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Two Cases of Invasive Vancomycin-resistant Group B Streptococcus Infection

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Keywords

Group B streptococcus; *S. agalactiae* ; vancomycin resistance; skin; soft tissue; bone infections

To the Editor: Group B streptococcus (GBS) has emerged as an important cause of invasive bacterial infections among adults, particularly the elderly and diabetics [1]. Leading clinical syndromes include bacteremia without focus, skin and/or soft-tissue infection (often accompanied by mixed infections with methicillin-resistant *Staphylococcus aureus* (MRSA)) and pneumonia [1]. Vancomycin is often initiated empirically pending organism details. Until now, vancomycin resistance among GBS has not been confirmed. We report two unrelated cases of adult invasive GBS infection with decreased vancomycin suspectibility.

The first was an 82-year-old woman with diabetes (Table) referred to a New York City emergency department for evaluation of fever, right ankle pain with swelling and drainage eight weeks after a fracture repair. A CT scan showed soft tissue edema and intra-articular gas consistent with a post-operative joint infection. Vancomcyin was started empirically. Blood and wound cultures taken at admission grew *Streptococcus agalactiae* with an unusually high minimum inhibitory concentration (MIC) of vancomycin (4 μg/ml; CLSI threshold for susceptibility </=1μg/ml [2]), determined by automated microdilution and e-test. The wound culture also grew MRSA. Her infection resolved after surgical incision and drainage of the ankle and a six-week course of daptomycin than linezolid.

The second patient was a 48-year-old man with end-stage renal disease on hemodialysis who presented to a New Mexico emergency room with fever and right chest wall erythema. He had recently completed an eight-week vancomycin course for GBS bacteremia from a left hip sacroiliitis. The patient had a history of anaphlyaxis to penicillin and was initiated on vancomycin. His initial blood cultures grew *S. agalactiae* with a vancomycin MIC of 4 μg/ml, noted twelve days later. His infection was clinically resolved at that time so vancomycin was stopped.

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Isolates were confirmed for identification and susceptibility by local and state health authorities and sent to the Streptococcal Reference Laboratory at the Centers for Disease Control and Prevention for further characterization (Table). Both strains tested positive by polymerase chain reaction for a 941-bp *vanG* amplicon found in *Enteroccus faecalis* employing primers EG1 and EG2 [3]. Subsequent unidirectional and conventional PCR and sequencing [4] from the *vanG* amplicon termini revealed putative *vanW* and *vanXY* counterparts in each strain, with each of the three gene pairs sharing high sequence similarity (89.8%, 91.0%, and 95.7% identity between *vanW*, *vanG*, and *vanXY*, respectively). Further, the New York strain shared complete sequence identity over the contiguous 2658-bp overlap with the corresponding *E. faecalis vanG* sequence (GenBank accession DQ212986).

To our knowledge, we report the first laboratory-confirmed GBS isolates exhibiting vancomycin resistance. The divergence in vanG sequences and lack of an epidemiologic link suggest independent resistance acquisitions. Further studies are necessary to identify the origin and mode of acquisition of the resistance mechanism, and the clinical impact. These cases emphasize the importance of continued surveillance for resistant GBS. It may be important to establish vancomycin breakpoints for GBS and guidance for clinical laboratory testing. Clinicians and laboratories should be encouraged to report suspected vancomycin resistant GBS to health authorities for confirmation as this resistance profile may be emerging.

References

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Table 1:

Comparison of Clinical and Microbiologic Characteristics of New York and New Mexico GBS strains with reduced susceptibility to vancomycin

Characteristic	NY Case	NM Case
Age	82 years-old	48 years-old
Co-morbidities	Diabetes Hypertension Hypercholesteremia Congestive Heart Failure	Endstage renal disease on hemodialysis Cor pulmonale Obesity Chronic osteomyelitis
Clinical syndrome	Sepsis from complicated septic joint infection	Sepsis/bacteremia from skin/soft tissue infection
Vancomycin exposure	None	Prolonged
History of prior GBS infection	None	Yes
GBS capsular serotype and MLST *	Capsular serotype II, MLST type 22	Capsular serotype II, MLST type 22
Susceptibility profile (MICs in μg/ml) **	Vancomycin (4) Tetracycline (>16) Clindamycin (>32) Erythromycin (>32) Penicillin G (0.06) Cefotaxime (0.12)	Vancomycin (4) Tetracycline (>16) Clindamycin (0.12) Erythromycin (0.06) Penicillin G (0.06) Cefotaxime (0.12)
***VanG* element resistance genes**	Strong PCR signal of 941-bp amplicon generated with primers EG1 and EG2 [3] Contiguous *vanW*, *vanG*, *vanXY* gene cluster sharing sequence identy over 2658-bp overlap with *Enterococcus faecalis vanG* element (GenBank accessionDQ212986)	Weak PCR signal of 941-bp amplicon generated with primers EG1 and EG2 [3] Contiguous *vanW*, *vanG*, *vanXY* gene cluster sharing 91.9% identity in its overlap with New York strain and *Enteroccocus faecalis vanG* element (GenBank accessionDQ212986)

* Verification of species *S. agalactiae* was performed by Lancefield serotype grouping, CAMP factor testing, multilocus sequence typing (MLST) and 16S rRNA gene sequencing.

** Based on confirmatory testing by CDC via CLSI recommended procedures, including broth microdilution and e-test.