# Microbiology of Healthcare-Associated Infections

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2025

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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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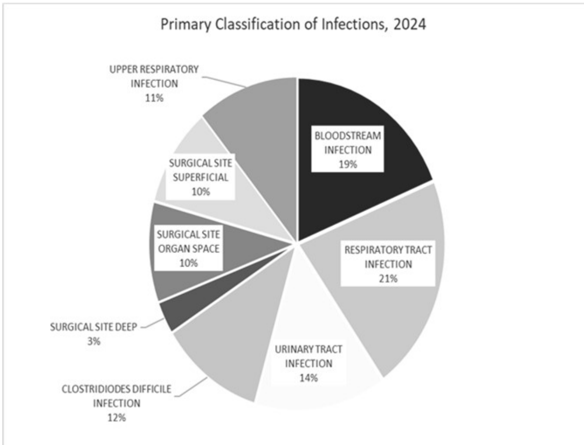


*In 2024, surgical site infections remained the most prevalent type of HAI, accounting for ~23% of infections, followed by HAP/VAP/VAE and bloodstream, each accounting for 20% and 19% of infections, respectively. In 2024, URI accounted for 11% of all HAI (an increase from previous years) and CDI accounted for 12% of all HAI (an increase compared to 2023), while UTI accounted for lower percentage of HAI than previous years.*

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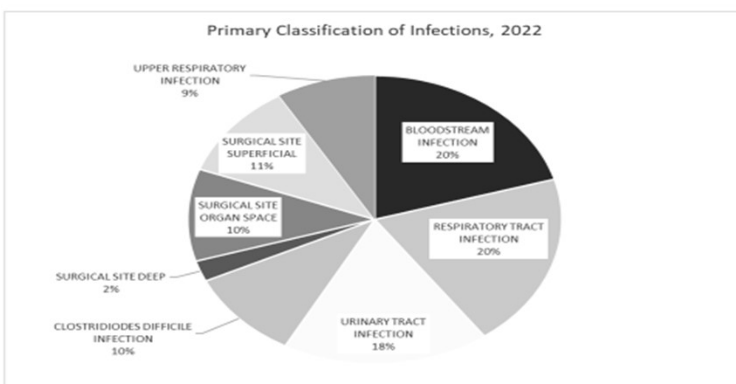


*In 2022, surgical site infections remain the most prevalent type of HAI, accounting for 23% of infections, followed by bloodstream infections and HAP/VAP/VAE, each accounting for 20% of infections. In 2021, URI only accounted for 2% of the total HAI, however in 2022, URI accounted for 9% of all HAI*

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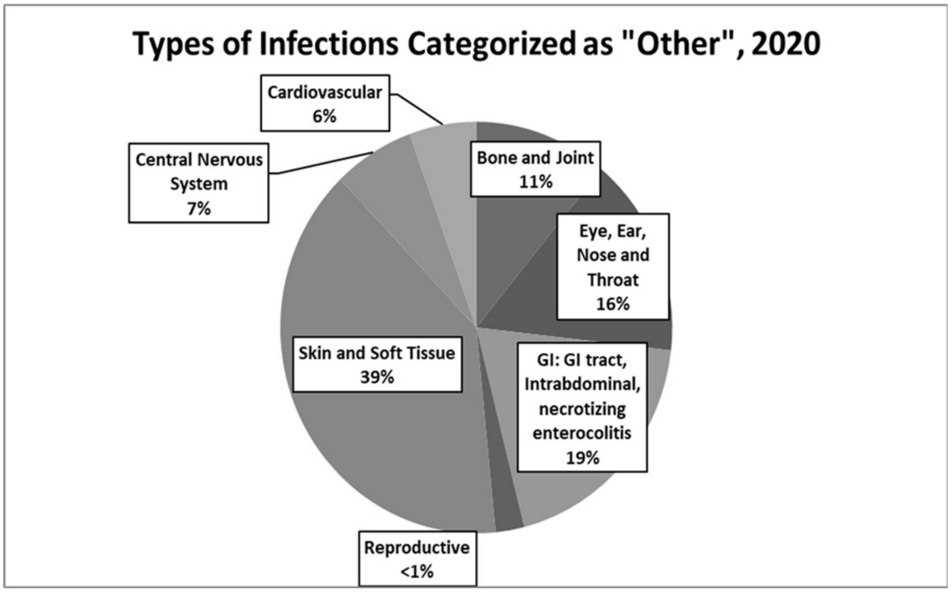


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# PATHOGENS CAUSING HAIs, NHSN, 2006-2007

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

| | Overall | | CLABSI | | CAUTI | | VAP[a] | | SSI | |
|---|---|---|---|---|---|---|---|---|---|---|
| Pathogen | No. (%) of pathogens | Rank[b] | No. (%) of pathogens | Rank[b] | No. (%) of pathogens | Rank[b] | No. (%) of pathogens | Rank[b] | No. (%) of pathogens | 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 |
| [illegible] | [illegible] | [illegible] | [illegible] | [illegible] | [illegible] | [illegible] | [illegible] | [illegible] | [illegible] (4.7) | 7 |
| Other pathogen | 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) | |

%MRSA by site: CLABSI, 50.7% (2014); VAP, 42.4% (2012); SSI, 42.6% (2014); CAUTI, 5(2014)

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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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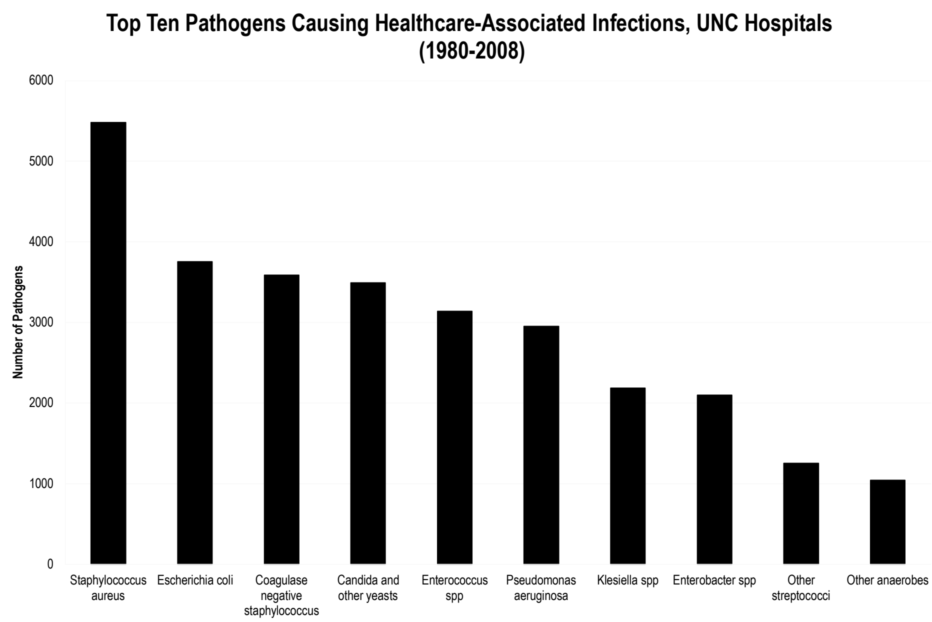


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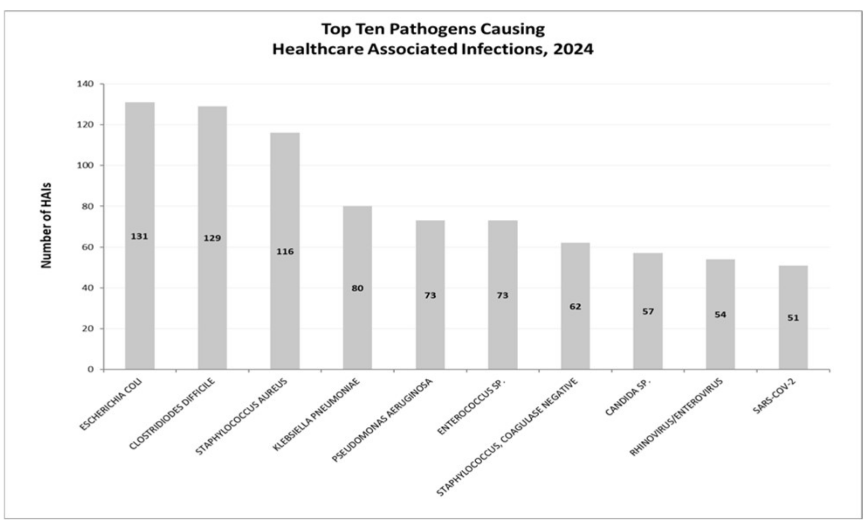


*Similar list in 2024 (same top 3 pathogens) compared to previous recent years, however: 1) there was a ~25% increase in the number of HAI with Staphylococcus aureus, 2) there was a ~10% increase in the number of rhinovirus/enterovirus HAI and of SARS-CoV-2 HAI in 2024 compared to 2023*

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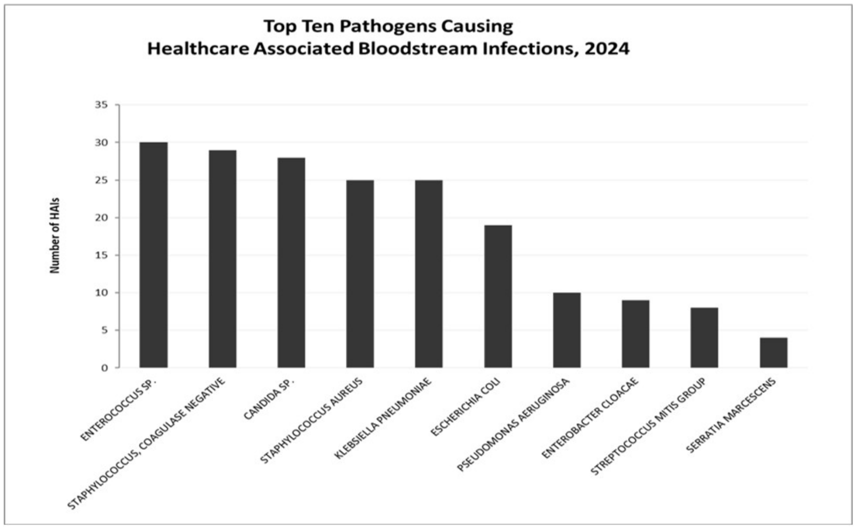


*In 2024, Enterococcus sp. and klebsiella pneumoniae accounted for a higher proportion of bloodstream infections than in 2023, while there were fewer bloodstream infections with Staphylococcus aureus and Staphylococcus, coagulase negative.*

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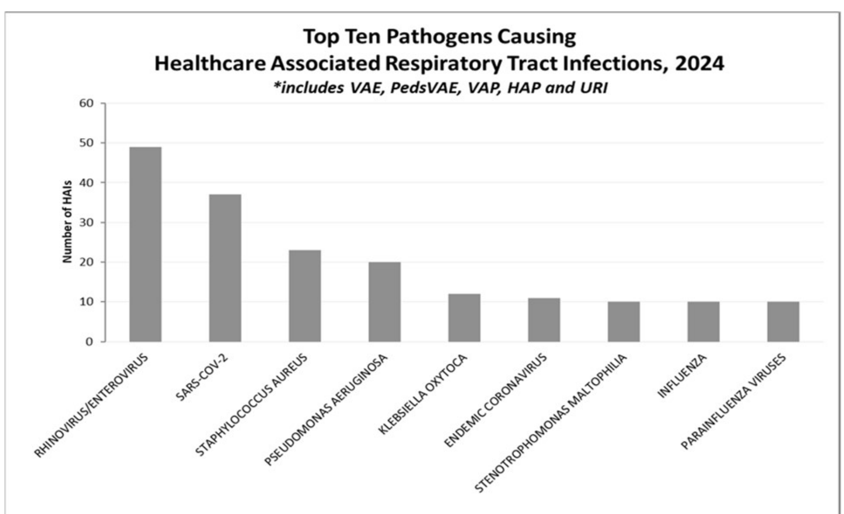


*~30% of these infections did not have a pathogen associated with it (not necessary to meet NHSN definition). In 2024, there were more respiratory HAI staphylococcus aureus and klebsiella pneumoniae and fewer with klebsiella oxytoca and influenza. Otherwise, proportions of HAI with remaining pathogens remained the same.*

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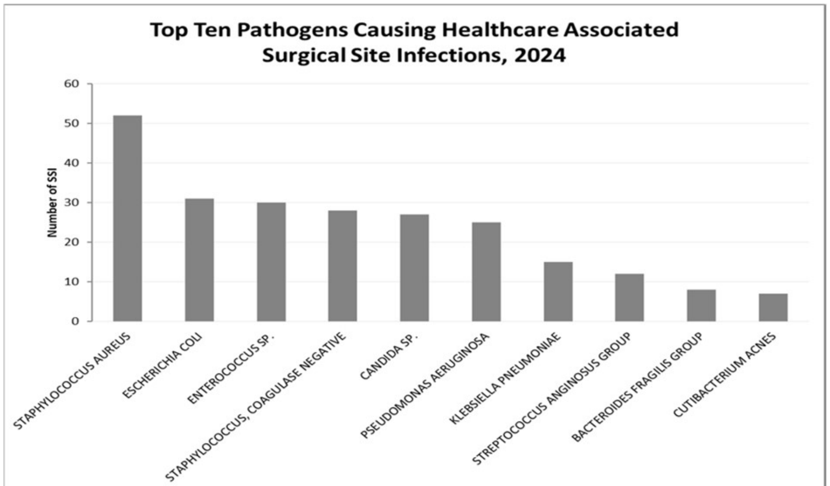


*~15% of these infections (lower percentage than previous years) did not have a pathogen associated with it (not necessary to meet NHSN definition). Of those infections with an organism, ~40% are skin flora. The number of SSI HAI with Staphylococcus aureus increased in 2024. Otherwise, proportions of these pathogens did not shift in 2024 compared to 2023.*

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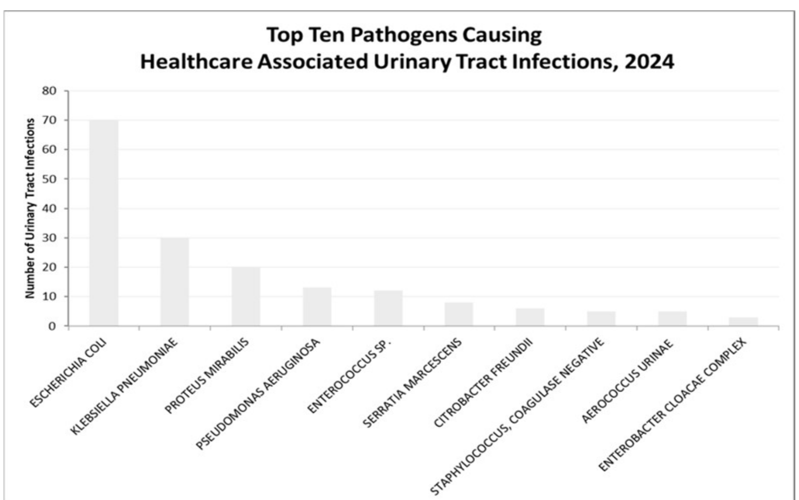


*Escherichia coli again accounted for >40% of all 2024 hospital-associated urinary tract infections. Proportions of these pathogens did not shift in 2024 compared to previous few years.*

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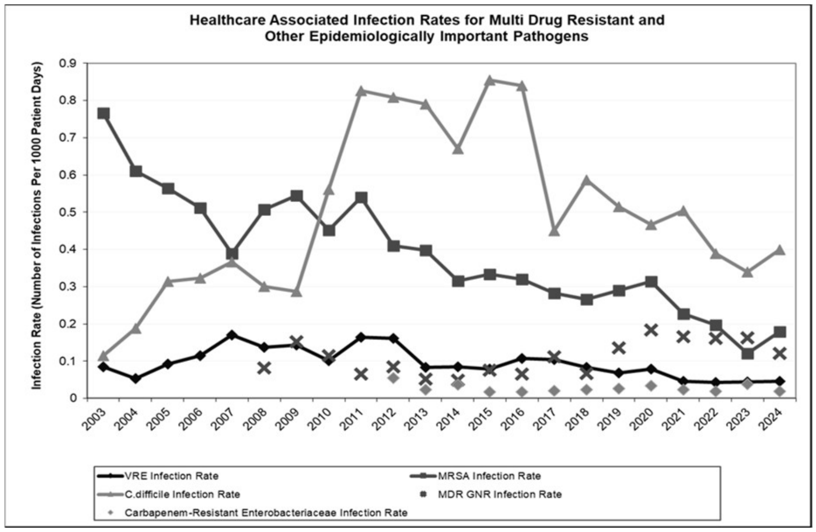


*In 2024, after several years of steady decreases, the MRSA and C. difficile infection rates per 1000 patient days increased. The infection rates per 1000 patient days remained relatively stable for VRE and infections for MDR-GNR and CRE slightly decreased.*

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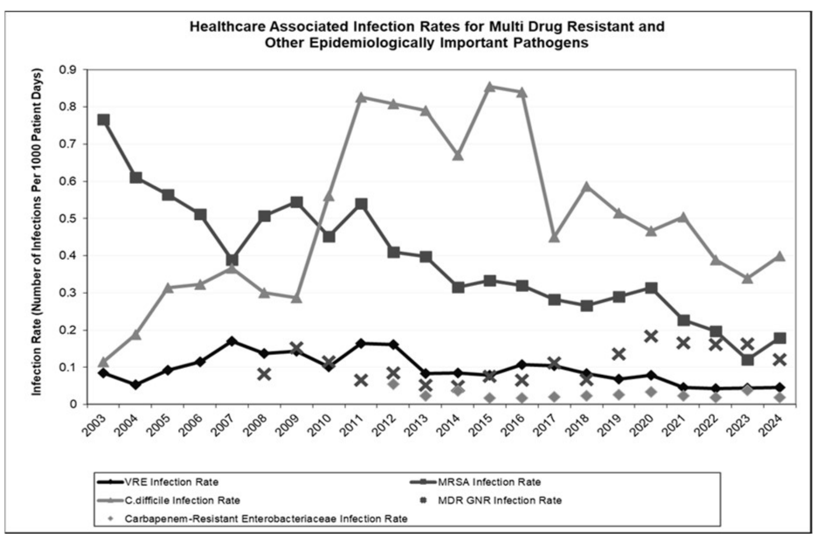


*C. difficile* increase in 2010 associated with reduced susceptibility to antibiotics, frequent antibiotic use, hypervirulent *C. difficile* strain. After experiencing a significant decrease in 2017, a slight increase in 2018, *C. difficile* HAI rates remained stable in 2021.In 2021, UNC had 33% fewer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

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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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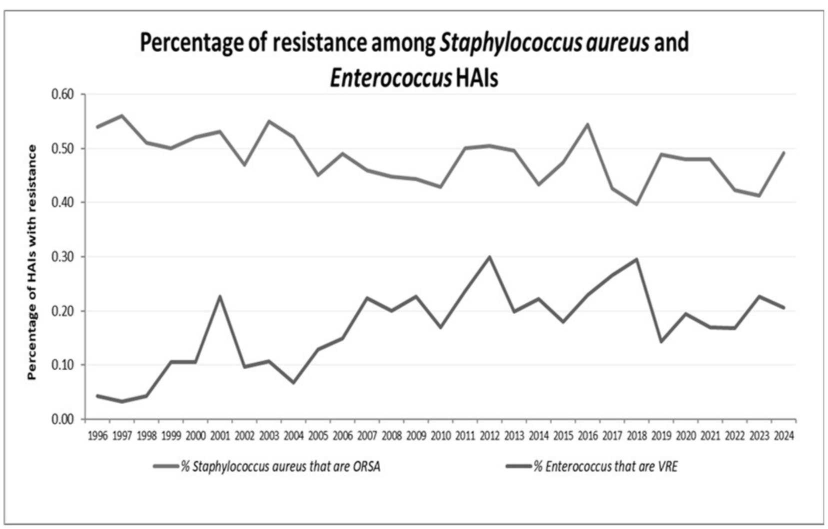


*The percentage of resistance among Enterococcus HAIs slightly decreased in 2024 (when compared to 2023) while the percentage of resistance among Staphylococcus aureus HAIs increased in 2024 compared to past couple of years.*

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## Pathogens of Epidemiologic Importance

- **Carbapenem resistant**
  - 3 of 28 (11%) *Enterobacter cloacae*
  - 2 of 131 (1.5%) *Escherichia coli*
  - 1 of 80 (1.3%) *Klebsiella pneumoniae*
- **Multi-drug resistant**
  - 5 of 28 (18%) *Enterobacter cloacae*
  - 16 of 131 (12%) *Escherichia coli*
  - 1 of 9 (11%) *Acinetobacter sp.*
  - 8 of 73 (11%) *Pseudomonas aeruginosa*
  - 1 of 10 (10%) *Klebsiella aerogenes*
  - 4 of 80 (5%) *Klebsiella pneumoniae*
- **Other drug resistant**
  - 15 of 73 (20.5%) *Enterococcus* were vancomycin resistant
  - 58 of 116 (50%) *Staphylococcus aureus* were oxacillin resistant

*These percentages are relatively similar to percentages for CRE and MDR reported in past few years*

2024

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## Other Pathogens of Epidemiologic Importance

- 129 *Clostridioides difficile*
- 54 Rhinovirus/enterovirus
- 51 SARS-CoV-2
- 14 Parainfluenza viruses
- 10 Respiratory Syncytial virus
- 9 endemic coronaviruses
- 9 Adenovirus
- 8 Group B *Streptococcus*
- 4 Influenza A
- 4 *Haemophilus influenzae*
- 3 *Aspergillus sp.*
- 3 Metapneumovirus
- 1 *Fusarium*
- 2 *Mycobacterium abscessus*
- 1 *Mycobacterium mucogenicum*
- 1 *Mycobacterium chelonae*

2024

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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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## Conclusions and Recommendations

**UNC Medical Center, 2024**

- **HAI pathogens recovered at UNC Hospitals are similar in spectrum to nationally reported data.**
- **The proportion of vancomycin-resistance among *Enterococcus* decreased slightly and the VRE HAI rate remained relatively stable in 2024 compared to 2023.**
- **The proportion of oxacillin-resistance among *Staphylococcus aureus* and the MRSA HAI rate increased in 2023 compared to 2023.**
- **HAI rates of MDR Gram negative bacteria and CRE decreased in 2024 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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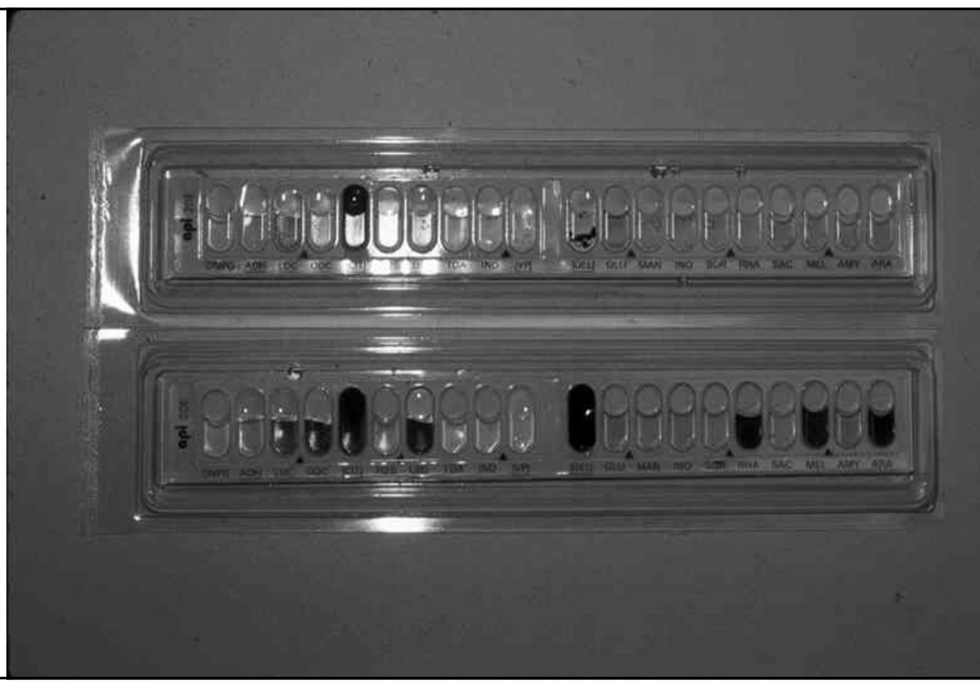


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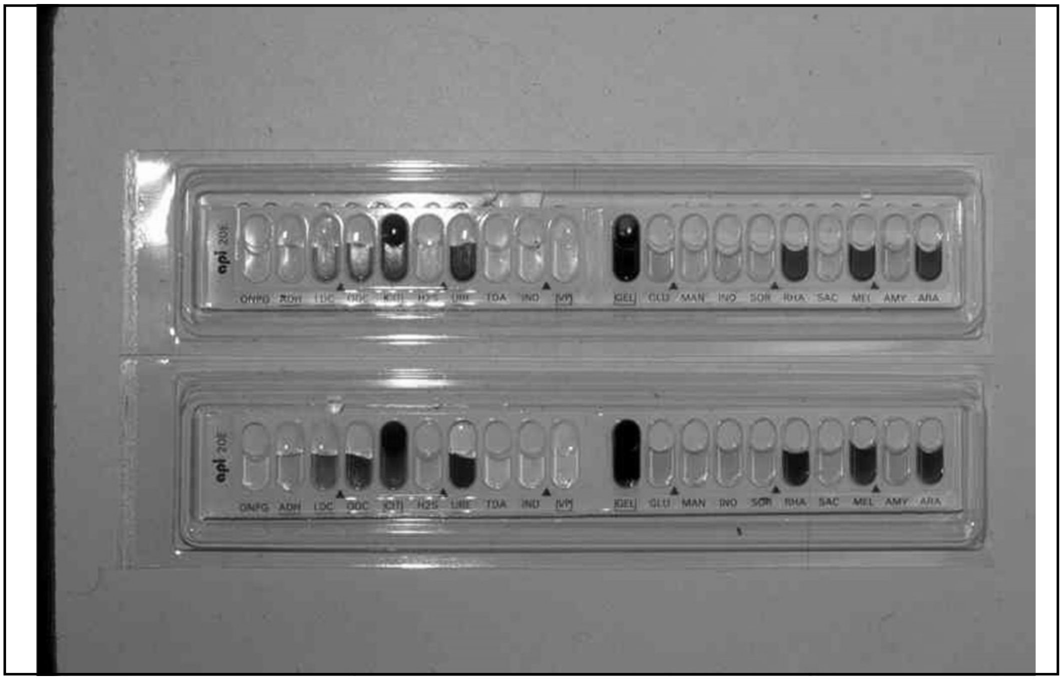
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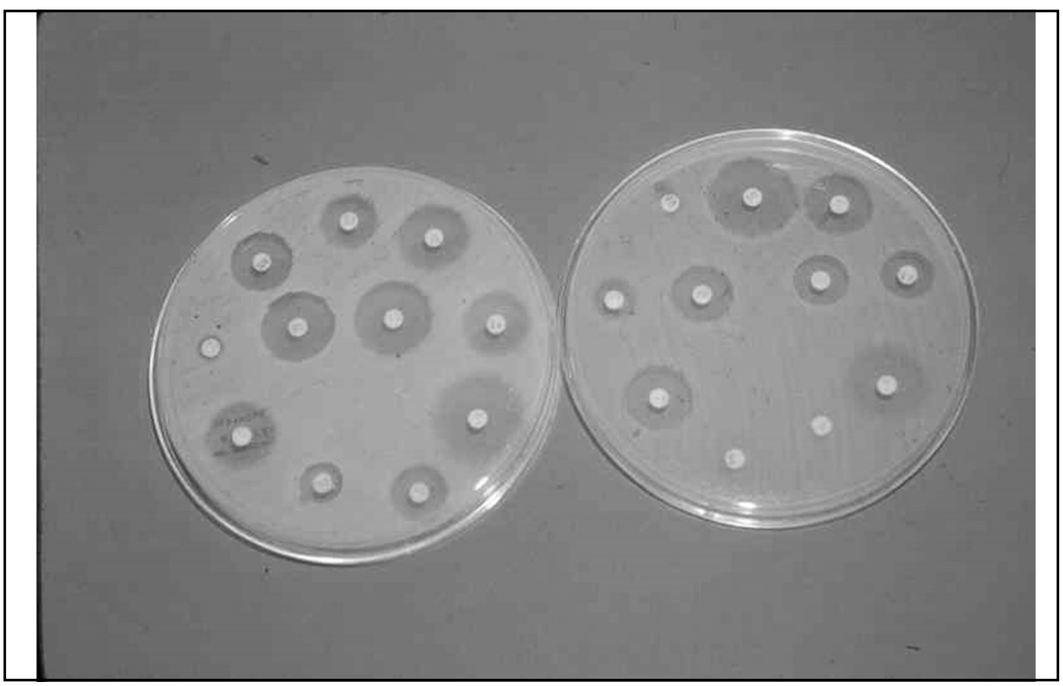

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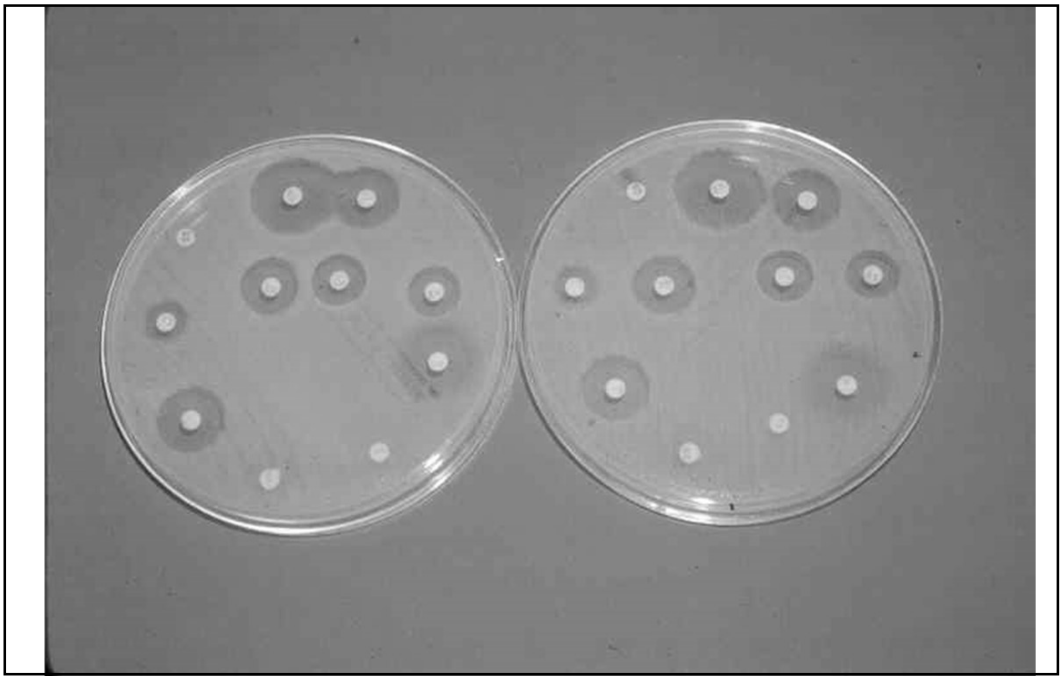

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# Outbreak of *P. cepacia* Bacteremia Associated with IABP

**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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0 10 20 30 40 50 60
BALLOON DISPLACEMENT cc's
RESET
BALLOON OFF
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INFLATED > 2 Sec.
VOLUME GAIN
VOLUME LOSS

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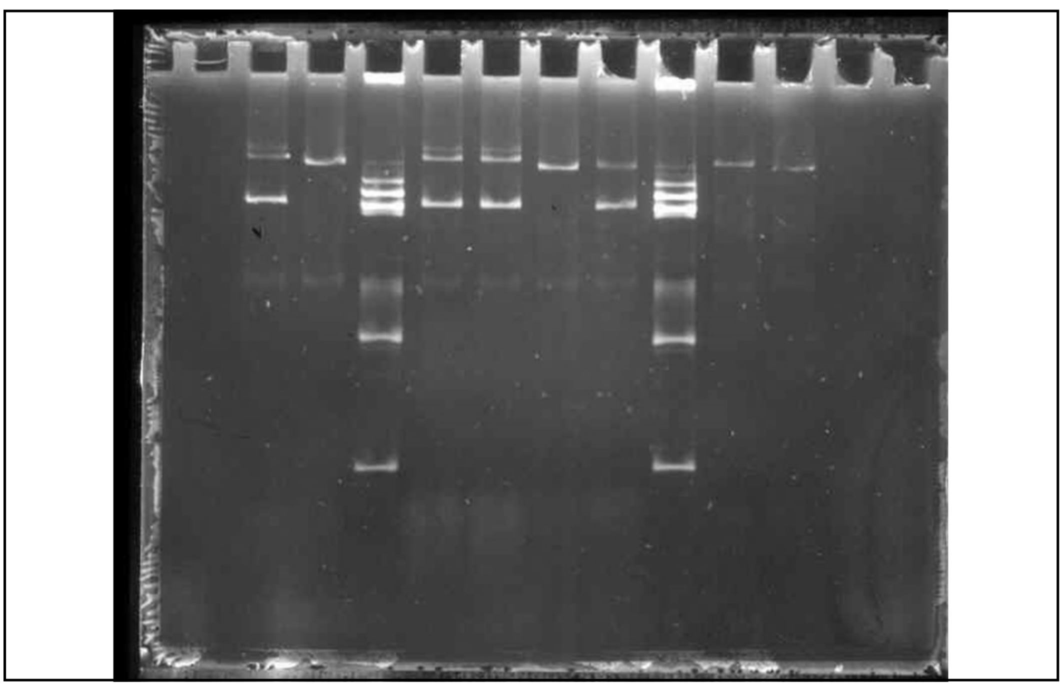

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# Faucet Aerators: Source of Patient Colonization with *S. maltophilia*

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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## Whole Genome Sequencing

**Heater Cooler Units**

- Current manufacturers
  - LivaNova (Sorin)
  - Maquet
  - Cardioquip
  - Terumo
  - Cincinnati-Sub-Zero

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## SOURCE OF *M. CHIMAERA* OUTBREAK

- Point-source contamination of 3T HCU suggested by 2 studies
  - Europe: *M. chimaera* isolates from 5 patients, 3T HCU from 3 different countries and from new 3T HCU and environment at manufacturer facility – identical by sequencing (typing unpublished – preliminary)
  - US: *M. chimaera* isolates from 11 patients and 5 3T HCU from PA and Iowa were the same by whole genome sequencing
- Manufacturing facility added disinfection and active drying procedures to production line in Sept 2014 due to *M. chimaera* contamination

Contamination during production of heater-cooler units by *Mycobacterium chimaera* potential cause for invasive cardiovascular infections: results of an outbreak investigation in Germany, April 2015 to February 2016

*Mycobacterium chimaera* Contamination of Heater-Cooler Devices Used in Cardiac Surgery — United States

Haller S, et al. Euro Surveill 2016;21(17), April 28 Perkins KM, et al. MMWR 2016;65:1117

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# THANK YOU!
# www.disinfectionandsterilization.org


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