Microbiology of Healthcare-Associated Infections

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2024

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Goals

- Microorganisms causing healthcare-associated infections
- Microbiological tools that can be used to "fingerprint" microorganisms

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Properties of Microorganisms

	Size	Growth on Non-Living Media	DNA and RNA	Sensitivity to Antibiotics
Mycotic Agents				
Yeasts	3-15 µm	+	+	+
Molds	2-20 µm	+	+	+
Bacteria	1-5 µm	+	+	+
Mycoplasma	0.1-0.25µm	+	+	+
Rickettsiae	0.3-0.7µm	-	+	+
Chlamydiae	0.1-1.5µm	-	+	+
Viruses	20-300nm	-	-	-

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Sources of Healthcare-Associated Pathogens

Weinstein RA. Am J Med 1991:91 (suppl 3B):179S

- Endogenous flora (SSI, UTI, CLABSI): 40-60%
- Exogenous: 20-40% (e.g., cross-infection via contaminated hands [staff, visitors])
- Other (environment): 20%
  - Medical devices/inanimate objects
  - Contact with environmental surfaces (direct and indirect)

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Nosocomial Infections

Chain of Infection

- Agent
- Mode of transmission
  - Contact (direct, indirect, droplet spread)
  - Airborne
  - Common-vehicle spread
- Host

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Mechanisms of Transmission

- Airborne-true airborne phase in route of dissemination
- Contact-victim has contact with source
  - Direct: Person-to-person (physical contact)
  - Indirect: Person-to-object-to-person (contact with contaminated intermediate object)
  - Droplet: <3 feet (brief passage of infectious agent through the air)
- Common-vehicle: Food, water, medical devices (contaminated inanimate vehicles serves as vector of agent to multiple persons)
- Vector-borne

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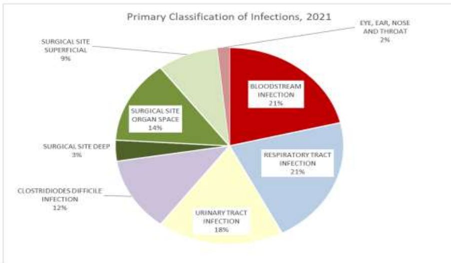

In 2021, surgical site infections still remain the most prevalent type of HAI, accounting for 26% of infections, followed by bloodstream infections and respiratory tract infections, each accounting for 21% of 2021 infections.

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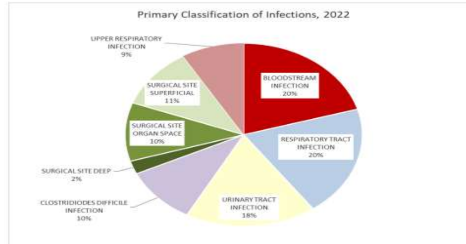

In 2022, surgical site infections remain the most prevalent type of HAI, accounting for 23% of infections, followed by bloodstream infections and HAP/VAP/VAE, each accounting for 20% of infections. In 2021, URI only accounted for 2% of the total HAI, however in 2022, URI accounted for 9% of all HAI

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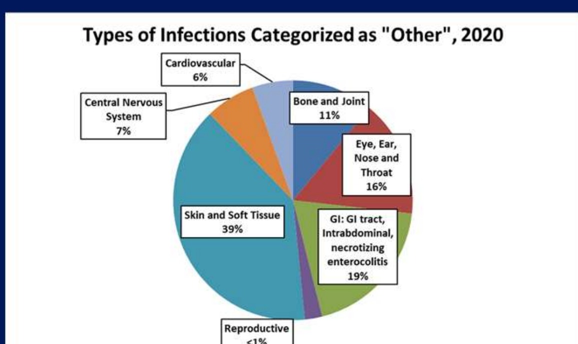

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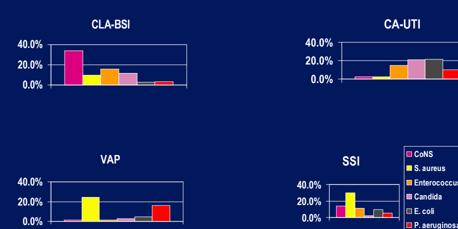
PATHOGENS CAUSING HAIs, NHSN, 2006-2007



Hidron AI, et al. ICHE 2008;29:996-1011

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HAI PATHOGENS, NHSN, 2011-2014

Weiner LM, et al. ICHE 2016;37:1288-130

TABLE 4. Distribution and Rank Order of Pathogens Frequently Reported to the National Healthcare Safety Network (NHSN), by Type of Healthcare-Associated Infection (HAI), 2011–2014

Pathogen	Overall No. (%) of pathogens	Overall Rank[b]	CLABSI No. (%) of pathogens	CLABSI Rank[b]	CAUTI No. (%) of pathogens	CAUTI Rank[b]	VAP[a] No. (%) of pathogens	VAP[a] Rank[b]	SSI No. (%) of pathogens	SSI Rank[b]
Escherichia coli	62,904 (15.4)	1	5,193 (5.4)	7	36,806 (23.9)	1	476 (5.4)	6	20,429 (13.7)	2
Staphylococcus aureus	48,302 (11.8)	2	12,706 (13.2)	2	2,515 (1.6)	14	2,179 (24.7)	1	30,902 (20.7)	1
Klebsiella (pneumoniae/oxytoca)	31,498 (7.7)	3	8,062 (8.4)	4	15,471 (10.1)	4	898 (10.2)	3	7,067 (4.7)	6
Coagulase-negative staphylococci[c]	31,361 (7.7)	4	15,794 (16.4)	1	3,696 (2.4)	13	72 (0.8)	13	11,799 (7.9)	3
Enterococcus faecalis[d]	30,034 (7.4)	5	8,118 (8.4)	3	10,728 (7.0)	5	32 (0.4)	21	11,156 (7.5)	4
Pseudomonas aeruginosa	29,636 (7.3)	6	3,881 (4.0)	10	15,848 (10.3)	3	1,449 (16.5)	2	8,458 (5.7)	5
Candida albicans[d]	27,231 (6.7)	7	5,761 (6.0)	6	17,926 (11.7)	2	193 (2.2)	10	3,351 (2.2)	12
Enterobacter spp[c]	17,235 (4.2)	8	4,204 (4.4)	9	5,689 (3.7)	9	727 (8.3)	4	6,615 (4.4)	8
Enterococcus faecium[d]	14,942 (3.7)	9	6,567 (6.8)	5	4,212 (2.7)	11	23 (0.3)	24	4,140 (2.8)	11
Other *Enterococcus* spp.[d]	14,694 (3.6)	10	1,974 (2.0)	14	6,291 (4.1)	7	19 (0.2)	27	6,410 (4.3)	9
Proteus spp.[c]	11,249 (2.8)	11	820 (0.8)	17	6,108 (4.0)	8	125 (1.4)	12	4,196 (2.8)	10
Yeast NOS[e]	10,811 (2.6)	12	763 (0.8)	18	9,443 (6.1)	6	54 (0.6)	16	551 (0.4)	25
Other *Candida* spp.[d]	10,641 (2.6)	13	4,730 (4.9)	8	5,178 (3.4)	10	37 (0.4)	19	696 (0.5)	19
Candida glabrata[d]	8,121 (2.0)	14	3,314 (3.4)	11	4,121 (2.7)	12	12 (0.1)	33	674 (0.5)	20
Bacteroides spp.	[illegible]	15	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	72	7,011 (4.7)	7
[illegible]	51,932 (12.7)		14,130 (14.6)		9,771 (6.4)		2,507 (28.5)		25,524 (17.1)	
Total	408,151 (100)		96,532 (100)		153,805 (100)		8,805 (100)		149,009 (100)	

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Relative Frequency of HA Pathogens, 1980-2008

Kang, Sickbert-Bennett, Brown, Weber, Rutala. AJIC, 2012

Table 1
Changes in relative frequency of health care-associated pathogens by time blocks from 1980 to 2008

	Total (1980-2008)			Percent of each time blocks						Trend analysis	
Organism	Rank	No.	%	1980-1984	1985-1989	1990-1994	1995-1999	2000-2004	2005-2008	% Change	*P* value
Staphylococcus aureus	1	5,483	15.4	11.8	11.2	16.0	18.2	17.3	15.5	5.3	<.0001
Escherichia coli	2	3,753	10.6	12.6	12.7	11.3	9.2	8.2	11.5	−3.1	<.0001
Coagulase negative staphylococci	3	3,587	10.1	6.9	7.6	8.1	12.7	13.2	9.2	4.8	<.0001
Candida and other yeasts	4	3,494	9.8	7.7	10.4	11.0	10.3	11.1	8.1	3.0	.1890
Enterococcus spp	5	3,138	8.8	8.1	5.8	8.0	8.8	10.2	10.7	3.8	<.0001
Pseudomonas aeruginosa	6	2,954	8.3	9.5	9.5	9.7	8.6	6.7	7.1	−3.1	<.0001
Klebsiella spp	7	2,186	6.2	7.3	7.7	5.9	6.3	4.9	5.7	−2.4	<.0001
Enterobacter spp	8	2,097	5.9	7.2	8.2	6.3	4.8	4.7	5.7	−2.7	<.0001
Other streptococci	9	1,252	3.5	5.0	4.1	2.8	3.6	3.1	2.9	−1.8	<.0001
Clostridium difficile and other anaerobes	10	1,044	2.9	3.3	3.2	2.9	1.5	1.9	5.5	0.8	.0025
Proteus spp	11	946	2.7	5.4	3.9	2.1	1.6	1.9	2.1	−1.8	<.0001
Serratia spp	12	802	2.3	3.8	2.5	2.1	1.8	2.1	1.7	0.8	<.0001
Acinetobacter spp	13	593	1.7	1.2	1.4	2.2	1.4	2.1	1.6	−1.5	.0163
Haemophilus spp	14	494	1.4	1.6	2.5	2.2	1.1	0.9	0.8	−2.0	<.0001
Bacteroides spp	15	349	1.0	2.6	1.6	1.0	0.3	0.4	0.7	−0.8	<.0001
Citrobacter spp	16	325	0.9	1.1	1.1	0.9	0.8	0.9	0.8	0.5	.0488
Group B streptococci	17	324	0.9	1.4	1.3	1.1	0.5	0.6	0.9	−0.3	<.0001
Other	18	2,689	7.6	3.5	5.2	6.2	8.5	10.0	9.5	6.7	<.0001
Total (n)		35,510		5,217	4,336	4,904	6,964	7,999	6,090		

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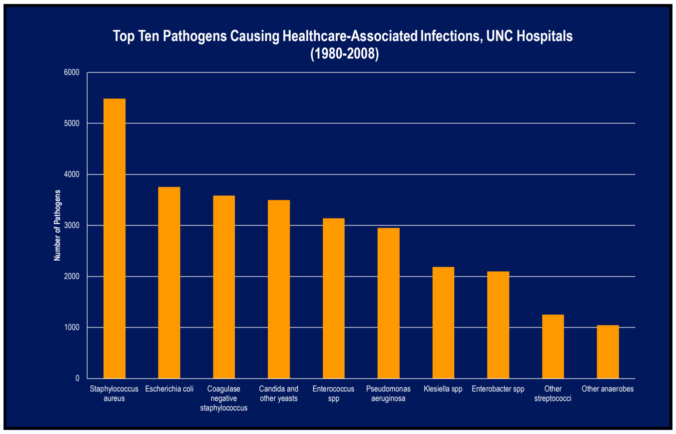

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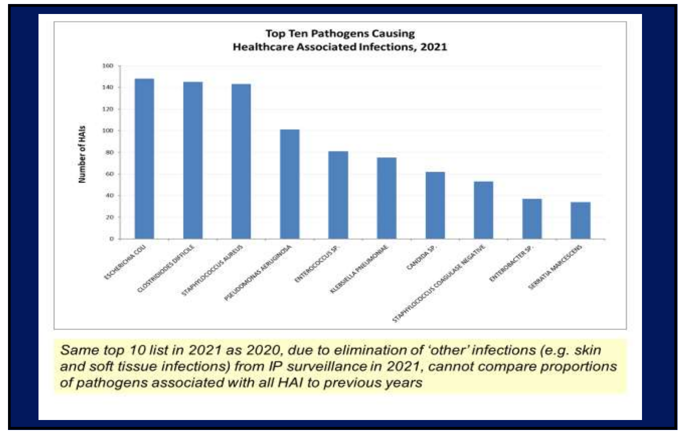

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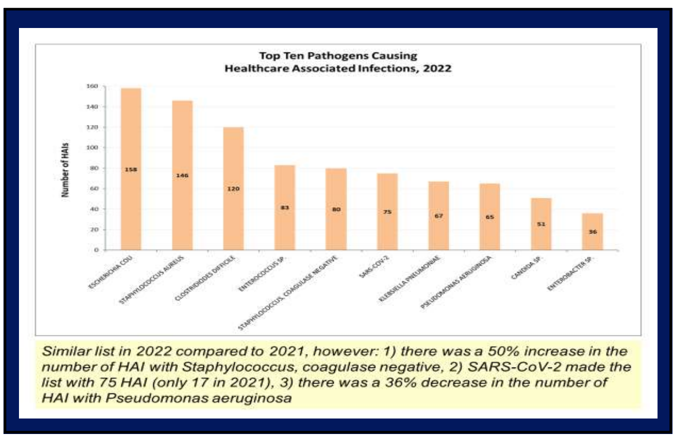

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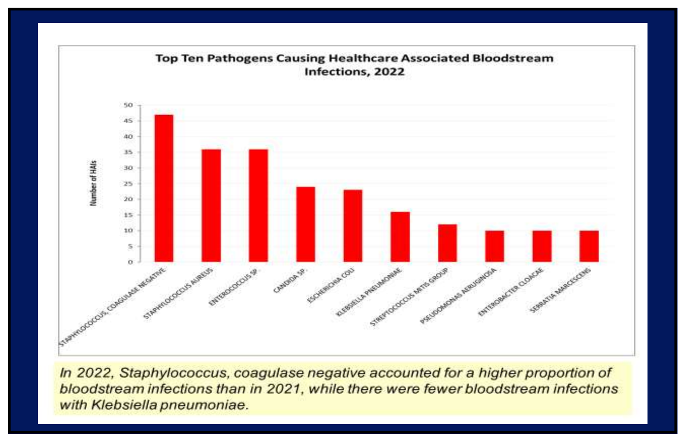

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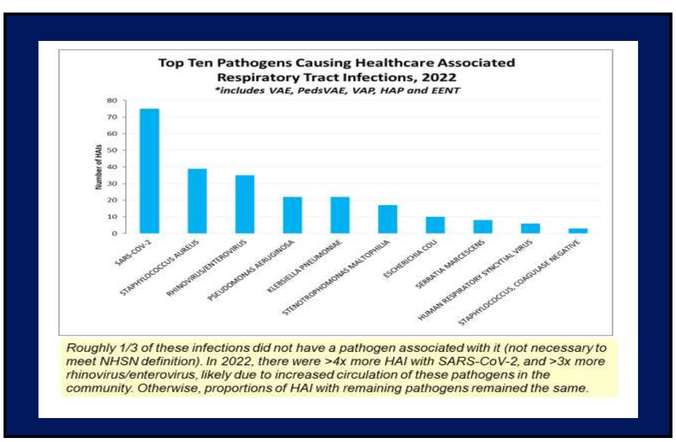

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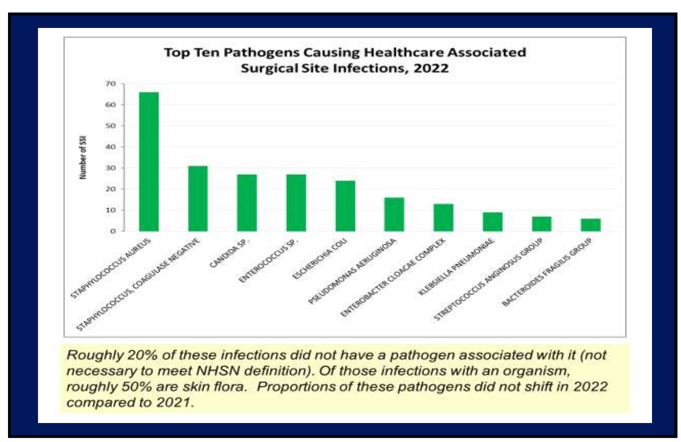

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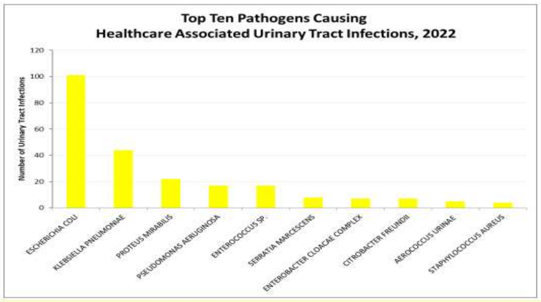

Escherichia coli accounted for 47% of all 2022 hospital-associated urinary tract infections. There was a higher proportion of UTI with proteus mirabilis and lower proportion of UTI with pseudomonas aeruginosa in 2022 compared to 2021.

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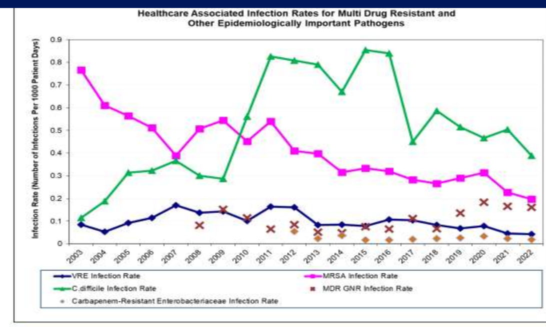

In 2022, infection rates per 1000 patient days remained relatively stable for VRE, MDR-GNR and CRE. There was a decrease in the C. difficile and MRSA infection rate per 1000 patient days in 2022.

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After experiencing a significant decrease in 2017, a slight increase in 2018, *C. difficile* HAI rates remained stable in 2021. In 2021, we had 33% fewer CDI infections than predicted when compared to the 2015 national baseline experience (most recent available national benchmarking data). *C. difficile* increase in 2010 associated with reduced susceptibility to antibiotics, frequent antibiotic use, hypervirulent *C. difficile* strain

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Bundled Approach to Reduce *C. difficile*

(two-step GDH-glutamate dehydrogenase/toxin and NAAT-nucleic acid amplification) (2015-2017)
Schultz et al. J Clin Microbiol 2018;56:1-10

- Diagnostic Stewardship
  - Only unformed liquid stool tested
  - No testing from patients with positive *C. difficile* test in previous 14 days
  - Testing restricted for patients with negative *C. difficile* in previous 7 days
  - Discouraged testing patients who received laxatives and/or stool softeners in previous 48 hours
- Enhanced Isolation-to 30 days after cessation of antibiotics
- Environmental C/D-standardized plan; UV
- Antimicrobial stewardship-reduce 3rd/4th generation cephalosporins and fluoroquinolones
- Hand Hygiene-clean in, clean out; immediate feedback

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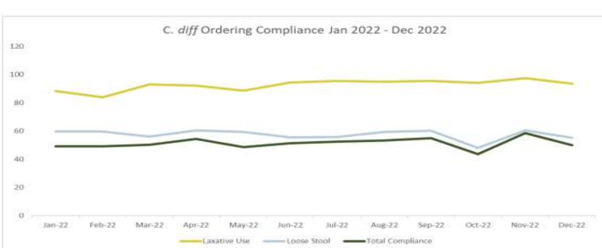

Despite relatively stable trend for CY2022 there were improvements in C. diff ordering compliance compared to CY2021, especially in laxative use. Laxative use component increased from 85% in CY2021 to 93% in CY2022. Compliance with loose stool documentation increased from 45% in CY2021 to 51% in CY2022.

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Pathogens of Epidemiologic Importance

- **Carbapenem resistant**
  - 4 of 65 (6%) *Pseudomonas aeruginosa*
  - 1 of 36 (3%) *Enterobacter cloacae*
  - 1 of 12 (8%) *Klebsiella oxytoca*
- **Multi-drug resistant**
  - 19 of 65 (29%) *Pseudomonas aeruginosa*
  - 10 of 158 (6%) *Escherichia coli*
  - 7 of 36 (19%) *Enterobacter cloacae*
  - 7 of 67 (10%) *Klebsiella pneumoniae*
  - 3 of 30 (10%) *Serratia marcescens*
- **Other drug resistant**
  - 14 of 83 (17%) *Enterococcus* were vancomycin resistant
  - 61 of 146 (42%) *Staphylococcus aureus* were oxacillin resistant

These percentages are similar to percentages for CRE, MDR and other drug resistant reported in past few years

2022

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Other Pathogens of Epidemiologic Importance

- 141 *Clostridiodes difficile*
- 75 SARS-CoV-2
- 35 Rhinovirus/enterovirus
- 8 Influenza A
- 6 Respiratory Syncytial Virus
- 6 *Mycobacterium abscessus*
- 5 endemic coronaviruses
- 3 Adenovirus
- 3 Group B *Streptococcus*
- 2 *Aspergillus sp.*
- 2 Metapneumovirus
- 2 Parainfluenza viruses
- 1 *Fusarium*
- 1 *Haemophilus influenzae*
- 1 *Mycobacterium immunogenum*
- *1 Mycobacterium fortuitum*
- 1 Mold
- 1 *Neisseria meningitidis*

In 2021, there were 17 HAI with SARS-CoV-2, however, in 2022 there were 75. Overall, there were more HAI with respiratory viruses (e.g. rhinovirus/enterovirus, influenza A) likely due to the increased prevalence of these pathogens in the community compared to 2020/2021, when COVID mitigation strategies were more widely/consistently implemented.

2022

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Pathogens of Epidemiologic Importance

- **Carbapenem resistant**
  - 4 of 37 (11%) *Enterobacter cloacae*
  - 1 of 10 (10%) *Klebsiella oxytoca*
  - 1 of 24 (4%) *Klebsiella aerogenes*
- **Multi-drug resistant**
  - 2 of 10 (20%) *Acinetobacter baumannii*
  - 16 of 101 (16%) *Pseudomonas aeruginosa*
  - 3 of 37 (8%) *Enterobacter cloacae*
  - 11 of 148 (7%) *Escherichia coli*
  - 5 of 75 (6%) *Klebsiella pneumoniae*
  - 2 of 34 (6%) *Serratia marcescens*
- **Other drug resistant**
  - 14 of 81 (17%) *Enterococcus* were vancomycin resistant
  - 69 of 143 (48%) *Staphylococcus aureus* were oxacillin resistant

These percentages are similar to percentages for CRE, MDR and other drug resistant reported in 2020

2021

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Other Pathogens of Epidemiologic Importance

- 145 *Clostridiodes difficile*
- 17 SARS-CoV-2
- 10 Rhinovirus
- 8 Group B *Streptococcus*
- 5 Respiratory Syncytial Virus
- 3 *Aspergillus sp.*
- 2 *Fusarium*
- 2 Parainfluenza viruses
- 1 *Streptococcus pneumoniae*
- 1 *Haemophilus influenzae*
- 1 *Legionella pneumophila*
- 1 *Mycobacterium abscessus*
- 1 Mucor
- 1 Mold
- 1 Salmonella
- 1 Human metapneumovirus

In 2020, there was just 1 HAI with SARS-CoV-2, but in 2021 there were 17. However, there were fewer HAI with some of the other respiratory viruses (e.g. no HAI with influenza, lower numbers of HAI with parainfluenza) likely due to the decreased prevalence of these pathogens in the community compared to previous years.

2021

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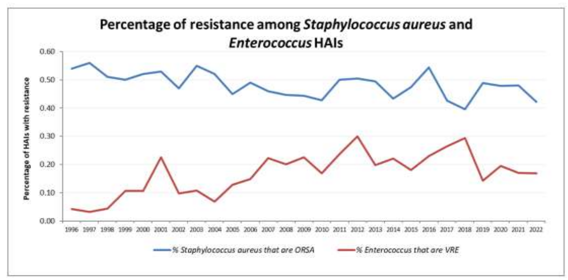

The percentage of resistance among Enterococcus HAIs remained stable in 2022 (when compared to 2021) while the percentage of resistance among Staphylococcus aureus HAIs slightly decreased in 2022.

2022

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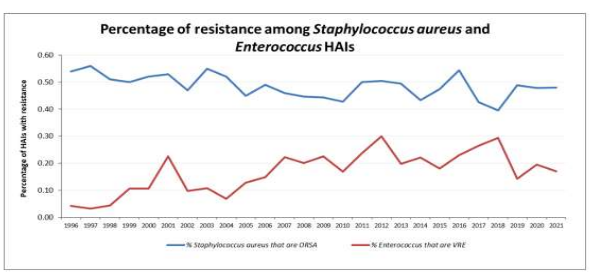

The percentage of resistance among Staphylococcus HAIs remained stable in 2021 (when compared to 2020) while the percentage of resistance among Enterococcus HAIs slightly decreased in 2021.

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UNC Medical Center, 2022

Conclusions and Recommendations

- HAI pathogens recovered at UNC Hospitals are similar in spectrum to nationally reported data.
- The proportion of vancomycin-resistance among *Enterococcus* and the VRE HAI rate remained stable in 2022 compared to 2021.
- The proportion of oxacillin-resistance among *Staphylococcus aureus* and the MRSA HAI rate decreased in 2022 compared to 2021.
- HAI rates of MDR Gram negative bacteria and CRE have been stable and remain low.

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Goals

- Microorganisms causing healthcare-associated infections
- Microbiological tools that can be used to “fingerprint” microorganisms

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Microbiological Tools That Can Aid an Infection Preventionists

- Biotyping: use of biochemical reactions to differentiate bacteria
- Antibiograms: antimicrobial susceptibility
- Phage Typing: certain bacteria under bacterial phage attachment and subsequent lysis
- Serotyping: whole microorganisms or its components can be used as antigenic sources for a variety of serologic schemes
- Molecular Typing: microbial DNA fingerprinting (e.g., PFGE, whole genome sequence analysis)
- MALDI-TOF mass spectrometry for organism ID (new tools bring efficiencies to ID process; peptide map used to search sequence database)

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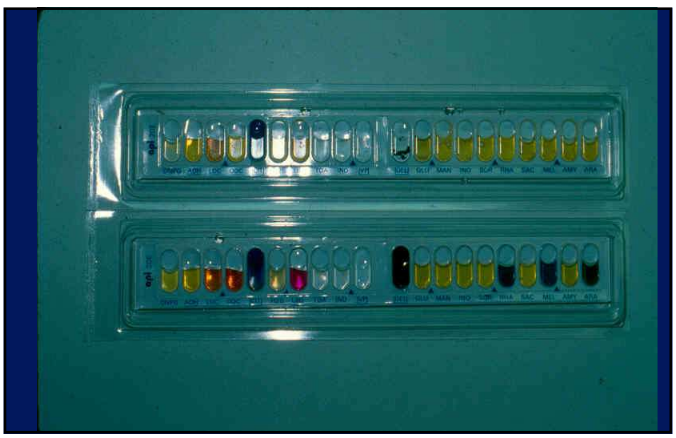

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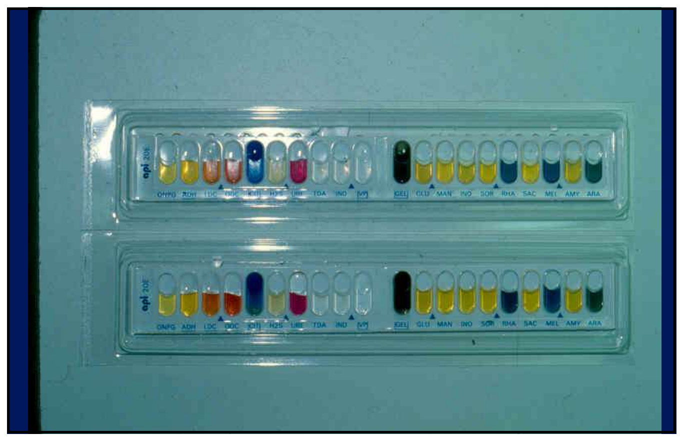

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Outbreak of *P. cepacia* Bacteremia Associated with IABP

Rutala et al. J Thoracic Cardio Surg 1988

- Cluster: Symptomatic *P. cepacia* bacteremia in 2 patients in CTICU within 3 days after insertion of IABP
- Evaluation: Both patients needed IABP for circulatory support
- Results: IABP water reservoir contained more than 10^5/ml *P. cepacia*. Also recovered from purge button, on-off switch, hands of HCP who manipulated the water reservoir
- Agarose gel electrophoresis of *P. cepacia* revealed 3 identical plasmids
- Transmission from workers hands to patients occurred by inoculation of intravascular lines during management

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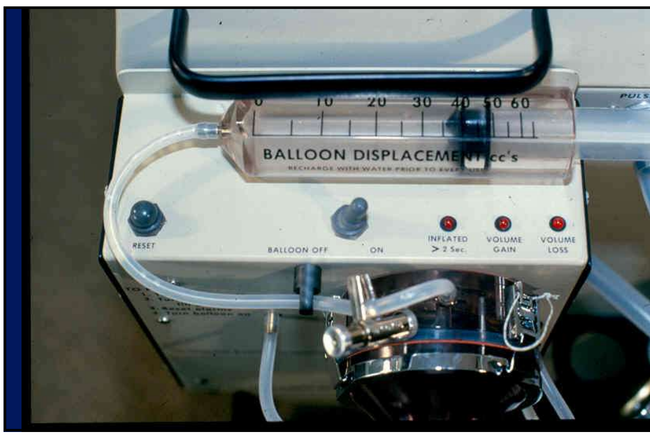

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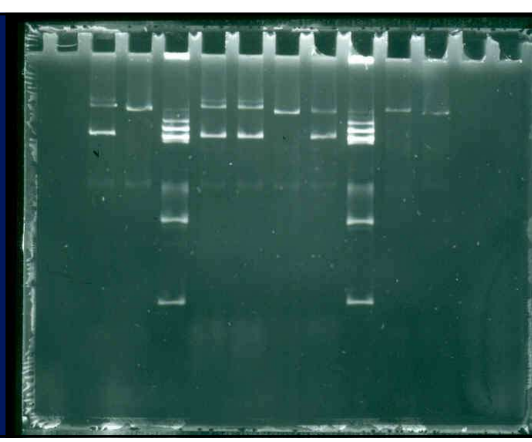

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Faucet Aerators: Source of Patient Colonization with *S. maltophilia*

Weber, Rutala et al. AJIC

- Cluster of patients in SICU C/I with *S. maltophilia*
- Environmental isolates obtained from water sources
- Two isolates of *S. maltophilia* were identical to strains isolated from the faucet aerators in sinks in the patients' rooms (lanes 3,4 and lanes 6,7-patient and sink aerator)
- Believed low-level contamination of water led to contamination of faucet aerators with amplification on the aerator.
- If clusters of C/I linked to aerators, consider given to routine disinfection or removal

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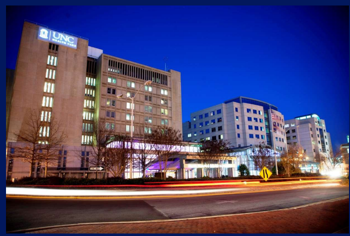
THANK YOU!

www.disinfectionandsterilization.org



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