



Descriptive Epidemiology of Antimicrobial Resistance in ESKAPE-E Pathogens Among Military Health System Beneficiaries, 2014-2024

Nicholas Seliga, MPH¹, Upendra Bhattarai, MD, MPH^{1,2}, Melissa Marcia, MPH^{3,4}, Kenji Matsumoto, MSc, MPH^{1,2}, Michael Ritsick, MSc, MPH^{1,2}, Allison Drew, DrPH, MPH¹, Hunter Jackson Smith, MD, MPH, MBE, FACPM³

¹Defense Centers for Public Health-Portsmouth, Portsmouth, Virginia ²Battelle Memorial Institute, Defense Centers for Public Health-Portsmouth, Portsmouth, Virginia ³Armed Forces Health Surveillance Division, Silver Spring, Maryland, USA. ⁴General Dynamics Information Technology, Silver Spring, Maryland



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Across the MHS, the overall rate of ESKAPE-E pathogens decreased from 2014 to 2024, with the most common pathogens *E. coli* and *S. aureus* averaging 60,206 and 13,198 isolates per year, respectively. Forty-nine percent of all ESKAPE-E isolates displayed varying degrees of antimicrobial resistance. Among all ESKAPE-E isolates, 10% had MDR. Between 2014 and 2024, 22% of all ESKAPE-E isolates were collected from ACSM, of which 49% displayed antimicrobial resistance, representing a direct concern for force readiness.

Background

The National Action Plan for Combatting Antibiotic-Resistant Bacteria (CARB) tasks many stakeholders within the federal government, including the Department of War (DoW), to reduce the impact of antimicrobial resistant (AMR) infections. Within the DoW, the Defense Centers for Public Health–Portsmouth (DCPH-P) EpiData Center (EDC) and Defense Health Agency (DHA) Public Health’s Armed Forces Health Surveillance Division (AFHSD) Global Emerging Infection Surveillance (GEIS), among others, are further tasked with surveilling AMR infections in order to reduce their impact on force readiness.^{1,2} Of particular interest are the ESKAPE-E pathogens: *Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, *Enterobacter* spp., and *Escherichia coli*, as these organisms represent the most common, and most concerning, AMR infections. In particular, ESKAPE-E infections displaying AMR, represent a critical threat to active-component service member (ACSM) readiness through prolonged recovery times and burdens on the Military Health System (MHS), with increased health care costs and increasingly complex treatment plans.^{3,4,5} This analysis seeks to support force and medical readiness by providing a descriptive epidemiological profile of ESKAPE-E infections detected within the MHS and examining the temporal changes in infection rates.

Methods

The analysis identified positive ESKAPE-E cultures among DoW MHS beneficiaries collected between January 1, 2014, and December 31, 2024. Cases were identified utilizing Composite Health Care System (CHCS) and MHS GENESIS microbiology results and antibiotic susceptibility data from cultures collected within the MHS. Theater, shipboard, and private care data were omitted from this analysis. Cases were matched to personnel, medical encounter, and pharmacy databases to capture additional demographic data. Based on reported antimicrobial susceptibility testing cases were grouped into 1 of 5 AMR categories:

- Not resistant:** No non-susceptible medications in any drug classes tested.
- Antimicrobial resistant (AMR):** Non-susceptible to one or more medications in at least 1 drug class.
- Multidrug resistant (MDR):** Non-susceptible to one or more medications in at least three drug classes.
- Extensively drug resistant (XDR):** Non-susceptible to one or more medications in all but two or fewer drug classes.
- Pan-drug resistant (PDR):** Non-susceptible to all tested medications across all drug classes.

Table 1. Demographics of All MHS Beneficiaries and Active-Component Service Members with an ESKAPE-E Isolate, 2014-2024

Category	All MHS Beneficiaries n(%)	Active-Component Service Members n(%)
Sex		
Female	767,891 (79.2)	153,961 (72.0)
Male	201,544 (20.8)	59,881 (28.0)
Missing	1 (<0.1)	0 (0)
Age Group		
0-4 years	36,310 (3.8)	N/A
5-16 years	49,077 (5.1)	N/A
17-24 years	204,443 (21.1)	103,514 (48.4)
25-34 years	180,881 (18.7)	70,976 (33.2)
35-54 years	206,873 (21.3)	37,819 (17.7)
55+ years	291,824 (30.1)	1,531 (0.7)
Missing	28 (<0.1)	2 (<0.1)
Race		
API	37,252 (3.8)	11,321 (5.3)
AIAN	5,254 (0.5)	2,382 (1.1)
Black	104,648 (10.8)	44,834 (21.0)
White	324,272 (33.5)	117,320 (54.9)
Other	188,118 (19.4)	16,906 (7.9)
Missing	309,892 (32.0)	21,079 (9.9)
Service		
Army	408,948 (42.2)	84,367 (39.5)
Air Force	225,753 (23.3)	49,565 (23.2)
Marine Corps	82,303 (8.5)	25,707 (12.0)
Navy	196,690 (20.3)	51,779 (24.2)
Space Force	426 (<0.1)	203 (0.1)
Other	55,099 (5.7)	2,221 (1.0)
Missing	217 (<0.1)	0 (0)
DHA Networks		
Atlantic	124,062 (12.8)	33,650 (15.7)
Central	167,251 (17.3)	29,363 (13.7)
Continental	93,556 (9.7)	18,393 (8.6)
East	136,291 (14.1)	31,458 (14.7)
Europe	38,064 (3.9)	12,031 (5.6)
Indo-Pacific	84,314 (8.7)	16,881 (7.9)
National Capital Region	81,065 (8.4)	12,800 (6.0)
Pacific Rim	118,817 (12.3)	31,308 (14.6)
West	107,807 (11.1)	21,824 (10.2)
Missing	17,939 (1.8)	6,134 (2.9)

Data Source(s): Composite Health Care System (CHCS) and MHS GENESIS Microbiology results and susceptibility data. Abbreviation: DHA, Defense Health Agency, MHS, Military Health System, ESKAPE-E, *Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, *Enterobacter* spp., and *Escherichia coli*; API, Asian and Pacific Islanders, AIAN, American Indian and Alaskan Native. Prepared by the EpiData Center, Defense Centers for Public Health – Portsmouth, July 1, 2026.

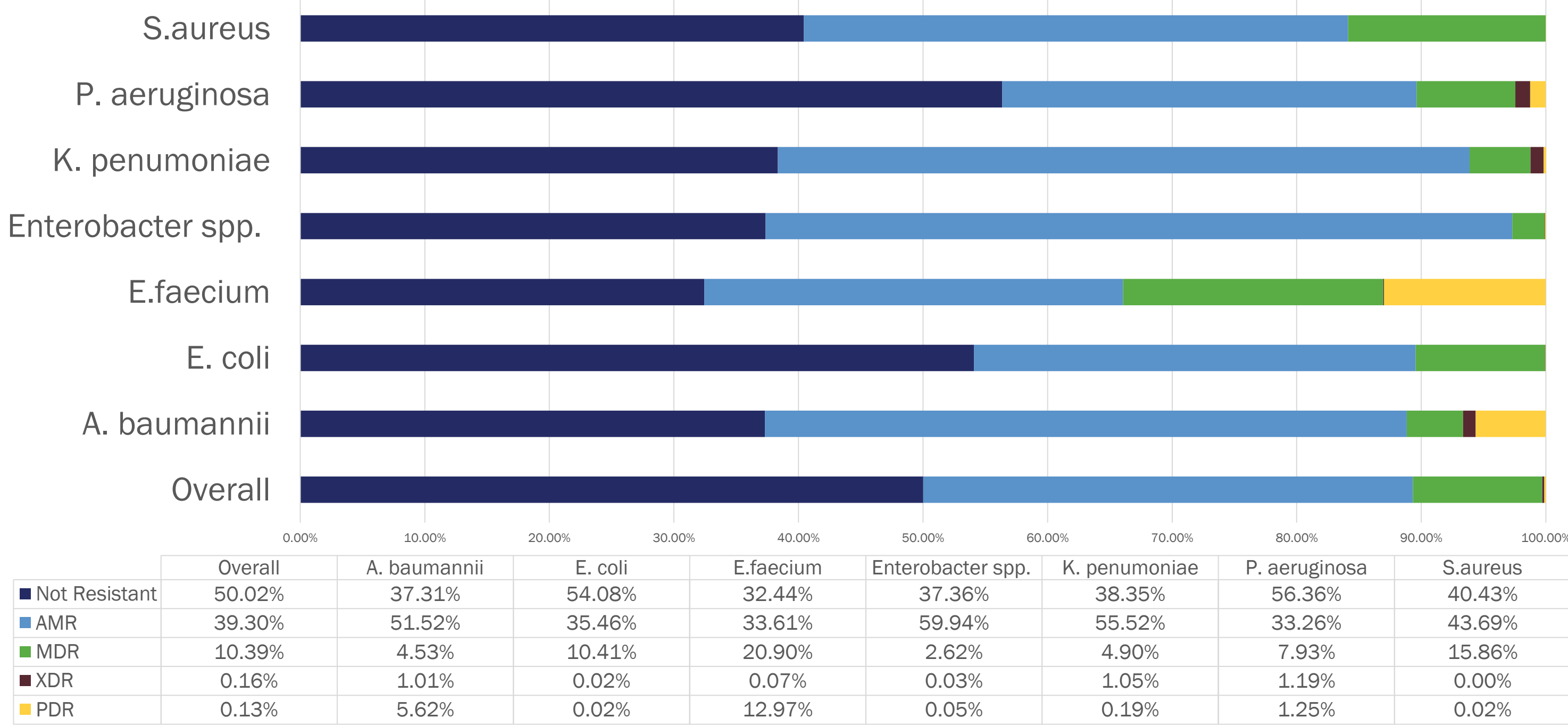
Table 2. Counts of ESKAPE-E Pathogens among MHS Beneficiaries and Active-Component Service Members, 2014-2024

ESKAPE-E Pathogen	All MHS Beneficiaries, n (%)	Active-Component Service Members, n (%)
<i>A. baumannii</i>	1,281 (0.1)	331 (0.2)
<i>Enterobacter</i> spp.	29,200 (3.0)	6,992 (3.3)
<i>E. faecium</i>	2,722 (0.3)	203 (0.1)
<i>E. coli</i>	662,267 (68.3)	138,709 (64.9)
<i>K. pneumoniae</i>	93,260 (9.6)	14,066 (6.6)
<i>P. aeruginosa</i>	35,527 (3.7)	3,595 (1.7)
<i>S. aureus</i>	145,179 (15.0)	49,946 (23.4)

Data Source(s): Composite Health Care System (CHCS) and MHS GENESIS Microbiology results and susceptibility data. Abbreviation: MHS, Military Health System, ESKAPE-E, *Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, *Enterobacter* spp., and *Escherichia coli*. Prepared by the EpiData Center, Defense Centers for Public Health – Portsmouth, July 1, 2026.

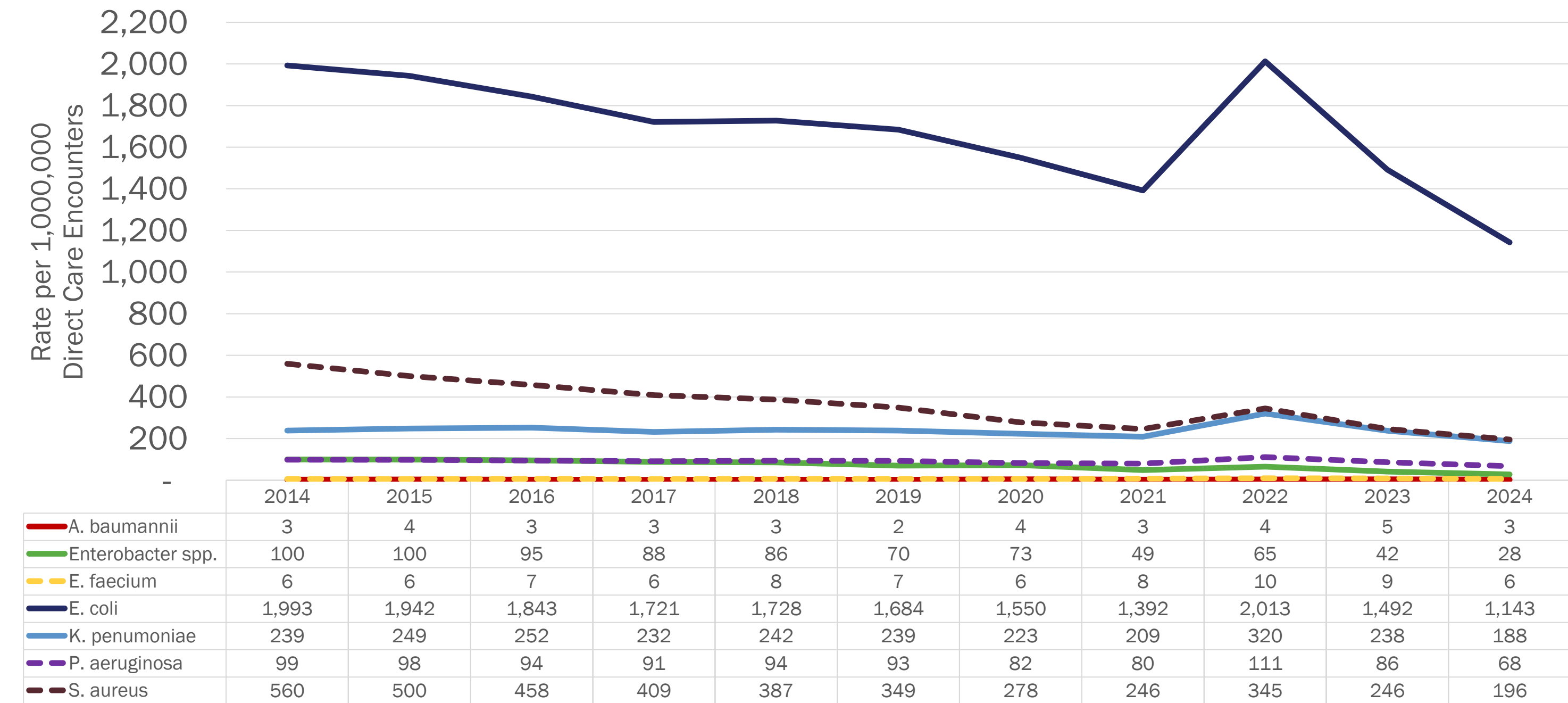
Results

Figure 1. ESKAPE-E Organisms by Antimicrobial Resistance Categories among All MHS Beneficiaries, 2014-2024



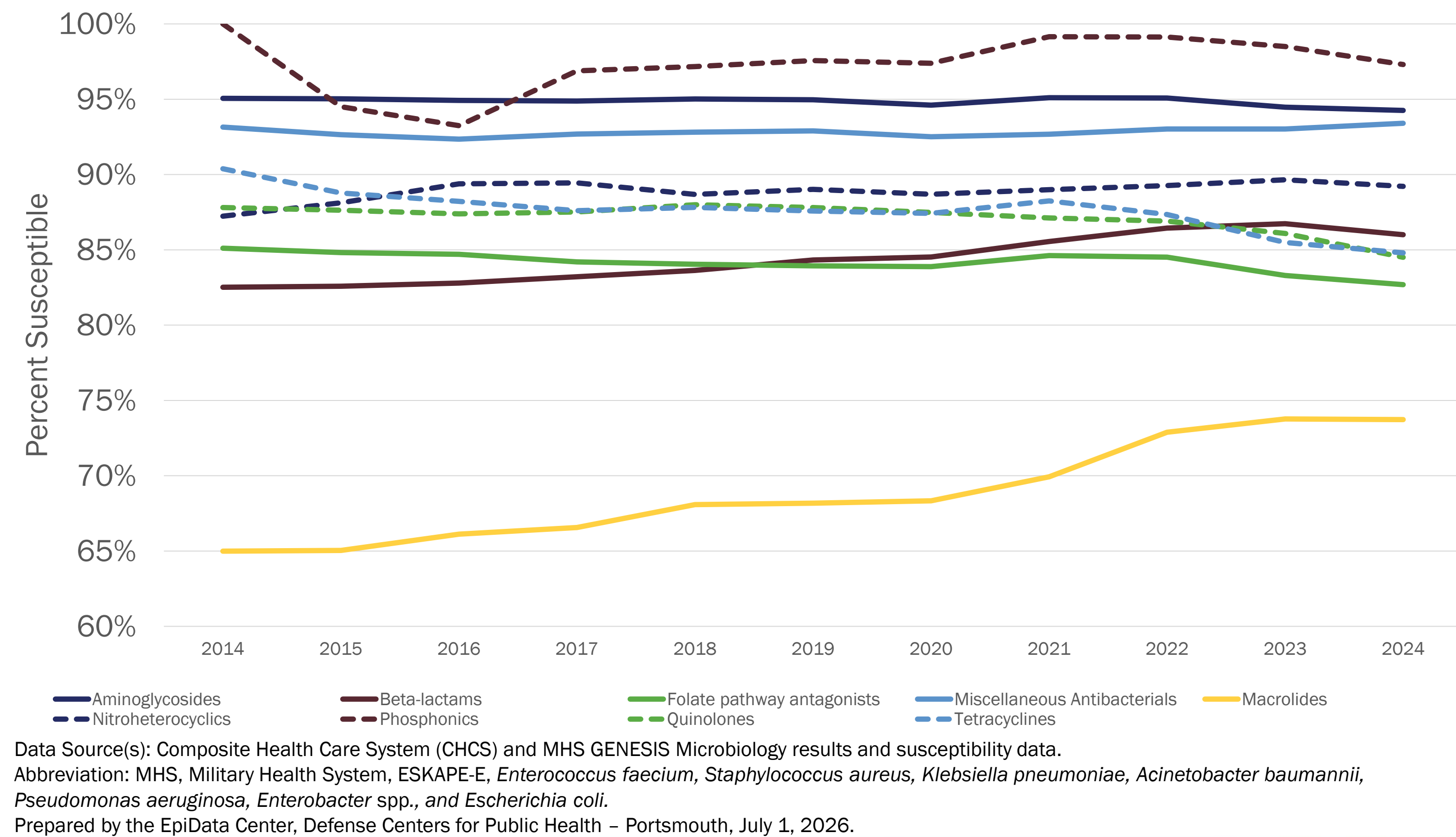
Data Source(s): Composite Health Care System (CHCS) and MHS GENESIS Microbiology results and susceptibility data. Abbreviation: MHS, Military Health System, ESKAPE-E, *Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, *Enterobacter* spp., and *Escherichia coli*. Prepared by the EpiData Center, Defense Centers for Public Health – Portsmouth, July 1, 2026.

Figure 2. Rate of ESKAPE-E Pathogen Isolates among MHS Beneficiaries by Year, 2014-2024



Data Source(s): Composite Health Care System (CHCS) and MHS GENESIS Microbiology results and susceptibility data. denominator data is a count of direct care inpatient and outpatient encounters from DHA's Fiscal Year TRICARE Program Evaluation Reports⁶. Abbreviation: MHS, Military Health System, ESKAPE-E, *Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, *Enterobacter* spp., and *Escherichia coli*. Prepared by the EpiData Center, Defense Centers for Public Health – Portsmouth, July 1, 2026.

Figure 3. Annual Susceptibility Trends of Antibiotic Classes among ESKAPE-E Isolates within MHS Beneficiaries, 2014-2024



Data Source(s): Composite Health Care System (CHCS) and MHS GENESIS Microbiology results and susceptibility data. Abbreviation: MHS, Military Health System, ESKAPE-E, *Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, *Enterobacter* spp., and *Escherichia coli*. Prepared by the EpiData Center, Defense Centers for Public Health – Portsmouth, July 1, 2026.

Conclusions

During the surveillance period, a total of 969,436 clinical ESKAPE-E isolates were identified; of these, 49% displayed resistance to at least one antimicrobial agent. *E. coli* and *S. aureus* were the most frequent pathogens isolated overall (68% and 15%, respectively), and the most common isolates displaying AMR (63% and 18%, respectively). The decreasing trend of ESKAPE-E isolates over the surveillance period requires further investigation. This reduction may be due, in part, to better prevention and control strategies, policies, and awareness. Other contributors may be due to changes in the utilization of MHS laboratories and the electronic medical record, such as the implementation of MHS GENESIS, impacting the capture of data. Understanding and combating AMR is a critical part of the force. MDR ESKAPE-E infections in ACSMs represent a direct threat to force health protection. These cases can lead to prolonged return-to-duty times, complex logistical demands for treatment, and a potential degradation of medical readiness, particularly in operational environments.

Limitations

Classifying laboratory tests involved the search of free-text fields. Misclassification is possible, though validation steps were included to reduce error. Tests ordered within the MHS and sent to commercial laboratories for further testing are included. However, some records may be missed, and the number of missing tests is unknown. These data do not include laboratory orders from outside the MHS, including out-of-network or private sector care. In addition, these data do not include in-theater or shipboard laboratory tests. Laboratory data do not capture cases where a physician chooses to treat presumptively without laboratory confirmation. Clinical culture practices vary among providers and facilities. The use of microbiology data for antibiotic resistance analysis is limited by the practice of selective and/or cascade reporting, in which antibiotic sensitivity results are conditionally reported to the provider to guide treatment decisions. Selective and/or cascade reporting is practiced to varying degrees at MHS Military Treatment Facilities (MTFs). Data in this report are based on electronically available laboratory results; therefore, multidrug-resistant organisms at MTFs that practice cascade reporting may be underestimated.

Citations

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