ g/ml. This observation differed slightly from 2006 results (for LEADER and ZAAPS), where MSSA strains had a two-fold higher linezolid MIC mode.
- A total of 1,020 CoNS isolates were processed by CLSI reference tests for linezolid and 15 comparison agents. The all region linezolid MIC<sub>90</sub> was 1  $\mu$ g/ml (Table 3) and no significant differences were noted in linezolid MIC distributions when comparing methicillin (oxacillin)-resistant and -susceptible isolates. The oxacillin-resistant (OR) rates varied by census region (58.7 to 78.9%) with the highest rates detected in the WN Central, ES Central and Mid-Atlantic regions. The overall OR CoNS rate was 72.7%, decreased from 76.9% in 2006.
- Linezolid potency tested against CoNS isolates demonstrated a MIC<sub>50/90</sub> of only 1 µg/ml (Table 1) without any adverse influence by oxacillin susceptibility or resistance. However, 18 (1.76%) isolates were observed to have linezolid MIC results at  $\geq 8 \mu g/$ ml, e.g. non-susceptible (Tables 2 and 3). These strains were isolated from 13 hospitals in eight states (New York [3], Texas [5], New Jersey [4], Arizona [2] and one strain each from Kentucky, Massachusetts, Tennessee and Wisconsin). The most frequent linezolid-resistant CoNS species were: S. epidermidis (10 strains), S. haemolyticus (two), S. simulans (two), S. xylosis (two), S. capitis (one) and S. hominis (one).
- The tested enterococcal species strains (705) were most likely to be identified as *E. faecalis* (436; 61.8%) or *E. faecium* (249; 35.3%%). Among these strains, the ampicillin-susceptible rate was only 67.0% and VRE rates varied by census region ranging from 24.5% (WN Central) to 41.3% (Mid-Atlantic). The VRE rate for the entire enterococcal sample was 29.8% (28.0% in 2006) and the VanA resistance phenotype represented 93.0% of the VRE isolates. High-level aminoglycoside resistance (gentamicin and streptomycin) was only 25.2 to 29.2%.
- Linezolid and daptomycin were the most active agents tested against enterococci with susceptibility rates at 98.9% and 100.0%, respectively (Tables 2 and 3). A total of eight enterococci (all *E. faecium*) had a linezolid MIC at  $\ge 8 \mu g/ml$ (Table 4). These strains were found in Kansas (2), Kentucky (1), Maryland (1), Tennessee (1), Texas (1), Utah (1) and Virginia (1).

Table 1.	Inducible clindamycin resistance among <i>S. aureus</i> listed by census region.					
	Regior	n (%2007/2006)				
	1.	Pacific (20.5/21.5)				
	2.	Mountain (29.2/30.8)				
	3.	West North Central (39.0/39.7)				
	4.	West South Central (16.9/25.5)				
	5.	East North Central (37.8/44.6)				
	6.	East South Central (39.3/33.1)				
	7.	New England (61.7/65.2)				
	8.	Mid-Atlantic (52.9/53.6)				
	9.	South Atlantic (39.6/48.4)				

Table 2.	Linezolid activity comp	pared to	o 14 otl	her agents w	hen tested in the
	LEADER Program (US	A, 2007	7), 6,30	5 strains.	
			MIC (µ	ıg/ml)	% by category:
Pathogen (no	. tested/antimicrobial agent)	50%	90%	Range	Susceptible/Resistant
<i>S. aureus</i> (3,3	318)				
Linezolid		1	2	0.25->8	99.9 / -
Ciprofloxa	acin	1	>4	≤0.03->4	51.2 / 47.3
Clindamy	cin	≤0.25	>2	≤0.25->2	75.8 / 24.2
Erythromy	ycin	>2	>2	≤0.25->2	33.3 / 66.4
Gentamic	in	≤2	≤2	≤2->8	97.5 / 2.4
Oxacillin		>2	>2	≤0.25->2	41.8 / 58.2
Quinupris	tin/daltopristin	0.5	0.5	≤0.25-2	99.9 / 0.1
Vancomy		≤0.3 1	≤0.5 1	≤0.3->2	90.0 / 2.0 \\0.0 \ 0.0
	orativa ataphylacacci (1.020)	1	I	<u>≤0.12-4</u>	>99.97 0.0
Lipozolid	egative staphylococci (1,020)	4	1	<0.06 > 8	08.2 /
Ciprofloya	acin	т Д	۱ ۸	≤0.00->0 <0.03->4	430/556
Clindamy	cin	+ <0.25	>2	<0.25->2	62 5 / 35 1
Frythrom	vcin	>2	>2	<0.25->2	29.3 / 70.3
Gentamic	in	<2	>8	<2->8	71.9 / 17.7
Oxacillin <sup>a</sup>		 >2	>2	≤0.25->2	27.3 / 72.7
Quinupris	tin/dalfopristin	≤0.25	0.5	≤0.25-2	99.8 / 0.0
Trimethop	orim/sulfamethoxazole	≤0.5	>2	≤0.5->2	65.2 / 34.8
Vancomy	cin	1	2	≤0.12-8	99.9 / 0.0
Enterococci (	705)				
Linezolid		1	2	0.25->8	98.9 / 1.1
Ampicillin	a	≤1	>16	≤1->16	67.0 / 33.0
Ciprofloxa	acin	>4	>4	0.25->4	43.3 / 53.6
Gentamic	in (high-level)	≤500	>1000	≤500->1000	74.8 / 25.2
Quinupris	tin/dalfopristin	>2	>2	≤0.25->2	32.2 / 62.7
Streptomy	ycin (high level)	≤1000	>2000	≤1000->2000	70.8 / 29.2
Teicoplan	in	≤2	>16	≤2->16	72.3 / 25.0
Vancomy	cin	1	>16	0.25->16	70.2 / 29.4
S. pneumonia	ae (622)				
Linezolid		1	1	≤0.12-2	100.0 / -
Amoxicilli	n/clavulanic acid	≤1	8	≤1-16	84.7 / 12.2
Ceftriaxor	ne	≤0.25	1	≤0.25-8	92.3 / 2.3
Ciprofloxa	acin	1	2	≤0.03->4	(2.3)
Clindamy	cin	≤0.25	>2	≤0.25->2	80.5 / 19.1
Erythromy	yCIN	≤0.25	>2	≤0.25->2	65.9/33.4
Levotioxa	CIN		I A	≤0.5->4	99.8 / 0.0
Vancomy	ain	≤0.03 ~1	4	≤0.03-8 ~1	01.0 / 19.0 100.0 /
	r atraptagged (240)	$\geq$ 1	21		100.07 -
Linezolid	p streptococci (249)	1	1	0 12_1	100 0 / -
		ı ح0 25	1	<0.12-1	032/32
Ciprofloxa	acin	≤0.23 1	т Д	≤0.23-0 ∩ 12->4	(14 1) <sup>b</sup>
Clindamy	cin	<0.25	0.5	<0.12 >4	884/96
Ervthrom	vcin	1	>2	<0.25->2	43.4 / 55.8
Levofloxa	cin	1	2	≤0.5->4	94.8 / 4.0
Penicillin <sup>a</sup>		0.06	1	≤0.015-32	71.5 / 4.4
Vancomy	cin	0.5	0.5	≤0.12-1	100.0 / -
ß-haemolvtic	streptococci (391)				
Linezolid		1	1	0.25-2	100.0 / -
Ceftriaxor	ne	≤0.25	≤0.25	≤0.25-0.5	100.0 / -
Ciprofloxa	acin	0.5	1	≤0.03->4	<b>(0.8)</b> <sup>b</sup>
Clindamy	cin	≤0.25	>2	≤0.25->2	88.2 / 11.3
Erythromy	ycin	≤0.25	>2	≤0.25->2	72.1 / 27.4
Levofloxa	cin	≤0.5	1	≤0.5->4	99.2 / 0.5
Penicillin <sup>a</sup>		≤0.015	0.06	≤0.015-0.12	100.0 / -
Vancomy	cin	0.5	0.5	0.25-1	100.0 / -
a. Criteria as p	oublished by the CLSI, B-lactam sus	ceptibility	should be	directed by the oxa	cillin test results with

staphylococci. Enterococcal susceptibility was predicted by ampicillin results and penicillin was the agent used for streptococcal activity for selected *B*-lactams.

Percentages in parentheses are the strains having a ciprofloxacin MIC at  $\ge 4 \mu g/ml$ , possible QRDR mutations.

- Linezolid was active against all streptococci (MIC<sub>50</sub> and MIC<sub>90</sub>, 1 µg/ml, Tables 2 and 3) and only 16 strains had MIC values of  $2 \,\mu g/mL$
- Two staphylococcus isolates (S. aureus and S. epidermidis) displayed linezolid-non-susceptible phenotypes and had a positive PCR result using *cfr*-specific primers (confirmed by sequencing). These isolates were the first noted in humans in the USA.

# **Table 3.** Cumulative percentage inhibited results at each linezolid MIC strains.

	Cum. % inhibited at linezolid MIC (µg/ml):							
Organism group (no. tested)	≤0.12	0.25	0.5	1	2	4	8	>8
Viridans group streptococci (249)	0.8	4.4	42.6	98.4	100.0	-	-	-
S. pneumoniae (622)	0.3	1.9	36.7	98.6	100.0	-	-	-
ß-haemolytic streptococci (391)	0.0	0.3	21.2	99.2	100.0	-	-	-
CoNS (1,020)	0.4	1.3	45.0	96.9	98.0	98.2	98.3 <sup>b</sup>	100.0 <sup>b</sup>
Enterococci (705)	0.0	0.4	4.3	68.1	98.9	98.9	99.4 <sup>°</sup>	100.0 <sup>c</sup>
<i>S. aureus</i> (3,318)	0.0	0.1	0.9	58.8	99.9	>99.9	>99.9 <sup>d</sup>	100.0 <sup>d</sup>
<ul><li>a. Organism groups were ranked in decreasing order of susceptibility to the oxazolidinone.</li><li>b. 18 strains from eight states, includes six species.</li></ul>								

. Eight *E. faecium* strains from seven states . One strain at each MIC (8 and >8  $\mu$ g/ml) from Texas and Ohio.

(MIC, ≥8 µg/ml).									
Isolate ID						LEADER			
number	Organism	State	Linezolid MIC	Mechanism	PFGE	sample <sup>a</sup>			
25-6328A	S. epidermidis	Texas	>8	G2576T		Yes			
15-5690A	S. epidermidis	New York	>8	G2576T		Yes			
129-1200A	S. epidermidis	New Jersey	>8	G2576T	129B	Yes			
426-3147L	S. epidermidis	Arizona	>8	cfr +	426A	Yes			
426-3159L	S. epidermidis	Arizona	>8	G2576T	426B	Yes			
442-3207L	S. epidermidis	New Jersey	>8	Negative <sup>b</sup>	442B	Yes			
442-3204L	S. epidermidis	New Jersey	8	Negative <sup>b</sup>	442A	Yes			
417-801L	S. epidermidis	Wisconsin	>8	G2576T		Yes			
82-3650A	S. epidermidis	New York	8	G2576T	82C	No			
82-7521A	S. epidermidis	New York	>8	G2576T	82D	Yes			
82-7522A	S. epidermidis	New York	>8	G2576T	82C1	No			
52-7675A	S. epidermidis	Massachusetts	>8	G2576T		Yes			
107-3386A	S. haemolyticus	Kentucky	>8	G2576T		Yes			
432-1923L	S. haemolyticus	Tennessee	>8	G2576T		Yes			
409-659L	S. simulans	Texas	>8	G2576T	409C	Yes			
409-660L	S. simulans	Texas	>8	G2576T	409C	Yes			
407-2847L	S. hominis	New Jersey	>8	G2576T		Yes			
409-664L	S. capitis	Texas	>8	G2576T	409C	Yes			
409-663L	S. xylosus	Texas	>8	G2576T	409D	Yes			
17-998C	S. xylosus	New York	>8	G2576T		Yes			
409-641L	S. aureus	Texas	>8	G2576T		Yes			
4-737X	S. aureus	Ohio	8	cfr +		Yes			
30-142A	E. faecium	Virginia	>8	G2576T	30F1	No			
30-3053A	E. faecium	Virginia	8	G2576T	30F1	No			
30-1896X	E. faecium	Virginia	>8	G2576T	30F	No			
30-6832A	E. faecium	Virginia	8	G2576T	30F	No			
30-901C	E. faecium	Virginia	>8	Negative <sup>b</sup>	30F1	No			
30-8040A	E. faecium	Virginia	8	G2576T	30F1	Yes			
425-394L	E. faecium	Kansas	>8	G2576T	425A	Yes			
425-381L	E. faecium	Kansas	>8	G2576T	425A	Yes			
401-559L	E. faecium	Maryland	8	G2576T		Yes			
51-1562A	E. faecium	Utah	8	G2576T		Yes			
24-5739A	E. faecium	Texas	>8	G2576T		Yes			
107-4184X	E. faecium	Kentucky	>8	G2576T		Yes			
436-1710L	E. faecium	Tennessee	>8	G2576T		Yes			
a. Yes = used in surveillance report and No = follow up studies of local clonality.									

b. Mechanism of resistance remains unknown.

# **ASM 2008**

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when testing six different groups of Gram-positive cocci isolated from all USA census regions (LEADER Program, 2007)<sup>a</sup>; 6,305 

 Table 4
 Staphylococcus and Enterococcus species resistant to linezolid

### CONCLUSIONS

- Linezolid susceptibility testing of Gram-positive isolates (6,305) from 60 USA medical centers showed excellent retained activity and a sustained susceptibility rate of 99.56% overall (99.55% in 2006).
- Linezolid MIC population distributions remained unchanged without evidence of "MIC creep" among indicated species (Table 3).
- Molecular epidemiology (PFGE) and mechanisms of resistance (target mutations or *cfr*) testing for the linezolid-resistant strains implicate epidemic clonal dissemination in monitored medical centers. This type of spread along with the novel emerging mobile resistance (plasmidic *cfr*) appears to be most responsible for the modest resistance rates observed in the LEADER Program (2007). Continued monitoring of the oxazolidinone resistance rates and mechanisms remain a prudent practice.

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