TABLE 99-4 PATHOGENIC ISOLATES RESISTANT TO SELECTED ANTIMICROBIAL AGENTS ACCORDING TO THE NHSN, 2009-2010

ORGANISM	ANTIMICROBIAL	CLABSI	CAUTI	VAP	SSI
Staphylococcus aureus	Oxacillin	54.6%	58.7%	48.4%	43.7%
Enterococcus faecium	Vancomycin	82.6%	82.5%	82.6%	62.3%
Klebsiella pneumoniae	Ceftriaxone or ceftazidime	28.8%	26.9%	23.8%	13.2%
	Carbapenems	12.8%	12.5%	11.2%	11.2%
Escherichia coli	Ceftriaxone or ceftazidime	19.0%	12.3%	16.3%	10.9%
	Fluoroquinolones	41.8%	31.2%	35.2%	25.3%
Enterobacter spp.	Ceftriaxone or ceftazidime	37.5%	38.5%	30.1%	27.7%
	Carbapenems	4.0%	4.6%	3.6%	2.4%
Pseudomonas aeruginosa	Fluoroquinolones	30.5%	33.5%	32.7%	16.9%
	Piperacillin-tazobactam	17.4%	16.6%	19.1%	6.8%
	Cefepime	26.1%	25.2%	28.4%	10.2%
	Carbapenems	26.1%	21.3%	30.2%	11.0%
Acinetobacter baumannii	Carbapenems	62.6%	74.1%	61.2%	37.3%

Modified from Sievert DM, Ricks P, Edwards JR, et al: Antimicrobial-resistant pathogens associated with healthcare-associated infection: summary of data reported to the National Healthcare Safety Network at the Centers for Disease Control and Prevention, 2009-2010, Infect Control Hosp Epidemiol 34:1–14, 2013.

CAUTI, Catheter-associated urinary tract infection; CLABSI, central line–associated bloodstream infection; NHSN, National Healthcare Safety Network; SSI, surgical site infection; VAP, ventilator-associated pneumonia.

The intermediate resistance or decreased susceptibility to vancomycin is thought to result from cell wall and biomatrix thickening, making the drug target more difficult to reach. Complete vancomycin resistance occurs by acquisition of the *vanA* gene from VRE. VRE, unlike many MRSA strains, is almost entirely a health care–associated phenomenon. Clusters of *vanA* or *vanB* genes are carried on mobile genetic elements that are readily transmitted between strains. These genes encode peptidoglycan precursors that have a low affinity for vancomycin.

Gram-negative MDROs have a greater tendency to form resistance to multiple antimicrobials, and new antimicrobials to target these pathogens are not available. The Enterobacteriaceae are gram-negative bacteria that usually reside in the gastrointestinal tract, are glucose fermenters, and account for about 29% of HAIs. These organisms tend to be the most common pathogens in SSIs associated with abdominal operations. The non–glucose fermenting organisms, including *P. aeruginosa, Acinetobacter baumannii,* and *Stenotrophomonas maltophilia,* account for about 9% of HAIs.

Multidrug-resistant gram-negative bacteria are making their way into the limelight largely due to the emergence of isolates that are resistant to most or all available antimicrobials (e.g., MDROs that exhibit β-lactamases, extended-spectrum β-lactamases, carbapenem and fluoroquinolone resistance). The predominant carbapenem-resistance mechanisms are the loss of OprD, an outer membrane protein, *Klebsiella pneumoniae* carbapenemases (KPCs), and the metalo-β-lactamases (MBLs), which hydrolyze the carbapenem. The New Delhi metalo-β-lactamase 1 (NDM1) is one of the first MBLs to cause outbreaks in the United States. The carbapenemases and MBLs are easily transmissible and tend to be associated with other genes encoding mechanisms of resistance to other antimicrobial classes. Fluoroquinolone resistance can occur by efflux pumps or mutations in genes encoding the drug targets DNA gyrase and topoisomerase IV.

Limiting the spread of MDROs in the health care setting should be a comprehensive and system-wide program at any institution. Infection prevention programs should include optimized surveillance practices to identify emerging MDROs and appropriate intervention strategies. The mainstay of these programs includes use of evidence-based prevention practices and antimicrobial stewardship programs.

SUGGESTED READINGS

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