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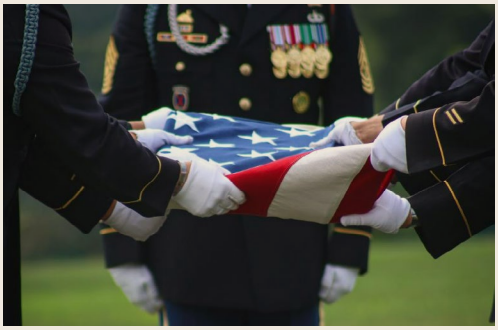

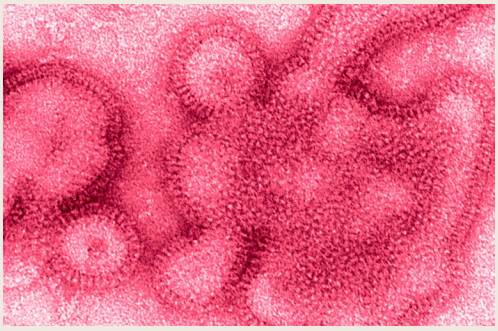

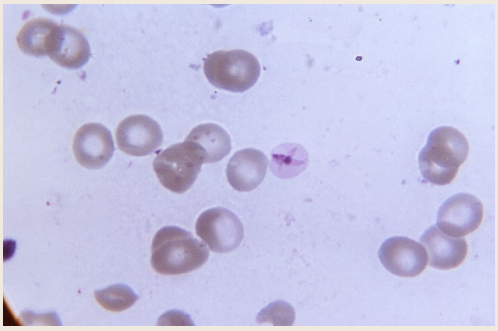

In this issue:

U.S. Army Mortality Surveillance in Active Duty Soldiers, 2014–2019

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Mortality surveillance is an important activity for capturing information on a population's health. This retrospective surveillance analysis utilizes administrative data sources to describe active duty U.S. Army soldiers who died from 2014 to 2019, and calculate mortality rates, assess trends by category of death, and identify leading causes of death within subpopulations. During the surveillance period, 2,530 soldier deaths were reported. The highest crude mortality rates observed during the 6-year surveillance period were for deaths by suicide, followed by accidental (i.e., unintentional injury) deaths. The crude mortality rates for natural deaths decreased significantly over the 6-year period, by an average of 6% annually. The leading causes of death were suicide by gunshot wound, motor vehicle accidents, suicide by hanging, neoplasms, and cardiovascular events. Significant differences were observed in the leading causes of death in relation to demographic characteristics, which has important implications for the development of focused educational campaigns to improve health behaviors and safe driving habits. Current public health programs to prevent suicide should be evaluated, with new approaches for firearm safety considered.

What are the new findings?

The mortality rate for natural causes declined 6% annually, from 18.8 deaths per 100,000 soldiers in 2014 to 13.4 deaths per 100,000 in 2019, which was statistically significant. During this period when annual mortality rates for natural deaths declined significantly, the highest Army mortality rates were for deaths due to suicide, followed by accidental death. Despite the decline in natural deaths, neoplasms remain the leading cause of death in women and older soldiers.

What is the impact on readiness and force health protection?

This report provides more accurate mortality surveillance for the Army population and is the only all-cause mortality report published by the Defense Health Agency since 2016. Preventable deaths are a significant issue in the Army population. A better understanding of preventable deaths can focus attention on both behavioral and medical factors that affect military readiness. This report reveals trends in mortality and related subject areas that require more active or renewed prevention efforts.

Mortality surveillance is an important activity for capturing information on a population's health, as it tracks new and emerging health trends in a population and informs future prevention efforts.[1] Mortality surveillance in the U.S. Army is essential for identifying and understanding the occupational exposures that increase risk of premature soldier death.[2] Given that approximately 70% of soldiers are young adults under 35 years of age, this translates to significant potential years of life lost.

Few public health investigations have focused on all-cause mortality in the U.S. Armed Forces.[2-4] Prior investigations within the military were restricted to specific categories and causes of death, such as neoplasms, infectious diseases, and suicide.[5-8] The few investigations that examined all-cause mortality concluded that male, non-Hispanic White, and 17-34-year-old service members had the highest mortality rates in the U.S. military.

No known prior studies have examined the differences in the leading causes of death among subpopulations, such as sex, age, and racial ethnicity, in the U.S. Army. Strata-specific analysis by demographic characteristics is an important epidemiological methodology that recognizes consequential social, environmental, and biological differences among subgroups.[9] The objectives of this study were to describe the demographic characteristics of U.S. Army active duty soldiers who died from 2014 to 2019, identify leading causes of death within subpopulations, and calculate mortality rates to assess trends by category of death.

Methods

Study Design and Population

This retrospective surveillance analysis included information on mortality among U.S. Army active duty (Army active component, activated National Guard or Reserve) soldiers from 2014 to 2019. Soldiers who were between 17 and 64 years of age at the time of their death were included in this study. This project was reviewed and approved by the Office of Human Protections Public Health Review Board, Defense Centers for Public Health–Aberdeen.

Data Sources and Study Variables

The Defense Casualty Information Processing System (DCIPS), which collects information on service members who die while in service, was the primary source of category of death, as its data are more complete. If information on category of death was not available in DCIPS, it was obtained from the Department of Defense (DOD) Medical Mortality Registry maintained by the Mortality Surveillance Division of the Armed Forces Medical Examiner System (AFMES). Category of death, determined by a civilian or AFMES coroner or medical examiner, was categorized as either accidental (i.e., unintentional injury), natural, suicide, homicide, combat (separate from homicide), undetermined, or pending (separate from undetermined). Combat and pending deaths are not consistent with National Association of Medical Examiner standards and guidelines of 5 "manners of death," so the term "category of death" is used instead, as "manner of death" has a specific definition.[10] Combat deaths occur in theater because of hostile actions. Deaths still under investigation are classified as pending but are typically reclassified within 12 months. Data from DCIPS and AFMES were obtained in November 2021.

For underlying causes of death, the Suicide Data Repository (SDR), created and maintained by the DOD and Veterans Affairs, served as the primary source of information, as this information is not available from the AFMES or DCIPS.[11] These data were obtained in November 2020. Cause of death is defined as the event that initiated the sequence of events resulting in death, recoded from International Classification of Diseases, 10th Revision (ICD-10) codes obtained from the National Death Index.[12,13] For example, if accident is a category of death, then possible causes of death could be drowning, poisoning, or falls. Causes are not presented for combat-related deaths, because this category is based on only 2 ICD-10 codes: Y36 (Operations of war) and Y89.1 (Sequelae of war operations); these definitions were obtained from the World Health Organization ICD-10 manual.[12]

Demographic characteristics such as sex (female, male) and age (17-24, 25-34, 35-44, 45-64 years) were obtained from the DCIPS. Race and ethnicity (non-Hispanic White, non-Hispanic Black, non-Hispanic Asian / Pacific Islander [A/PI], Hispanic, non-Hispanic American Indian / Alaskan Native, unknown) and Army population estimates were obtained from the Defense Manpower Data Center (DMDC). To obtain the total U.S. Army active duty population, each component's troop counts for September of each year were derived from DMDC.

Analytical Approach

Univariate statistics (counts, percentages) were used to report the distribution of the categories of death, stratified by cause, age, sex, and race and ethnicity, from 2014 to 2019. The 5 leading underlying causes of death were reported overall as well as stratified by age, sex, and race and ethnicity based on counts. Leading underlying causes of death refers to the 5 most frequently occurring causes with the largest number of deaths reported over the 6-year period.

Crude annual mortality rates by category of death from 2014 to 2019 were calculated by dividing the number of deaths by the number of soldiers per year, multiplied by 100,000. Annual rates for the combat and homicide deaths were not included due to the high number of instances with less than 20 cases.[14] Rate ratios (RRs) and 95% confidence intervals (CIs) of trend analyses were calculated using Poisson regression. Mortality data are not subject to sampling error because it is expected that all deaths in the population are captured, so 95% CIs are not reported for crude rates.[15] All data management and statistical analyses were conducted using SAS® (version 9.4, SAS Institute, Inc., 2013, Cary, NC).

Results

Category of Death

Between 2014 and 2019, 2,530 deaths occurred among U.S. Army soldiers **(Table 1)**. During this period, suicide (n=883, 35%) was the most common category of death, followed by accidental death (n=814, 33%). Gunshot wounds (GSWs) accounted for 65% of suicide deaths, and about two-thirds of accidental deaths were transportation-related (67%). Natural death (n=534, 21%), the next most frequent category, was often caused by neoplasms or cancer (49%). GSWs were the cause of 79% of homicide deaths, and if legal interventions (i.e., legal execution or death by law enforcement) are included, that number increases to 82%.

Cause of Death

Overall, the 5 leading causes of death from 2014 to 2019 were suicide by GSW (n=575), motor vehicle accidents (MVAs) (n=431), neoplasms (n=263), suicide by hanging or asphyxiation (n=228), and cardiovascular events (n=145). When stratified by age group, MVAs were the leading cause for soldiers aged 17-24 years **(Table 2)**. Accidental overdose (AOD) and homicide by GSW were the fourth and fifth leading causes for soldiers under age 35. Neoplasms were the leading cause in the oldest age group and women. The leading cause of death in non-Hispanic Black soldiers was MVAs (n=100). AOD was the fifth leading cause of death for non-Hispanic White soldiers.

Trends in Mortality Rates

From 2014 to 2019, suicide was generally the category with the highest cumulative mortality rate, followed by accidental death **(Figure)**, with the exception of 2017. The crude rate of accidental death showed a slight annual upward trend of 2% (RR=1.02, 95% CI: 0.99-1.06) as it increased from 24.7 deaths per 100,000 soldiers in 2014 to 26.3 deaths per 100,000 soldiers in 2019 **(Table 3)**. The annual rate of suicide death also showed a slight upward trend of 3% (RR=1.03, 95% CI: 1.00-1.07), as it increased from 25.4 deaths per 100,000 soldiers in 2014 to 28.8 deaths per 100,000 soldiers in 2019. Neither of these trends was statistically significant, however. The mortality rate for natural causes declined 6% (RR=0.94, 95% CI: 0.89-0.98) annually, from 18.8 deaths per 100,000 soldiers in 2014 to 13.4 deaths per 100,000 soldiers in 2019, which was statistically significant.

TABLE 1. Categories[a] and Causes[b] of Death Among U.S. Army Active Duty Soldiers[c],2014–2019 (n=2,530)[d]

	Year of Death, n (%)						
	2014 (n=434)	2015 (n=415)	2016 (n=385)	2017 (n=431)	2018 (n=427)	2019 (n=419)	2014-2019 (n=2,511)
Combat	**31 (7)**	**3 (1)**	**12 (3)**	**20 (5)**	**14 (3)**	**16 (4)**	**96 (4)**
Accident[e]	**136 (31)**	**137 (33)**	**123 (32)**	**154 (36)**	**128 (30)**	**136 (32)**	**814 (32)**
Motor vehicle	76 (56)	71 (52)	70 (57)	77 (50)	66 (52)	71 (52)	431 (53)
Motorcycle	15 (11)	13 (10)	12 (10)	10 (7)	11 (9)	2 (1)	63 (8)
Air, space, other transportation[f]	9 (7)	12 (9)	3 (2)	10 (7)	7 (5)	6 (4)	47 (6)
Drug / alcohol overdose[g]	16 (12)	21 (15)	18 (15)	31 (20)	24 (19)	11 (8)	121 (15)
Drowning[h]	6 (4)	7 (5)	9 (7)	9 (6)	5 (4)	12 (9)	48 (6)
Fall[i]	5 (4)	5 (4)	2 (2)	3 (2)	3 (2)	5 (4)	23 (3)
Other[j]	6 (4)	5 (4)	9 (7)	11 (7)	8 (6)	10 (7)	49 (6)
Unknown[k]	3 (2)	3 (2)	0	3 (2)	4 (3)	19 (14)	32 (4)
Natural[l]	**104 (24)**	**109 (26)**	**85 (22)**	**84 (20)**	**84 (20)**	**68 (16)**	**534 (21)**
Neoplasm	56 (54)	58 (53)	48 (57)	38 (45)	34 (40)	29 (43)	263 (49)
Circulatory system	30 (29)	36 (33)	19 (22)	23 (27)	30 (36)	7 (10)	145 (27)
Other[m]	17 (16)	11 (10)	12 (14)	11 (13)	11 (13)	8 (12)	70 (13)
Unknown[k]	1 (1)	4 (4)	6 (7)	12 (15)	9 (11)	24 (35)	56 (11)
Suicide[n]	**140 (32)**	**144 (35)**	**144 (37)**	**139 (32)**	**165 (39)**	**151 (36)**	**883 (35)**
Gunshot wound	99 (71)	92 (64)	99 (69)	95 (68)	103 (62)	87 (58)	575 (65)
Hanging / asphyxiation	28 (20)	38 (26)	34 (24)	36 (26)	44 (27)	48 (32)	228 (26)
Drug / alcohol overdose[g]	7 (5)	8 (6)	5 (4)	6 (4)	6 (4)	1 (1)	33 (4)
Other[o]	5 (4)	5 (3)	3 (2)	2 (1)	7 (4)	3 (2)	25 (3)
Unknown[k]	1 (1)	1 (1)	3 (2)	0	5 (3)	12 (8)	22 (2)
Homicide	**17 (4)**	**14 (3)**	**16 (4)**	**17 (4)**	**17 (4)**	**13 (3)**	**94 (4)**
Gunshot wound	11 (65)	12 (86)	9 (56)	16 (94)	15 (88)	11 (85)	74 (79)
Sharp object	3 (18)	2 (14)	4 (25)	0	1 (6)	2 (15)	12 (13)
Legal intervention[p]	2 (12)	0	1 (6)	0	0	0	3 (3)
Other[q]	0	0	1 (6)	1 (6)	1 (6)	0	3 (3)
Unknown[k]	1 (6)	0	1 (6)	0	0	0	2 (2)
Undetermined[r]	**5 (1)**	**8 (2)**	**5 (1)**	**15 (3)**	**5 (1)**	**3 (1)**	**41 (2)**
Pending[s]	**1 (<1)**	**0**	**0**	**2 (<1)**	**14 (3)**	**32 (8)**	**49 (2)**

Abbreviation: n, number.

[a] Category of death was obtained from the Defense Casualty Information Processing System or the Armed Forces Medical Examiner System.

[b] Underlying cause of death was obtained from the Suicide Data Repository (SDR), maintained by the DOD and Veterans Affairs.

[c] Includes Army active component, activated National Guard, and activated Reserve soldiers. Due to rounding, some percentages may add up to more than 100.

[d] Total includes all 19 deaths with missing category or cause information.

[e] Excludes 8 deaths that were missing cause of death information.

[f] Other transportation includes rail, water transport, and all other transportation.

[g] Drug/alcohol overdose includes poisonings from other solids and liquids, including medications.

[h] Includes accidental drowning in any body of water.

[i] Includes falls from high places, ladders, and any other type of fall.

[j] Includes explosions, pending, and all other accidental deaths.

[k] Includes any deaths that have no known cause of death or are classified as unknown.

[l] Excludes 5 deaths missing cause of death information.

[m] Includes diseases related to nervous system, respiratory system, digestive system, musculoskeletal system, mental and behavioral disorders, congenital malformations, blood, endocrine, skin, pregnancy, infections, surgical complications, and all other natural conditions.

[n] Excludes 3 deaths missing cause of death information.

[o] Includes carbon monoxide and other gas/vapor poisonings, jumping from a high place, and all other means.

[p] Legal intervention includes legal execution and deaths by police or other law enforcement agents.

[q] Includes strangulation, blunt object, bodily force, and all other means.

[r] Excludes 2 deaths missing cause of death information.

[s] Excludes 1 death missing cause of death information.

TABLE 2. Leading Underlying Causes[a] of Death Among U.S. Army Active Duty Soldiers, 2014–2019 (n=2,530)

Subgroup[b]	Cause of Death[c]	Death Count (n)
Sex		
Male	Suicide by gunshot wound	538
	Motor vehicle accident[d]	401
	Suicide by hanging/asphyxiation	214
	Neoplasm[e]	211
	Cardiovascular disease and events[f]	130
Female	Neoplasm[e]	52
	Suicide by gunshot wound	37
	Motor vehicle accident[d]	30
	Cardiovascular disease and events[f]	16
	Suicide by hanging/asphyxiation	14
Age, y		
17–24	Motor vehicle accident[d]	215
	Suicide by gunshot wound	195
	Suicide by hanging/asphyxiation	106
	Accidental overdose	44
	Homicide by gunshot wound	34
25–34	Suicide by gunshot wound	245
	Motor vehicle accident[d]	152
	Suicide by hanging/asphyxiation	74
	Accidental overdose	48
	Homicide by gunshot wound	31
35–44	Suicide by gunshot wound	108
	Neoplasm[e]	91
	Cardiovascular disease and events[f]	60
	Motor vehicle accident[d]	51
	Suicide by hanging/asphyxiation	42
45–64	Neoplasm[e]	106
	Cardiovascular disease and events[f]	41
	Suicide by gunshot wound	27
	Other Illness[g]	22
	Motor vehicle accident[d]	19
Race and ethnicity		
White, non-Hispanic	Suicide by gunshot wound	383
	Motor vehicle accident[d]	252
	Neoplasm[e]	162
	Suicide by hanging/asphyxiation	145
	Accidental overdose	98
Black, non-Hispanic	Motor vehicle accident[d]	100
	Suicide by gunshot wound	85
	Neoplasm[e]	63
	Cardiovascular disease and events[f]	42
	Suicide by hanging/asphyxiation	27
Hispanic	Suicide by gunshot wound	64
	Motor vehicle accident[d]	50
	Suicide by hanging/asphyxiation	33
	Neoplasm[e]	21
	Cardiovascular disease and events[f]	17
Asian/Pacific Islander, non-Hispanic	Suicide by gunshot wound	19
	Suicide by hanging/asphyxiation	16
	Neoplasm[e]	12
	Motor vehicle accident[d]	10
	Accidental drowning	5
American Indian/Alaskan Native, non-Hispanic	Suicide by gunshot wound	6
	Motor vehicle accident[d]	6
	Suicide by hanging/asphyxiation	2
	Homicide by gunshot wound	2
	Accidental overdose	1

Abbreviations: n, number; y, years.

[a] Cause of death based on the ICD-10 National Center for Health Statistics records and obtained from the Suicide Data Repository.

[b] Information on demographic characteristics was obtained from the Defense Casualty Information Processing System or Defense Manpower Data Center.

[c] Rank based on number of deaths.

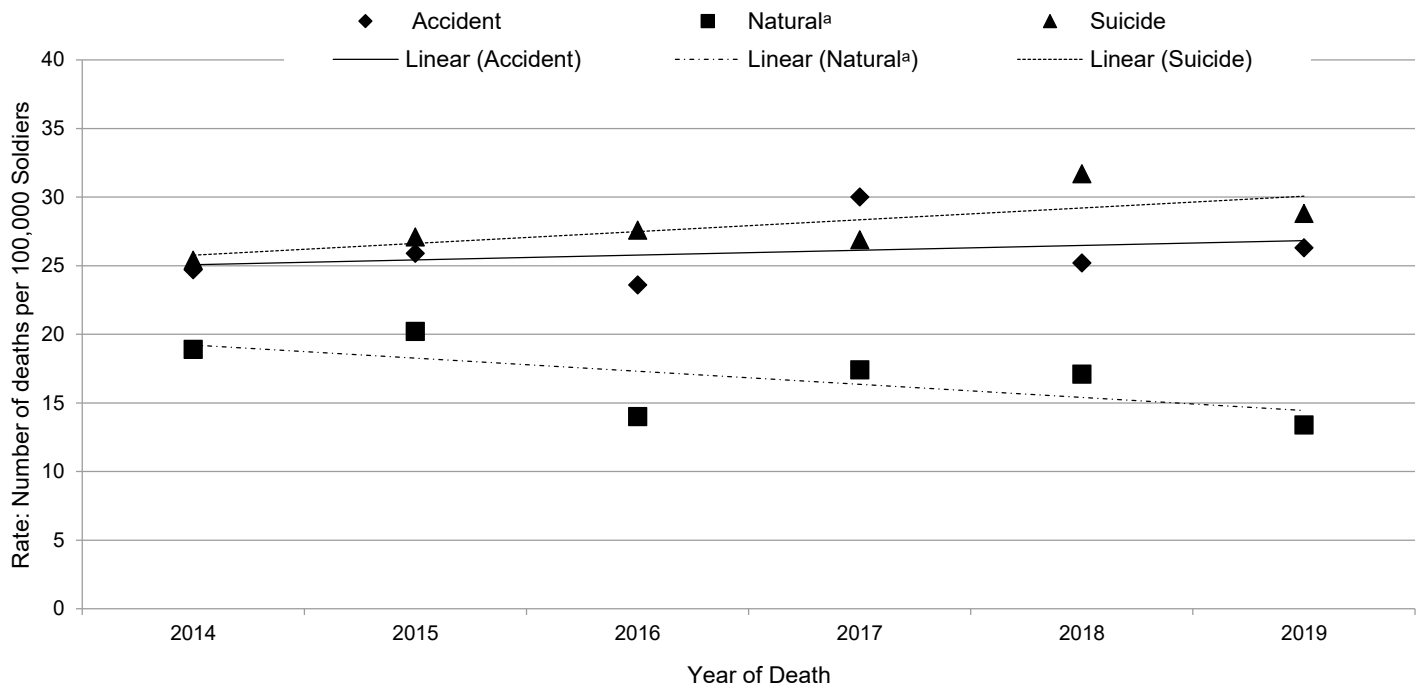
[d] Includes accidents involving heavy transport vehicles, buses, and individuals injured in collisions with motor vehicles, regardless of whether passenger, driver, or pedestrian.

[e] Includes deaths directly attributed to primary or secondary neoplasms and complications of neoplasms.

[f] Includes cardiac events, embolisms, aneurysms, strokes, and hemorrhages.

[g] Includes diseases related to nervous system, respiratory system, digestive system, musculoskeletal system, mental and behavioral disorders, congenital malformations, blood, endocrine, skin, pregnancy, infections, surgical complications, and all other natural conditions.

FIGURE. Annual Crude Mortality Rates by Category of Death Among U.S. Army Active Duty Soldiers, 2014–2019



Abbreviations: RR, rate ratio; CI, confidence interval.
[a]Indicates a statistically significant trend observed over time based on RRs calculated using Poisson regression: Accident (RR=1.02; 95% CI= 0.99-1.06), Natural (RR=0.94; 95% CI= 0.89-0.98), Suicide (RR=1.03; 95% CI=1.00-1.07).
Note: Annual crude rates for homicide and combat deaths are not shown because there were less than 20 homicide and combat deaths in all or most years. Rates are interpreted as the number of deaths per 100,000 soldiers. Denominator data were obtained from the Defense Manpower Data Center; numerator data were obtained from the Defense Casualty Information Processing System or the Armed Forces Medical Examiner System.

TABLE 3. Annual Crude Mortality Rates[a] for U.S. Army, 2014–2019

	Category of Death[b]		
Year of Death	Accident	Natural	Suicide
2014	24.7	18.9	25.4
2015	25.9	20.2	27.1
2016	23.6	14.0	27.6
2017	30.0	17.4	26.9
2018	25.2	17.1	31.7
2019	26.3	13.4	28.8
Rate Ratio[c] (95% CI[d])	1.02 (0.99–1.06)	**0.94 (0.89–0.98)**	1.03 (1.00–1.07)

Abbreviation: CI, confidence interval.
[a]Mortality rates are interpreted as the number of deaths per 100,000 soldiers. Numerator data were obtained from the Defense Casualty Information Processing System and the Armed Forces Medical Examiner System; denominator data were obtained from the Defense Manpower Data Center.
[b]Combat and, homicide death rates are not presented due to less than 20 deaths for all or most years.
[c]Rate ratios, calculated using Poisson regression, assessed trends in mortality rates from 2014 to 2019, **bolded** numbers are statistically significant.

Discussion

This is the first report since 2016 to expand on the underlying leading causes of death stratified by each demographic characteristic in the U.S. Army. The highest mortality rates by category were for suicide, and suicide by GSW remained the leading cause of death. The Army implements various initiatives that evaluate, identify, and track high-risk individuals for suicidal behavior and other adverse outcomes.[16,17] Current measures are used to track and educate soldiers on securing privately-owned weapons—as the literature has concluded that storing firearms locked, unloaded, or both are associated with a lower risk of suicide mortality—but findings on the effectiveness of these programs are limited.[18,19] A more passive approach, such as strict gun control policies, should also be considered.[19-21] For instance, in a report released in 2023 by the Suicide Prevention and Response Independent Review Committee (SPRIRC)

recommendations included establishing and updating gun control and safety policies to include requiring all privately-owned weapons in DOD military property to be registered and properly stored, and implementing waiting periods and minimum age requirements for privately-owned weapons and ammunition purchases on DOD property.[22]

Accidental death was the next most frequent category of mortality. Although no significant trend was detected in this study, the rate has decreased substantially since 2011.[23,24] MVAs were the second leading cause of death overall, and for the youngest age group as well as non-Hispanic Black soldiers. Prior studies have suggested this may be due to inexperience, high rates of alcohol use, and lower likelihood of wearing seatbelts increasing odds of death.[25,26] The United States Army Combat Readiness Safety Center's mass safety campaigns aim to reduce transportation-related crashes, but programs tailored to these high-risk groups may be necessary to affect change.[27] AOD was the fifth leading cause of death for non-Hispanic White service members, as well as the fourth leading cause for soldiers under age 35, which aligns with findings from prior reports that demonstrated higher rates of substance abuse and dependence among these groups.[28]

During this same period, the mortality rate for natural deaths declined significantly. Similar decreasing trends in deaths from natural causes such as heart disease and cancer were observed within the U.S. population from 2018 to 2019.[29,30] Neoplasms are still the leading cause of death for female and older soldiers, and among women this result may be related to low cancer screening rates, based on findings in the literature. Recent studies have concluded that female service members were not compliant with breast or cervical cancer screening guidelines despite universal access to health care and completion of the Periodic Health Assessment (PHA) every 13 months.[31-34] The PHA tracks cancer screening for breast, cervical, and colorectal cancers, as well as risk factors for lung cancer (e.g., smoking and tobacco use). Cardiovascular diseases and events were also a leading natural cause of death. This may be related to several cardiovascular risk factors observed in soldiers such as high blood pressure, smoking, and high body mass index.[35] To improve the health and well-being of its service members, the DOD has implemented initiatives such as the Performance Triad (P3), which establishes guidelines for increasing physical activity, eating a well-balanced diet, and receiving adequate sleep, and which have shown to be protective against adverse health outcomes in service members.[36-37]

Due to the 2-year data lag in mortality data, the number of cases missing underlying causes of death was highest in 2019. As a result, reporting for that year may underestimate the true mortality burden. Active duty soldiers who separated from the Army were excluded, thereby underestimating a soldier's risk of death, as previous studies have found higher mortality rates among separated soldiers compared to those who did not.[38] Small sample sizes were an issue for some subgroups, particularly American Indian / Alaskan Natives, and findings for this group should be interpreted with caution. Furthermore, population estimates for September of each year were used to calculate rates, which may have led to inaccurate estimates. Despite these limitations, these data are comprehensive and capture all deaths among active duty soldiers while in service during the surveillance period.

From 2014 to 2019, when annual mortality rates for natural deaths significantly declined, the highest Army mortality rates were for suicide, followed by accidental death. Evaluation of various public health suicide prevention programs and services, and a greater emphasis on firearm storage and safety, may be needed to reduce suicide. Public health campaigns promoting safe driving habits and healthy behaviors can be refined by examining a combination of the underlying causes of death and contributing factors that provide contextual information for developing effective targeted prevention efforts. Despite the decline in natural deaths, neoplasms remain the leading cause of death in women and older soldiers, underscoring the importance of promoting healthy behaviors and staying up-to-date with cancer screenings.

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Human Participant Protection
The Defense Centers for Public Health–Aberdeen Office of Human Protections Director determined this activity to be public health practice under OHP 19-802 (16-500).

Disclaimer
The views expressed in this presentation are those of the authors and do not necessarily reflect the official policy of the Department of Defense, Defense Health Agency, nor the U.S. Government.

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Outbreak of Influenza and SARS-CoV-2 at the Armed Forces of the Philippines Health Service Education and Training Center, September 25–October 10, 2023

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In the last week of September 2023, a surge of influenza-like illness was observed among students of the Armed Forces of the Philippines (AFP) Health Service Education and Training Center, where 48 (27 males and 21 females; age in years: mean 33, range 27-41) of 247 military students at the Center presented with respiratory symptoms. Between September 25 and October 10, 2023, all 48 symptomatic students were evaluated with real-time reverse transcription polymerase chain reaction and sequencing for both influenza and SARS-CoV-2. Thirteen (27%) students were found positive for influenza A/H3 only, 6 (13%) for SARS-CoV-2 only, and 4 (8%) were co-infected with influenza A/H3 and SARS-CoV-2. Seventeen influenza A/H3N2 viruses belonged to the same clade, 3C.2a1b.2a.2a.3a, and 4 SARS-CoV-2 sequences belonged to the JE1.1 lineage, indicating a common source outbreak for both. The influenza A/H3N2 circulating virus belonged to a different clade than the vaccine strain for 2023 (3C.2a1b.2a.2a). Only 4 students had received the influenza vaccine for 2023. In response, the AFP Surgeon General issued a memorandum to all military health institutions on October 19, 2023 that mandated influenza vaccination as a prerequisite for enrollment of students at all education and training centers, along with implementation of non-pharmaceutical interventions and early notification and testing of students exhibiting influenza-like-illness.

What are the new findings?

This report demonstrates a common source outbreak of influenza and SARS-CoV-2 among students of the AFP Health Service Education and Training Center. Potential contributing factors to the outbreak included low influenza vaccine coverage, mismatch with the clade of the influenza vaccine strain for 2023, close living conditions, in addition to other factors conducive to the transmission of respiratory infections.

What is the impact on readiness and force health protection?

Conditions during military schooling, such as close living quarters and sustained personal interactions, can significantly increase risk of morbidity related to outbreaks of respiratory pathogens. Prevention measures including requiring vaccination prior to enrollment may mitigate outbreaks of respiratory pathogens.

Because influenza and SARS-CoV-2 share similarities in their modes of transmission as well as common symptoms and clinical presentation, they can be challenging to distinguish.[1] Laboratory testing can help differentiate influenza from SARS-CoV-2 infection and inform clinical management. Accurate diagnosis is particularly important for patients admitted to emergency medical departments with suspected influenza, as well as determining the cause of a respiratory illness outbreak. Reports of co-infection of SARS-CoV-2 and other respiratory viruses, as well as bacterial and fungal infections, have been reported.[2,3]

Both viruses exhibit a propensity for rapid spread within confined settings, such as households and military barracks.[4] Conditions unique to military populations such as habitation in close quarters and sustained interactions during deployments can place those individuals at higher risk for respiratory disease outbreaks compared to the general population.[5-7]

The Walter Reed Army Institute of Research-Armed Forces Research Institute of Medical Sciences (WRAIR-AFRIMS) and the Armed Forces of the Philippines (AFP) began collaborations on influenza-like-illness (ILI) surveillance in 2008. This collaboration resulted in the establishment of the Philippines-AFRIMS Virology Research Unit (PAVRU) in Manila, one of the WRAIR-AFRIMS network of sentinel sites in Southeast Asia, on the grounds of the Victoriano Luna Medical Center

Hospital (VLMC), a tertiary hospital of the AFP. PAVRU was instrumental in detecting emerging and re-emerging diseases including the first cases of the pandemic influenza A(H1N1) 2009 (influenza A[H1N1]pdm09) in the AFP and providing laboratory confirmation and containment of influenza A(H1N1)pdm09 in several AFP camps.[8] Establishment of the AFP-AFRIMS Collaborative Molecular Laboratory in March 2011 further increased laboratory testing capability and research activities for other diseases important to the military, such as arboviral, vector-borne and diarrheal diseases, wound and blood-borne infections, in addition to characterizing multi-drug resistant bacteria. Existing collaborative relationships ensured PAVRU and the AFP-AFRIMS Collaborative Molecular Laboratory were strategically positioned to assist the AFP during the SARS-CoV-2 pandemic. The AFP-AFRIMS Collaborative Molecular Laboratory was one of the first laboratories accredited by the Philippines Department of Health for SARS-CoV-2 testing in the country.[9,10]

During the COVID-19 pandemic influenza circulation declined globally,[11,12] to the extent to which an influenza B lineage was reported as becoming extinct.[13-15] As COVID-19 cases decreased due to non-pharmaceutical interventions (e.g. mask wearing, social distancing, cleaning of frequently-touched surfaces, frequent handwashing with soap or use of hand sanitizers, closure of places where people gather, etc.), vaccination, and validated treatment options, the World Health Organization (WHO) announced in May 2023 that COVID-19 was no longer a public health emergency of international concern.[16] Movement restrictions, non-pharmaceutical interventions and low natural exposure to respiratory viruses during this 3-year period[12] may have created an environment conducive to respiratory disease resurgence and outbreaks due to decreased probability of occurrence by recent natural influenza infections and limited generation of more durable and cross-reactive immune responses.[17,18]

The risk of respiratory disease resurgence was evidenced during the last week of September 2023, when local Philippine newspapers reported an increase of ILI in several schools, prompting suspension of in-person classes.[19] Concurrently, a surge of ILI among students of the AFP Health Service Education and Training Center (AFPHSETC) triggered an outbreak investigation. This report describes the results of that investigation of the respiratory outbreak at the AFPHSETC detected by the AFP-AFRIMS Collaborative Molecular Laboratory.

Methods

Forty-eight students enrolled at AFPHSETC who presented with ILI, defined as objective or subjective history of fever (>99.5^{0}F; within 3 and 5 days from onset of fever for outpatients and inpatients, respectively) and cough or sore throat were tested as part of this outbreak investigation. Nasal and/or throat swabs were collected by hospital and study staff at the swabbing and triage area beside the VLMC emergency room. A standard form recorded demographic and clinical data, including, but not limited to, patient sex, occupation, age, town or city residence, date of fever onset, travel and exposure history, medical and vaccination history, signs and symptoms, and recent laboratory tests. The AFPHSETC Commandant advised the symptomatic students to have themselves tested. The students belonged to 7 different class cohorts with varying term durations—September and October, July through September, July through November, and June through December—that were coincident during the outbreak period.

One respiratory swab was tested using Quickvue influenza A+B rapid test (Quidel, CA, US) and a second respiratory swab was stored in universal transport media (Remel, KS, US) from which viral ribonucleic acid (RNA) was extracted using a QIAamp viral RNA mini kit (QIAGEN, US). The AFP-AFRIMS molecular laboratory performed real-time reverse transcription-polymerase chain reaction (RT-PCR) for influenza and SARS-CoV-2 using methods described previously.[20,21] Next generation sequencing (NGS) was performed on an iSeq100 instrument using the iSeq100 reagent kit version 2 (Illumina, US).

Viral RNA extracted from SARS-CoV-2-positive samples (Ct≤28) was used as a template for amplicon sequencing with ARTIC SARS-CoV-2 version 5.3.2 primers. For SARS-CoV-2 genome sequences analysis, the Burrows-Wheeler Aligner MEM algorithm (BWA-MEM v.0.7.17) was used for reference mapping, with the Wuhan-Hu-1 genome sequence (GenBank accession NC_045512.2) as the reference. Consensus sequences were generated using iVAR version 1.3.1[22] with specified criteria: mapping quality threshold ≥30, base quality ≥30, and a minimum depth of coverage of 10. Lineage and clade assignments were determined using Pangolin version 4.3.1[23] and Nextclade version 2.14.1.

For influenza A genome sequencing, viral RNA was extracted from all influenza A PCR-positive samples, and the RNA was used as a template for amplicon sequencing using a primer set previously described by Zhou et al.[24] including an additional primer, MBTuni-12G(5-ACGCGTGATCAGCGAAAGCAGG).[24] DNA libraries were constructed and multiplexed using an Illumina DNA prep kit and pooled prior to sequencing. For influenza genome sequences analysis, the hemagglutinin (HA) consensus sequences were generated using the same tools and criteria mentioned, with appropriate reference sequences selected from the GenBank database. The HA gene sequences were used to identify the genotype and clade with Nextclade version 2.14.1. Percentage of nucleotide and amino acid similarity among influenza HA sequence results were then compared to the WHO vaccine-recommended H3N2 vaccine strains for 2023.

Maximum-likelihood trees were constructed using IQ-TREE version 2.03 with 1,000 bootstrap replicates and the GTR+F+I and TVM+F+G4 models for SARS-CoV-2 and influenza trees, respectively. The phylogenetic trees were visualized using FigTree version 1.4.4.

The AFP Health Service Command (AFPHSC) Research Ethics Committee and the WRAIR Institutional Review Board approved the protocol.

Results

Forty-eight (27 males and 21 females; age in years: mean 33, range 27-41) military students who presented with ILI, out of 247 students in total, were enrolled in the investigation, with 13 (27%) positive for influenza A(H3) only and and 6 (13%) positive for SARS-CoV-2 only by real-time PCR, while 4 (8%) were co-infected with influenza A/H3 and SARS-CoV-2. Symptoms in addition to fever, cough, or sore throat are listed, according to laboratory diagnosis, in the **Table.** Only 4 (8%) and 7 (15%) of the 48 students had received the influenza vaccines for 2023 and 2022, respectively. Among the 4 students co-infected with influenza A/H3 and SARS-CoV-2, half (n=2, 50%) had symptoms other than fever, particularly difficulty of breathing **(Table).**

Two (4%) students with an initial diagnosis of acute viral infection required hospital admission, but did not require intubation, with 1 positive for influenza A/H3 and the other negative for both influenza and SARS-CoV-2. All students had received at least 2 doses of a SARS-CoV-2 vaccine.

NGS of influenza A/H3 samples yielded the whole genome for 15 of 17 (88%) influenza RT-PCR-positive samples. Pathogen identification of influenza A/H3N2 and phylogenetic analysis using the HA gene of all 17 samples showed that they all belonged to the same clade, 3C.2a1b.2a.2a.3a.1 **(Figure 1)**. The clade of the influenza outbreak viruses differed from the clade of the WHO-recommended influenza A/H3N2 strains for the 2023 Northern and Southern influenza vaccines, A/Darwin/6/2021(H3N2)-like virus (cell culture or recombinant-based) and A/Darwin/9/2021(H3N2)-like virus (egg-based), respectively, which belonged to clade 3C.2a1b.2a.2a.

The percentage similarity of the influenza A/H3N2 outbreak viruses with the WHO-recommended influenza A/H3N2(A/Darwin/6/2021[H3N2]-like virus) strain for the cell culture or recombinant based Northern and Southern vaccine influenza vaccine for 2023 was 98.40% nucleotide and 97.79% amino acid similarity, respectively. The WHO-recommended influenza A/H3N2 Northern and Southern egg-based influenza vaccine strain (A/Darwin/9/2021[H3N2]-like virus) showed 98.03% nucleotide and 97.42% amino acid similarity, respectively. Sequencing of 4 of 10 SARS-CoV-2-positive samples showed that all belonged to the JE1.1 lineage (Pangolin) **(Figure 2)** and 23E clade (clades.nextstrain.org).

Influenza and SARS-CoV-2 sampling and RT-PCR testing were completed on September 29, 2023 and October 2, 2023, respectively, and an initial report was sent to AFRIMS for review and confirmation of laboratory findings. The AFP Surgeon General was briefed on the investigation results on October 3, 2023, and on the following day (Oct. 4, 2023) a report was sent to the AFPHSETC Commandant, AFPHSC Commander, AFP Public Health Service Center (PHSC) Chief, VLMC Chief, and VLMC hospital infection control committee (HICC). PAVRU leadership briefed the Commandant of AFPHSETC, AFP PHSC Chief, and VLMC HICC Chief on October 9, 2023, after which measures such as mask wearing, social distancing, quarantining of symptomatic students were instituted.

Cases had begun to decrease in the first week of October 2023. NGS and bioinformatics analysis of influenza-positive samples were completed on October 10, 2023, allowing for review of any vaccine mismatch concerns. On October 19, 2023, the AFP Surgeon General issued a respiratory illness prevention memorandum addressed

TABLE. Demographic, Clinical, and Vaccination Statuses of Students Included in the Outbreak Investigation

	No.	(%)
Total	48	(100)
Sex		
Male	27	(56)
Female	21	(44)
Age (average, range), y	33 (27 – 41)	
Influenza vaccination (year)		
2023	4	(8)
2022	7	(15)
Unvaccinated	37	(77)
Influenza A/H3 only	13	(27)
Male	9	(69)
Headache, malaise/fatigue, runny nose, nasal congestion, generalized body pain/muscle ache, injected pharynx[a]	2	(15)[b]
Runny nose/nasal congestion[a]	2	(15)[b]
SARS-CoV-2 only	6	(13)
Male	1	(17)
Breathing difficultly, runny nose/nasal congestion[a]	1	(17)[b]
Runny nose/ nasal congestion[a]	1	(17)[b]
Co-infected with influenza A/H3 and SARS-CoV-2	4	(8)
Male	2	(50)
Breathing difficulty, headache, malaise/fatigue[a]	1	(25)[b]
Breathing difficulty, headache, runny nose/nasal congestion, generalized body pain/muscle ache[a]	1	(25)[b]

Abbreviations: y, years; SARS-CoV-2, severe acute respiratory syndrome-associated coronavirus disease strain 2.

[a] Symptoms in addition to fever, cough, and/or sore throat.

[b] Percent among those who tested positive for the specified pathogen(s).

to the Chief Surgeon of the major services and the chiefs and commanders of major AFP health facilities. The memorandum included information on the respiratory outbreak and issued guidance for influenza vaccination as a prerequisite for enrollment of students at AFP education and training centers, implementation of preventive public health interventions (e.g., mask wearing, hand washing), early notification of ILI symptoms, and reporting of updated influenza and COVID-19 vaccination coverage.

Discussion

Influenza and SARS-CoV-2 pose significant threats to public health and have far-reaching consequences for operational readiness and armed force strategic capabilities due to their rapid spread within units and high rates of morbidity. Distinguishing etiologic agents for respiratory illness is clinically difficult due to their similar signs and symptoms. The responsible pathogens of this outbreak were able to be determined rapidly by employing onsite AFP-AFRIMS Molecular Laboratory capabilities that enabled a wide variety of advanced molecular testing and NGS.

By rapidly demonstrating that the outbreak was due to influenza A/H3N2 and SARS-CoV-2, additional targeted data (e.g., vaccination rates) could be obtained. The high influenza infection rates observed were most likely due to low influenza vaccination coverage.

This investigation was initiated as part of an ongoing study protocol that excludes testing of asymptomatic students, which could have underestimated actual infection rates. Co-infection with both influenza and SARS-CoV-2 was associated with increased morbidity, in particular difficulty of breathing **(Table)**.

There was high nucleotide and amino acid percentage similarity of the influenza A/H3N2 outbreak viruses with the WHO-recommended influenza A/H3N2 strains for the cell culture or recombinant-based Northern and Southern vaccine influenza vaccine for 2023, but the clade of the influenza outbreak strains, 3C.2a1b.2a.2a.3a.1, did not match with the clade of the influenza A/H3 strains in the 2023 Northern and Southern hemisphere influenza vaccine strains (clade 3C.2a1b.2a.2a). This mismatch may have implications on vaccine effectiveness, especially if the mutations occurred in pivotal antigenic sites affecting glycosylation sites.[24] Neither influenza A(H1N1)pdm09 nor influenza B were detected during this outbreak, but both subtypes and respiratory syncytial virus (RSV) have been observed in 2023 to be circulating, through our ongoing ILI surveillance (unpublished data). NGS results for influenza and SARS-CoV-2 indicated a combination of common source transmission, as all influenza A(H3)-positive samples and selected SARS-CoV-2 samples belonged to the same clade.

Timely and coordinated outbreak management is crucial for mitigating the impacts of both influenza and SARS-CoV-2. Minimizing the military implications from pathogens involves robust preventive measures, vaccination strategies, and effective surveillance to safeguard the health and operational capabilities of military forces. Rapid outbreak response and availability of confirmatory assays, which can identify the etiologic agent, are critical for both guiding immediate mitigation measures and formulating health policies to contain and prevent future outbreaks. Lessons from this report can inform strategies not only for future outbreak response but health policy formulation and targeted public health interventions, and can serve as a reminder of the importance of maintaining high vaccination rates with compatible vaccine strains.

Specimen collection involved nasal and throat swabs and not nasopharyngeal swabs, which may have affected assay yield and performance. The pathogen (or pathogens) causing respiratory symptoms among students who tested negative for both influenza and SARS-CoV-2 were not able to be determined. In addition, the clade/lineage of all SARS-CoV-2-positive samples were not able to be determined because some samples had low viral loads. Vaccine efficacy estimation was not performed due to low sample size and vaccination rates. Demographic, clinical, and vaccination data on the military students who did not present with ILI symptoms were unavailable, so comparisons to determine potential risk factors associated with infection could not be made.

This report underscores the need for increasing influenza vaccine coverage with well-matched vaccine strains, along with developing, maintaining, and sustaining rapid confirmatory testing capability, including pathogen discovery, for forward deployed laboratory sites. The 16-year, enduring collaboration and partnership of AFRIMS and the AFP made possible the rapid detection of this outbreak and subsequent translation of findings into actionable health policy. Rapid response capability is critical for timely detection and containment of outbreaks, as well as early detection of pathogens with potential to cause pandemics. Further testing with assays of broader detection capability for other respiratory pathogens is recommended.

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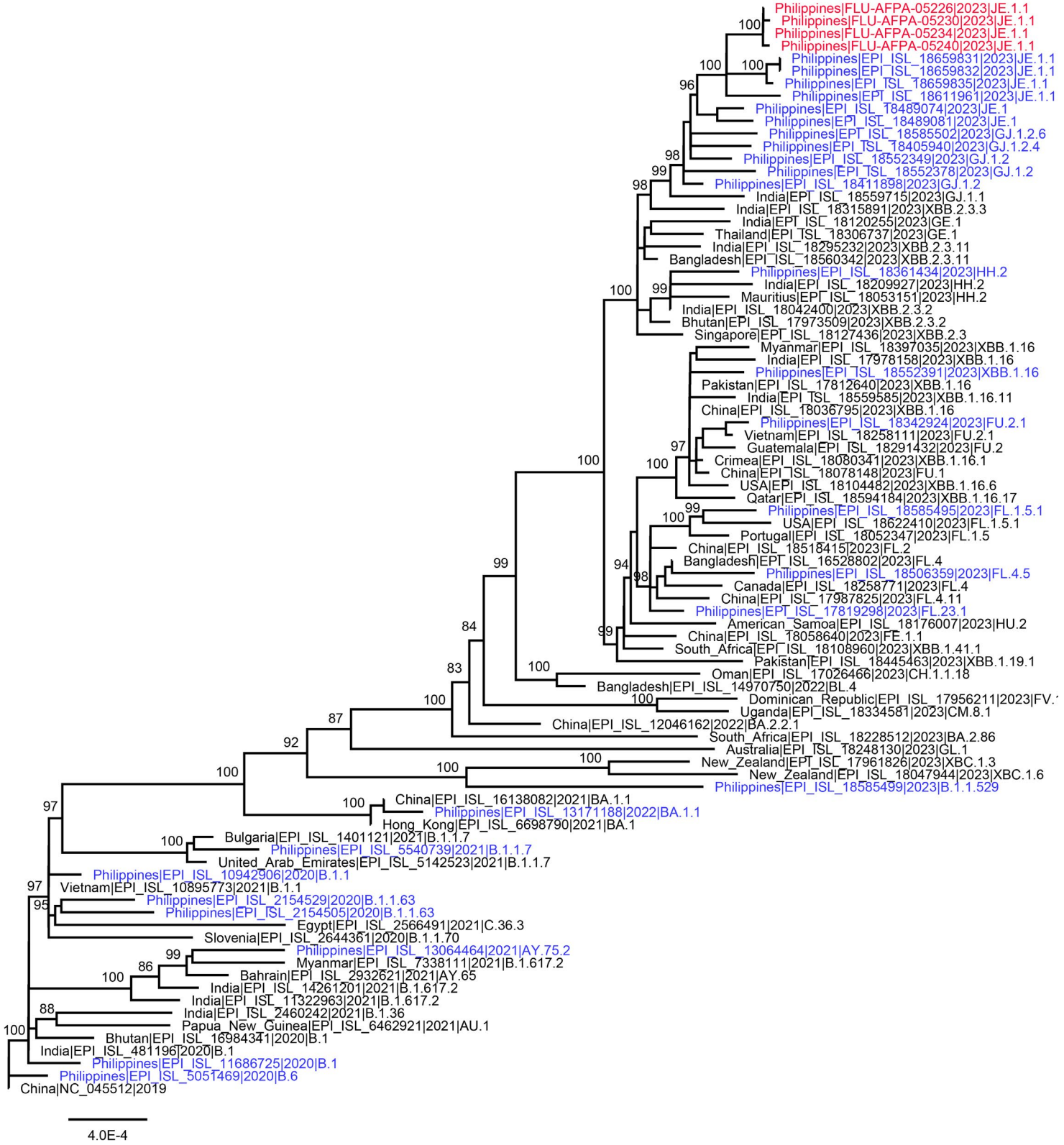
FIGURE 1. Maximum Likelihood Tree of 82 Influenza A / H3 HA Gene Sequences (1,701 nt) Including 17 New Sequences from the Philippines (red), and Sequences from GISAID and Genbank (15 sequences from the Philippines in blue, 10 sequences from WHO-recommended influenza A/H3 vaccine strains for 2019 to 2024 in **bold black**, and 40 sequences from other countries in black)

Legend:
Red-colored sequences: new influenza sequences from this outbreak report.
Blue-colored sequences: influenza sequences from the Philippines downloaded from GISAID and Genbank.
Bold black-colored sequences: WHO-recommended influenza A/H3 vaccine strains for 2019 to 2024.
Black-colored sequences: influenza sequences from other countries downloaded from GISAID and Genbank.

FIGURE 2. Maximum Likelihood Tree of 87 SARS-CoV-2 CDS Sequences (29,409 nt) Including 4 New Sequences from the Philippines (red), and 83 Sequences from GISAID and Genbank (27 sequences from the Philippines in blue and 56 sequences from other countries in black)



Legend:
Red-colored sequences: new SARS-CoV-2 sequences from this outbreak report.
Blue-colored sequences: SARS-CoV-2 sequences from the Philippines downloaded from GISAID and Genbank.
Black-colored sequences: SARS-CoV-2 sequences from other countries downloaded from GISAID and Genbank.

New sequences obtained from this study have been submitted to the GISAID database with the IDs EPI_ISL_18741371-74 for SARS-CoV-2 genome sequences and EPI_ISL_18740021-37 for influenza genome sequences.

Material has been reviewed by the Walter Reed Army Institute of Research. There is no objection to its presentation or publication.

The opinions or assertions herein are the views of the authors, not to be construed as official nor reflecting the views of the Department of the Army or the Department of Defense. The study investigators have adhered to policies for the protection of human subjects prescribed in AR 70–25.

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Surveillance Outcomes of Respiratory Pathogen Infections During the 2021–2022 Season Among U.S. Military Health System Beneficiaries, October 3, 2021–October 1, 2022

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The Department of Defense Global Respiratory Pathogen Surveillance Program conducts continuous surveillance for influenza, severe acute respiratory syndrome 2 (SARS-CoV-2), and other respiratory pathogens at 104 sentinel sites across the globe. These sites submitted 65,475 respiratory specimens for clinical diagnostic testing during the 2021-2022 surveillance season. The predominant influenza strain was influenza A(H3N2) (n=777), of which 99.9% of strains were in clade 3C.2a1b.2a2. A total of 21,466 SARS-CoV-2-positive specimens were identified, and 12,225 of the associated viruses were successfully sequenced. The Delta variant predominated at the start of the season, until December 2021, when Omicron became dominant. Most circulating SARS-CoV-2 viruses were subsequently held by Omicron sublineages BA.1, BA.2, and BA.5 during the season. Clinical manifestation, obtained through a self-reported questionnaire, found that cough, sinus congestion, and runny nose complaints were the most common symptoms presenting among all pathogens. Sentinel surveillance can provide useful epidemiological data to supplement other disease monitoring activities, and has become increasingly useful with increasing numbers of individuals utilizing COVID-19 rapid self-test kits and reductions in outpatient visits for routine respiratory testing.

What are the new findings?

Department of Defense Global Respiratory Pathogen Surveillance Program data show that influenza A(H3N2) was the dominant subtype of influenza throughout the 2021-2022 surveillance season. Three coincident waves, 1 of influenza and 2 of SARS-CoV-2 activity, were observed during the season. The wave of influenza occurred in April 2022, while the SARS-CoV-2 waves occurred from January 2022 through April 2022 and again in July 2022.

What is the impact on readiness and force health protection?

As the coronavirus disease (COVID-19) outbreak continues to evolve, it is crucial for health care providers and public health officials to be aware of the similarities as well as differences between SARS-CoV-2 (the causative agent of COVID-19), influenza, and other respiratory infections. These findings may contribute to improved clinical diagnoses and more effective management of respiratory infections among beneficiaries of the Military Health System.

In 1976, the U.S. Air Force Medical Service began conducting routine, global, laboratory-confirmed influenza surveillance. Efforts expanded when it became part of the Department of Defense Global Emerging Infections Surveillance and Response System (DOD-GEIS) in 1997.[1] Since then, GEIS has provided central coordination and financial support for the Department of Defense Global Respiratory Pathogen Surveillance Program (DODGRPSP), which routinely collects respiratory specimens from U.S. Military Health System (MHS) beneficiaries who meet the COVID-19-like illness (CLI) or influenza-like illness (ILI) case definition or symptoms determined by a physician to be a CLI / ILI case (physician-diagnosed CLI/ILI).

Respiratory infections are common among U.S. military personnel, who often live in crowded conditions, work in stressful environments, and are frequently exposed to a variety of respiratory pathogens during deployments.[2] It is crucial to conduct annual surveillance, to determine the circulating pathogens and detect changes for informing the DOD combatant commands' critical decisions about force health protection. This report presents the incidence of respiratory pathogen infections and genetic characteristics of influenza, and severe acute respiratory syndrome-related coronavirus strain 2 (SARS-CoV-2) among MHS beneficiaries during the 2021-2022 surveillance season.

Methods

DODGRPSP, a sentinel site-based program, requests that each site submit 6 to 10 specimens weekly with patient questionnaires from individuals who meet the CLI / ILI case definition or are physician-diagnosed CLI or ILI. Patient questionnaires

are distributed with each collection kit and requested to be completed with each submitted specimen, but compliance is not always guaranteed. The CLI and ILI case definitions, respiratory specimen collection, and testing criteria, as well as other program information, have been previously described.[3-5]

Testing analyzed for this study was conducted in laboratories at Landstuhl Regional Medical Center (LRMC), Incirlik Medical Center, and the U.S. Air Force School of Aerospace Medicine (USAFSAM). Specimens positive for influenza or SARS-CoV-2 underwent genetic sequencing for further characterization, as previously described.[5] Patients were classified by age group (children, 0-17 years; adults, 18-64 years, and elderly, 65+ years), geographic region (Eastern U.S., Western U.S., and outside continental U.S. [OCONUS]), and month of collection. Any specimens that the laboratory cancelled (52), rejected (347), did not test (795), or returned as an inconclusive test (141) were excluded. Individuals with multiple specimens (3,770) collected during the season were also removed from the study to avoid duplication, as they could have encountered several pathogens over the season.

All statistical analyses were performed using SAS version 9.4 (SAS Institute, Cary, NC). A p-value of <0.05 was considered statistically significant. Basic descriptive epidemiology was employed to obtain counts and rates of outcomes by sex, military beneficiary category, age group, month of collection, and geographic region. Patient symptoms among the 5 groups—influenza, other respiratory pathogens (adenovirus, seasonal coronavirus, human bocavirus, human metapneumovirus, and parainfluenza), respiratory syncytial virus (RSV), rhinovirus/enterovirus, and SARS-CoV-2—were performed using a chi-square or Fisher's exact test, limited to those specimens associated with DODGRPSP questionnaires.

Results

Between October 3, 2021 and October 1, 2022, a total of 65,475 respiratory specimens were tested, among which 26,794 (41%) specimens tested positive for respiratory pathogens **(Table 1)**. About 61% of the specimens came from OCONUS, 22% were from the Western U.S., and 17% came from the Eastern U.S. SARS-CoV-2 (70.9%) and RSV (58.0%) were most detected at OCONUS sites, while influenza (45.0%) and rhinovirus/enterovirus (41.7%) were most detected in the Eastern U.S. Other pathogens (39.6%)—adenovirus, seasonal coronavirus, human bocavirus, human metapneumovirus, and parainfluenza—were detected more in the Western U.S. **(Table 1)**.

Of the 65,475 specimens collected during the surveillance season, SARS-CoV-2 was detected in 32.8%, of which 8 were co-infections with influenza, including 4 influenza A(H3N2), 3 influenza A/not subtyped, 1 dual influenza and RSV (data not shown), and 65 were co-infections with other respiratory pathogens **(Table 2)**. Rhinovirus/enterovirus (3.4%) was the second-most detected pathogen, followed by influenza (1.4%), seasonal coronavirus (0.9%), and RSV (0.6%). *Mycoplasma pneumoniae* and *Chlamydophila pneumoniae* were not detected during the season. The numbers of positive samples and positivity percentages, by specific pathogen and month of diagnosis, are shown in **Figures 1** and **2**.

SARS-CoV-2 percent positivity increased to to 52.0% in January 2022, then peaked at 60.0% in March 2022 **(Figure 2)**, corresponding to the predominance of Omicron BA.1 and BA.2 **(Figure 3b)**. Percent positivity decreased to as low as 35.0% during May 2022, then peaked again during early June 2022 (47.0%) through July 2022 (54.0%), before it decreased for the rest of the season **(Figure 2)**. SARS-CoV-2 was the most prevalent pathogen detected during the season. In November 2021, however, the percent positivity of other respiratory pathogens as well as rhinovirus/enterovirus were briefly higher than SARS-CoV-2 **(Figure 2)**.

DODGRPSP data showed 1 distinct wave of influenza between mid-March to April 2022, with percent positivity peaking at 20.0% **(Figure 2)**. Among the 905 influenza viruses that were subtyped, influenza A(H3N2) was the predominant virus throughout the 2021-2022 surveillance season, which was in agreement with U.S. Centers for Disease Control and Prevention (CDC) data and the European Center for Disease Prevention and Control (ECDC).[6,7] Most specimens testing positive for influenza A(H3N2) were detected in the Eastern U.S. (Health and Human Service regions 1, 2, 3).

The highest rates of influenza infections were observed among service members (72.0%), followed by children (15.8%). Positive influenza cases started relatively high (October 2021), then decreased until another positivity increase in March 2022, reaching the highest point in April 2022. This highest point was followed by a subsequent decrease around May 2022, through the end of the season. In contrast to the low October 2021 influenza activity demonstrated by the CDC and ECDC,[7,8] the elevated influenza activity in DODGRPSP data was due to an influenza A(H3N2) outbreak at the U.S. Naval Academy.

Rhinovirus / enterovirus (26.0%) peaked in November 2021, then increased again between July 2022 (15.0%) and September 2022 (35.0%). Peak RSV (9.0%) activity was in November 2021 **(Figure 2)**, then declined until May 2022 (1.0%), when it steadily increased through September 2022 (4.0%). The highest percent positivity for RSV in participants was among children (56.8%), followed by service members (32.2%) **(Table 1)**. Specimens grouped as other respiratory pathogens (22.0%) peaked in May 2022, but their activity and percent positivity remained steady throughout the season.

Symptomatic evaluation of patients was limited to those with a DODGRPSP questionnaire. Among the 65,475 specimens received and tested, 8,773 specimens also had DODGRPSP questionnaires, representing an approximate 13% questionnaire response rate. Questionnaires were not received from specimens tested at LRMC and Incirlik Medical Center during the season.

Table 3 shows the distribution of demographic, clinical characteristics, and outcomes by viral agent. Chi-square tests were used to obtain p-values for the significance of the differences among the 5 groups. Significant associations were found between viral agent and gender, age group,

TABLE 1. Characteristics of Surveillance Population and Specimen Sources, MHS Beneficiaries, 2021-2022 Surveillance Season

	SARS-CoV-2		Influenza		Rhino/Entero		RSV		ORP[a]		No Pathogen Detected[b]		Negative[c]		Total	
	No.	%	No.	%	No.	%	No.	%	No.	%	No.	%	No.	%	No.	%
Total	21,466	32.8	913	1.4	2,226	3.4	419	0.6	1,770	2.7	9,723	14.8	28,958	44.2	65,475	100.0
Sex																
Male	13,050	60.8	634	69.4	1,360	61.1	235	56.1	1,033	58.4	5,953	61.2	18,333	63.3	40,598	62.0
Female	8,416	39.2	279	30.6	866	38.9	184	43.9	737	41.6	3,770	38.8	10,625	36.7	24,877	38.0
Age group, y																
0-17	4,415	20.5	148	16.2	645	29.0	238	56.8	730	41.2	1,502	15.4	5,183	17.9	12,861	19.6
18-64	16,842	78.5	763	83.6	1,570	70.5	180	43.0	1,025	58.0	8,078	83.1	23,336	80.6	51,794	79.1
65+	209	1.0	2	0.2	11	0.5	1	0.2	15	0.8	143	1.5	439	1.5	820	1.3
Month of collection																
October	313	1.5	213	23.3	459	20.6	81	19.3	208	11.8	1,022	10.5	3,314	11.4	5,610	8.6
November	503	2.3	38	4.2	493	22.1	157	37.5	293	16.6	1,077	11.1	3,477	12.0	6,038	9.2
December	748	3.5	106	11.6	292	13.1	85	20.3	295	16.7	1,332	13.7	2,617	9.0	5,475	8.4
January	7,941	36.9	62	6.8	196	8.8	19	4.5	250	14.1	3,032	31.2	7,376	25.5	18,876	28.8
February	2,247	10.5	35	3.8	76	3.4	7	1.7	101	5.7	654	6.7	1,922	6.6	5,042	7.7
March	2,472	11.5	139	15.2	133	6.0	11	2.6	158	8.9	611	6.3	1,653	5.7	5,177	7.9
April	2,518	11.7	199	21.8	118	5.3	1	0.2	138	7.8	488	5.0	2,563	8.9	6,025	9.2
May	979	4.6	69	7.6	68	3.1	7	1.7	116	6.6	286	2.9	1,828	6.3	3,353	5.1
June	1,205	5.6	22	2.4	72	3.2	9	2.1	64	3.6	334	3.4	1,359	4.7	3,065	4.7
July	1,375	6.4	16	1.8	56	2.5	9	2.1	45	2.5	294	3.0	1,173	4.1	2,968	4.5
August	682	3.2	12	1.3	109	4.9	16	3.8	41	2.3	362	3.7	874	3.0	2,096	3.2
September	483	2.3	2	0.2	154	6.9	17	4.1	61	3.4	231	2.4	802	2.8	1,750	2.7
Geographic region[d]																
Eastern U.S.	2,447	11.4	411	45.0	928	41.7	73	17.4	597	33.7	3,669	37.7	2,985	10.3	11,110	17.0
Western U.S.	3,792	17.7	158	17.3	742	33.3	103	24.6	701	39.6	3,129	32.2	5,725	19.8	14,350	21.9
Outside continental U.S.	15,227	70.9	344	37.7	556	25.0	243	58.0	472	26.7	2,925	30.1	20,248	69.9	40,015	61.1
Beneficiary category																
Adult	5,520	25.7	110	12.0	294	13.2	45	10.7	214	12.1	1,829	18.8	6,098	21.1	14,110	21.5
Child	4,415	20.6	144	15.8	644	28.9	238	56.8	729	41.2	1,498	15.4	5,183	17.9	12,851	19.6
Elderly	209	1.0	2	0.2	11	0.5	1	0.2	15	0.8	143	1.5	439	1.5	820	1.3
Service member	11,322	52.7	657	72.0	1,277	57.4	135	32.2	812	45.9	6,253	64.3	17,238	59.5	37,694	57.6
Data source																
INCIRLIK	547	2.5	6	0.6	30	1.3	5	1.2	25	1.4	96	1.0	1,095	3.8	1,804	2.8
LRMC	14,558	67.8	165	18.1	310	13.9	196	46.8	287	16.2	2,004	20.6	19,152	66.1	36,672	56.0
USAFSAM	6,361	29.6	742	81.3	1,886	84.7	218	52.0	1,458	82.4	7,623	78.4	8,711	30.1	26,999	41.2

Abbreviations: MHS, Military Health System; SARS-CoV-2, severe acute respiratory syndrome-related coronavirus strain 2; Rhino/Entero, rhinovirus/enterovirus; RSV, respiratory syncytial virus; ORP, other respiratory pathogen; USAFSAM, U.S. Air Force School of Aerospace Medicine; LRMC, Landstuhl Regional Medical Center.

[a] Adenovirus, coronavirus, human bocavirus, human metapneumovirus, parainfluenza.

[b] No pathogen was identified via multiplex testing and may not include SARS-CoV-2 testing.

[c] Specimen was negative for SARS-CoV-2 and only tested for SARS-CoV-2.

[d] Eastern U.S. includes regions 1-5; Western U.S. includes regions 6-10; regions 1-10 are U.S. Health and Human Services Regions.

TABLE 2. SARS-CoV-2, Influenza, and Other Respiratory Pathogens Among MHS Beneficiaries, 2021–2022 Surveillance Season

Pathogen	No. of specimens	Total (%)
Total	65,475	100
SARS-CoV-2 detected	21,466	32.8
Single infection	21,401	99.7
Co-infection with non-influenza respiratory pathogen	65	0.3
Co-infection with influenza	8	<0.01
Influenza detected	905	1.4
A(H1N1)pdm09	8	0.9
A(H3N2)	777	85.9
A/not subtyped	119	13.1
Oher respiratory pathogen	4,415	6.7
Adenovirus	86	1.9
Coronavirus (seasonal)	573	13.0
Human bocavirus	66	1.5
Human metapneumovirus	348	7.9
Parainfluenza	357	8.1
Respiratory syncytial virus (RSV)	419	9.5
Rhinovirus/enterovirus	2,226	50.4
Non-influenza viral coinfection	340	7.7
Other	38,681	59.1
No pathogen detected[a]	9,723	25.1
Negative[b]	28,958	74.9

Abbreviations: SARS-CoV-2, severe acute respiratory syndrome-related coronavirus strain 2; MHS, Military Health System; No., number.

[a] No pathogen was identified via multiplex testing.

[b] Specimen was negative for SARS-CoV-2 and only tested for SARS-CoV-2.

and many symptoms. Males were more likely to be infected with influenza (69.3%) and SARS-COV-2 (68.0%) than with rhinovirus/enterovirus (58.6%), RSV (58.4%), or other respiratory pathogens (58.0%). Whereas the 0-17 year age group was more likely to be infected with RSV (57.6%), other pathogens (42.3%) or rhinovirus/enterovirus (34.0%) than influenza (14.6%) or SARS-COV-2 (11.6%). The 18-64 year age group was more likely to be infected with SARS-COV-2 (86.5%), influenza (85.4%) or rhinovirus/enterovirus (65.6%) than other respiratory pathogens (56.9%) or RSV (42.4%).

Cough (>80.0%), sinus congestion (>60.0%), and/or runny nose (>50.0%) were the most common presenting symptoms among all pathogens. Other frequent symptoms of patients with influenza, as well as SARS-CoV-2, were fatigue (>60.0%), headache (>70.0%), sore throat (>60.0%), body aches (>50.0%), and fever (>50.0%). Among participants positive for rhinovirus/enterovirus, RSV, or other pathogens, the most common symptoms were sore throat (>50.0%) and fatigue (>45.0%). The frequency of cough, sinus congestion, and runny nose symptoms among COVID-19 patients (>50.0%) was lower than in influenza patients (>60.0%); however, the frequency of patients with a loss of taste or smell (10.1%) was greater in patients with COVID-19 than in patients with any other pathogens (<8.0%) **(Table 3)**. No significant associations were found between viral agents and diarrhea, acute respiratory distress, and shortness of breath **(Table 3)**.

Genetic Characteristics of Influenza and SARS-CoV-2

From October 1, 2021 through September 30, 2022, USAFSAM conducted next-generation sequencing and analysis on both influenza- and SARS-CoV-2-positive specimens. In total, 1,350 influenza sequences were either generated at USAFSAM or contributed by partner laboratories at the Navy Medical Research Unit 6 (NAMRU-6) in Peru or the Naval Health Research Center (NHRC) in San Diego, California. Ten influenza A(H1N1)pdm09 hemagglutinin (HA) sequences were characterized, of which 2 were clade 6B.1A.5a1 and 8 were clade 6B.1A.5a2. Of the 1,339 influenza A(H3N2) HA sequences characterized, 1 was clade 3C.2a2b.1a and the remaining 1,338 were clade 3C.2a1b.2a2 (subgrouping shown in **Figure 3a**). The predominant influenza strain of the season was A(H3N2), of which 99.9% of strains were clade 3C.2a1b.2a2. The subgroup sharing D53G held the majority for most of the season, although at times the subgroup sharing D53N was in the majority. By the end of the season, the subgroup sharing E50K became the dominant group.

One influenza B / Yamagata HA sequence was characterized as clade Y3, however the possibility of this being a live, attenuated influenza vaccine (LAIV) strain has not been eliminated. In addition, 12,225 out of 21,466 SARS-CoV-2-positive specimens were sequenced, and 10,381 were assigned to PANGO lineages. Among those lineages, 1 was an Alpha variant, 1,864 were Delta variants, 8,510 were Omicron variants, and 6 were recombinant viruses. The Omicron variants were divided into sublineages: 3,794 BA.1; 2,572 BA.2 including 622 BA.2.12.1; 18 BA.3; 324 BA.4 including 65 BA.4.6; and 1,802 BA.5 **(Figure 3b)**.

Discussion

The DODGRPSP data, along with the U.S. general population, saw the return of influenza after being relatively absent in the previous season.[5,6] The overall results revealed a positivity rate of 41.0% among all viruses; SARS-CoV-2 remained prevalent,

TABLE 3. Demographic and Clinical Details of MHS Beneficiaries, by Viral Agent, 2020–2021 Surveillance Season

Variable	SARS-CoV-2 n=749		Flu n=570		Rhino/Entero n=1,629		RSV n=243		ORP[a] n=1,161		p-value
	No.	%	No.	%	No.	%	No.	%	No.	%	
Sex											<.001
Male	509	68.0	395	69.3	954	58.6	142	58.4	673	58.0	
Female	240	32.0	175	30.7	675	41.4	101	41.6	488	42.0	
Age group, y											<.001
0-17	87	11.6	83	14.6	555	34.0	140	57.6	491	42.3	
18-64	648	86.5	487	85.4	1,068	65.6	103	42.4	661	56.9	
65+	14	1.9	0	0.0	6	0.4	0	0.0	9	0.8	
Symptom											
Cough	562	79.9	502	91.4	1,234	79.4	213	90.3	919	82.7	<.001
Sore throat	471	69.0	385	73.9	953	64.9	107	51.4	579	57.0	<.001
Fatigue	407	61.3	388	75.9	798	54.9	101	47.9	508	50.4	<.001
Body aches	400	58.8	378	72.0	534	37.5	36	18.3	366	36.9	<.001
Chills	319	48.3	345	66.1	438	31.0	40	20.1	309	31.0	<.001
Headache	472	69.5	386	74.1	788	54.8	59	29.5	476	48.0	<.001
Runny nose	329	49.9	342	67.9	1,093	73.0	166	75.8	753	71.2	<.001
Sinus congestion	467	69.1	389	76.3	1,249	81.3	183	82.8	868	80.4	<.001
Fever	384	57.6	378	72.6	643	44.7	125	57.9	581	55.3	<.001
Shaking	104	16.7	115	24.2	108	7.9	4	2.0	68	7.1	<.001
Vomit	43	7.0	59	12.2	160	11.6	22	10.7	93	9.7	0.016
Taste/smell	62	10.1	23	4.9	100	7.4	15	7.7	58	6.2	0.014
Diarrhea	65	10.4	63	13.2	169	12.2	12	6.1	118	12.5	0.062
Acute respiratory distress	13	2.5	15	4.0	35	3.0	3	1.9	24	3.0	0.635
Shortness of breath	112	17.8	80	16.6	247	17.9	34	17.1	160	16.7	0.939

Abbreviations: MHS, Military Health System; SARS-CoV-2, severe acute respiratory syndrome-related coronavirus strain 2; Flu, influenza; Rhino/Entero, rhinovirus/enterovirus; RSV, respiratory syncytial virus; No., number; N, Number; ORP, other respiratory pathogen; y, years.

[a] Adenovirus, coronavirus, human bocavirus, human metapneumovirus, parainfluenza.

however, and continued to be the dominant virus circulating among MHS beneficiaries. These data also show that rhinovirus/enterovirus was the second-most dominant virus in circulation, which increased in positivity starting in July 2022.

The overwhelming majority of clade 3C.2a1b.2a2, also reflected in data from the CDC, prompted the selection of A/Darwin/9/2021-like virus for the egg-propagated strain and A/Darwin/6/2021-like virus for the cell- and recombinant-based strain of the 2022-2023 influenza vaccine A(H3N2) component.[9] Although this clade persisted throughout the season, several subgroups emerged that could have potentially altered vaccine strain efficacy. Following the 2021-2022 season, the subgroup sharing D53G was renamed clade 2a.1 with associated subclades, the subgroup sharing D53N was renamed clade 2a.3 with associated subclades, the subgroup sharing E50K was renamed 2b with associated subclades, and the subgroup sharing 205F was renamed clade 2c with associated subclades. No change was made to the influenza A(H1N1) pdm09 or influenza B/Yamagata vaccine component. While no influenza B/Victoria specimens were sequenced by USAFSAM, the vaccine component was changed for the 2022-2023 season due to global circulation of some diversified strains.

The 2021-2022 season started with almost entirely Delta variants of SARS-CoV-2 until December 2021, when Omicron emerged and became dominant. Sublineages BA.1, BA.2, and BA.5 then subsequently held most circulating SARS-CoV-2 viruses for the rest of the season. The positivity rates showed 2 distinctive peaks, 1 in January 2022 through March 2022 (coinciding with Omicron sub-lineage BA.1/BA.2) and 1 in July 2022 (coinciding with Omicron sub-lineage BA.5) **(Figures 2** and **3b)**, which qualitatively agree with previous reports on the positivity rate of Omicron worldwide.[10,11]

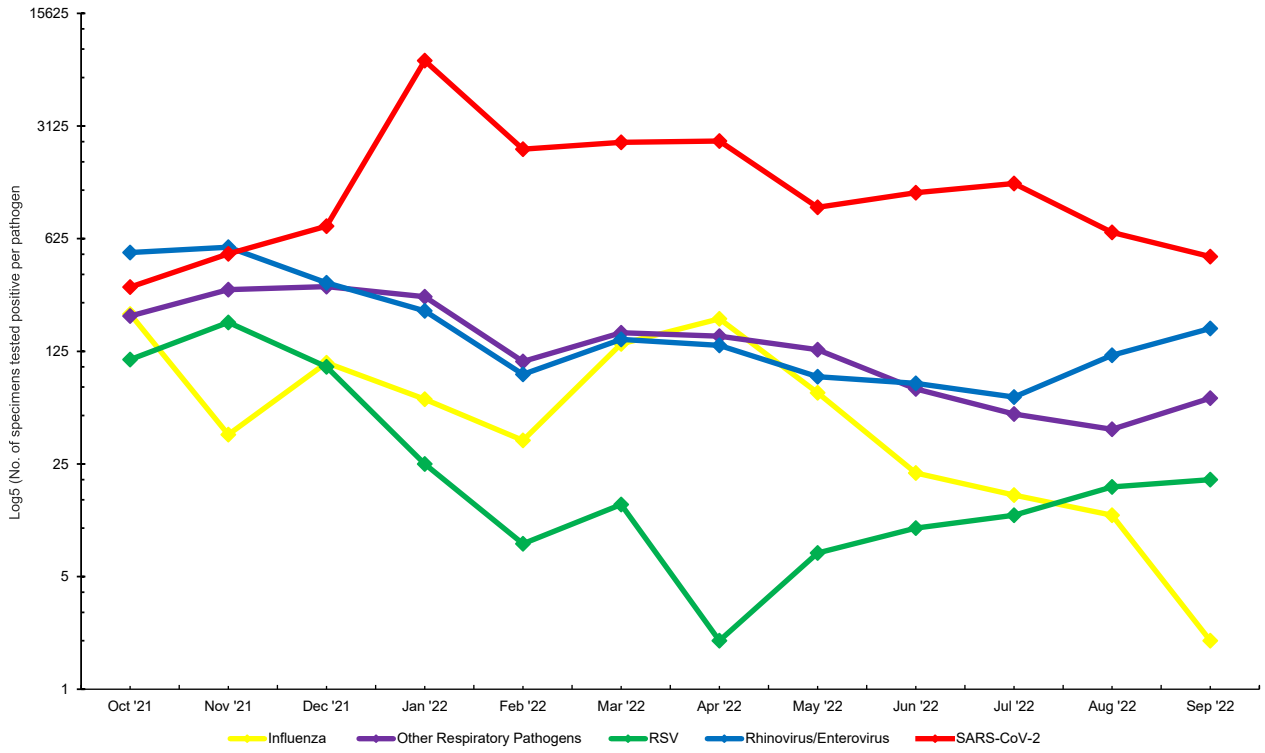
The end of September 2022 showed a reduction in the overall positivity rate. It should be noted that almost all detected influenza lineages, as well as SARS-CoV-2 variants and subvariants, were found in all geographic regions, suggesting that newly introduced viral strains can spread to all regions.

In this study, the SARS-CoV-2 infection rate in the 0-17 year age group was lower compared to any other pathogen, while RSV cases were predominantly among 0-17 year-olds. In contrast, SARS-CoV-2 was the most frequent virus detected among adults (18-64) **(Table 3)**. The findings of this report are consistent with other studies concerning the impact of SARS-CoV-2 among adults and RSV on children.[12-14]

This study had some limitations: First, the division of viral agents into only 5 groups, including 1 group representing 5 different pathogens, may be associated with different symptoms. Linking the other respiratory pathogens group as one group is due to small sample sizes, and this can only be possible when symptoms of the combined pathogens are similar. For instance, studies have shown that fever was not associated with adenovirus and parainfluenza virus.[15] The study also reveals that general symptoms such as cough, sinus congestion, and sore throat are more likely to be found in patients with other respiratory pathogens, of which it cannot be ascertained since it involves 5 different pathogens.

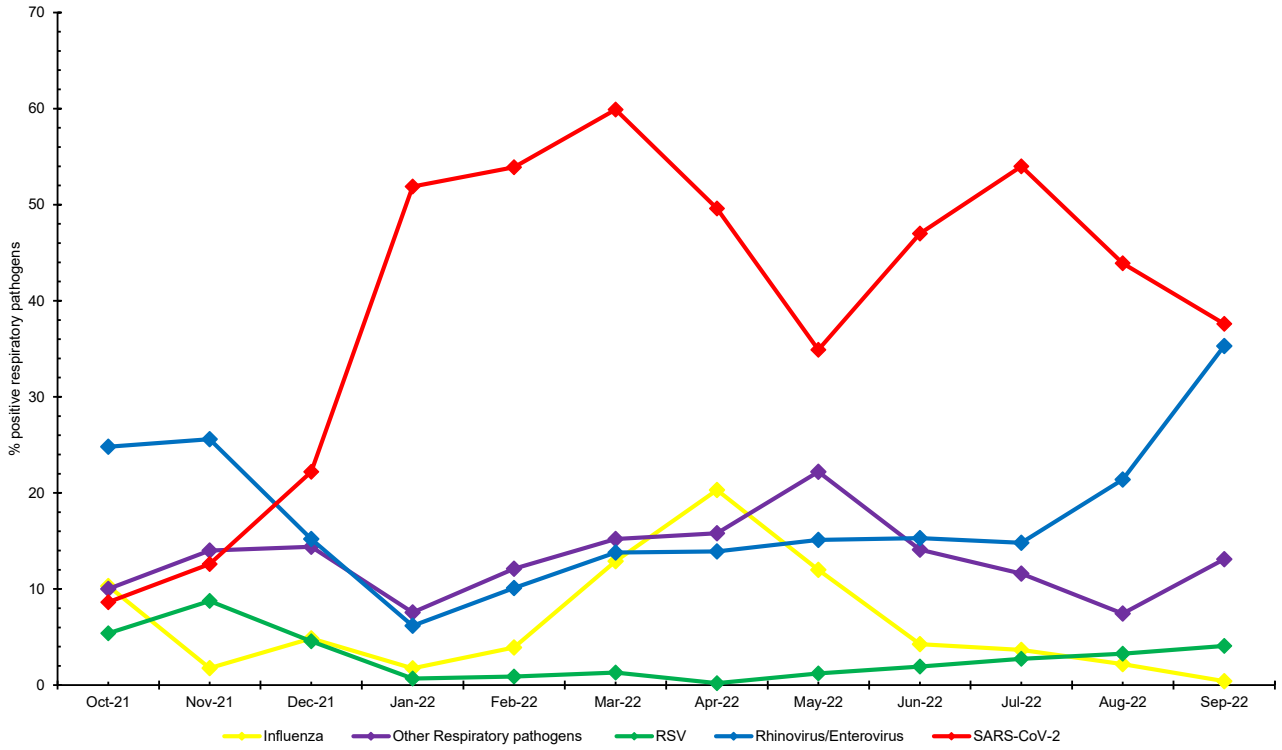
Secondly, DODGRPSP questionnaires had a low response rate, of about 13%. Even when statistically significant, symptomology results must be interpreted with

FIGURE 1. Numbers of Respiratory Pathogens that Tested Positive Among MHS Beneficiaries, October 2021–October 2022



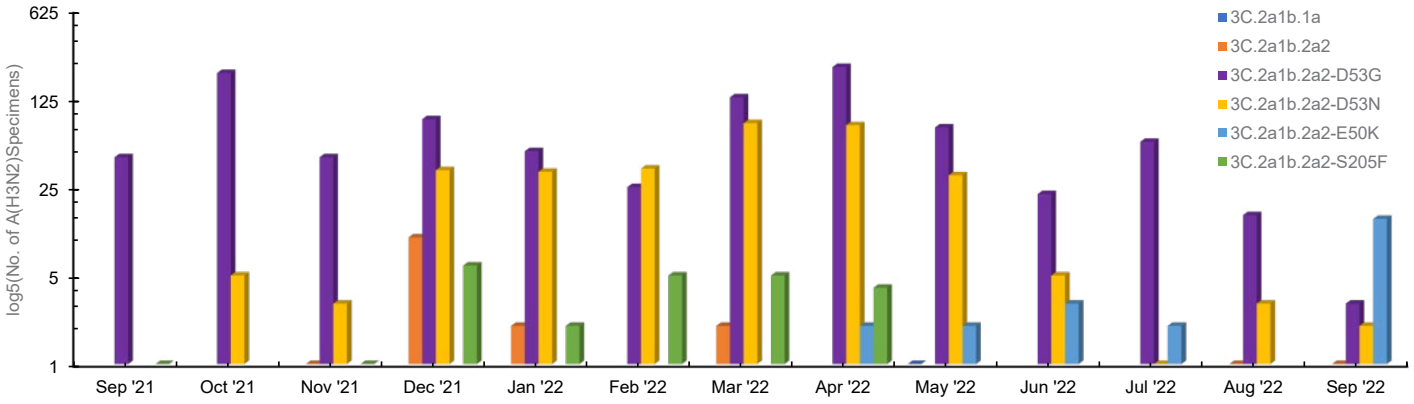
Abbreviations: MHS, Military Health System; No., number; RSV, Respiratory syncytial virus; SARS-CoV-2, severe acute respiratory syndrome-related coronavirus strain 2.
Note: Other respiratory pathogens include adenovirus, coronavirus, human bocavirus, human metapneumovirus, and parainfluenza.

FIGURE 2. Percentages of Respiratory Pathogens that Tested Positive Among MHS Beneficiaries, October 2021–October 2022



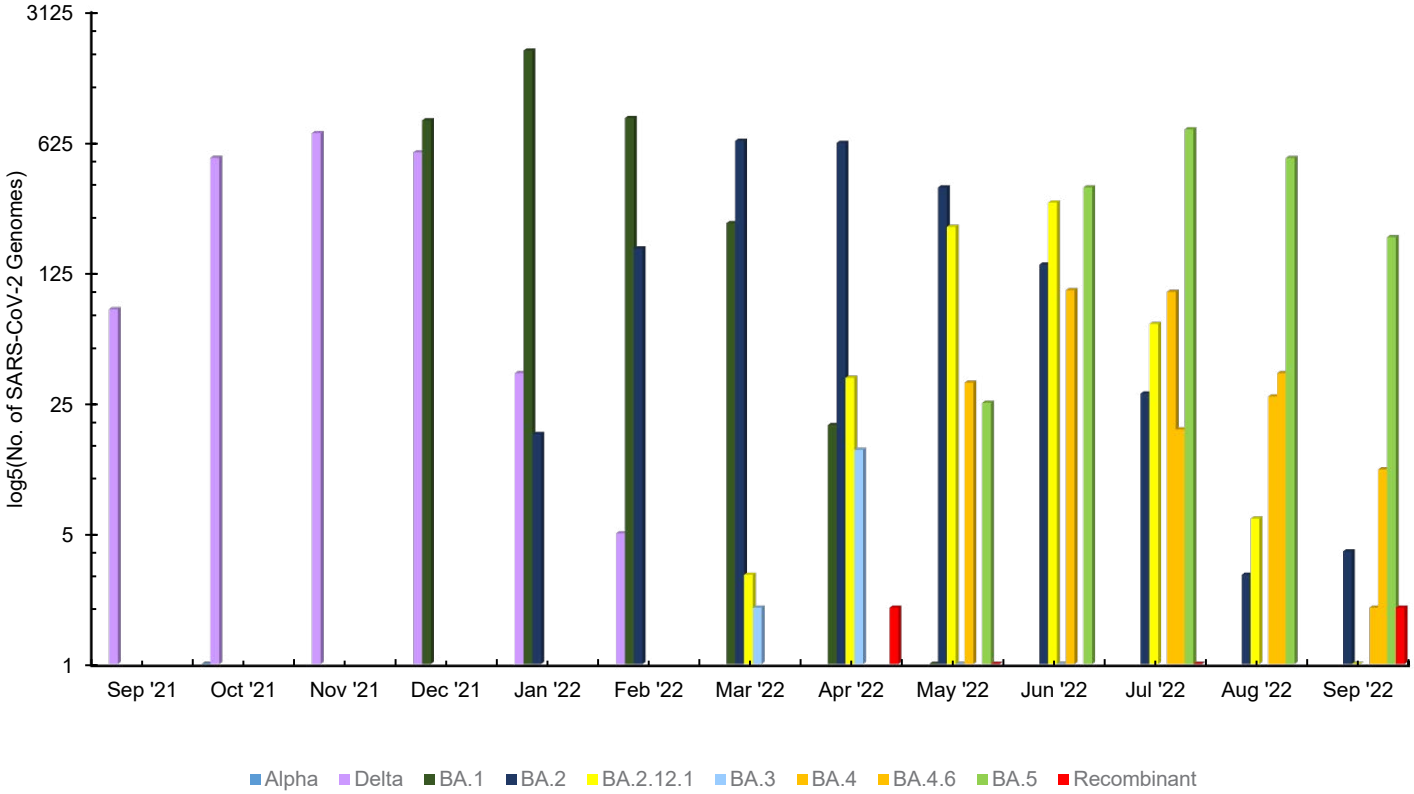
Abbreviations: MHS, Military Health System; RSV, Respiratory syncytial virus; SARS-CoV-2, severe acute respiratory syndrome-related coronavirus strain 2.
Note: Other respiratory pathogens include adenovirus, coronavirus, human bocavirus, human metapneumovirus, and parainfluenza.

FIGURE 3a. Influenza A(H3N2) Clade Proportions Among MHS Beneficiaries, 2021–2022 Surveillance Season (n=1,339)



Abbreviations: MHS, Military Health System, No., number.

FIGURE 3b. SARS-CoV-2 Lineages Identified Among MHS Beneficiaries, 2021–2022 Surveillance Season (n=12,225)



Abbreviations: SARS-CoV-2, severe acute respiratory syndrome-related coronavirus strain 2; MHS, Military Health System; No., number.

caution, as a large volume of specimens were submitted without a questionnaire. All specimens met the CLI / ILI case definition, however, or specimens were determined by a physician to be a CLI / ILI case.

During the 2021-2022 surveillance season, the temporal pattern of SARS-CoV-2 and influenza positivity among MHS beneficiaries was largely consistent with overall U.S. SARS-CoV-2 and influenza surveillance data, supporting the proposition that sentinel surveillance provides an accurate representation of respiratory pathogens trends.[6,16,17] These results emphasize the need for continuous surveillance of multiple respiratory pathogens and identification of novel pathogens, along with use of a CLI / ILI case definition for effective public health management and force health protection. Sentinel surveillance remains crucial for detecting emerging strains and guiding vaccine development efforts.

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Disclaimer

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Predicting COVID-19 and Respiratory Illness: Results of the 2022–2023 Armed Forces Health Surveillance Division Forecasting Challenge

Mark L. Bova, MPH; Sasha A. McGee, PhD; Kathleen R. Elliott, MPH; Juan I. Ubiera, MPH, MS

Since 2019, the Integrated Biosurveillance Branch of the Armed Forces Health Surveillance Division has conducted an annual forecasting challenge during influenza season to predict short-term respiratory disease activity among Military Health System beneficiaries. Weekly case and encounter observed data were used to generate 1- through 4-week advanced forecasts of disease activity. To create unified combinations of model inputs for evaluation across multiple spatial resolutions, 8 individual models were used to calculate 3 ensemble models. Forecast accuracy compared to the observed activity for each model was evaluated by calculating a weighted interval score. Weekly 1- through 4-week ahead forecasts for each ensemble model were generally higher than observed data, especially during periods of peak activity, with peaks in forecasted activity occurring later than observed peaks. The larger the forecasting horizon, the more pronounced the gap between forecasted peak and observed peak. The results showed that several models accurately predicted COVID-19 cases and respiratory encounters with enough lead time for public health response by senior leaders.

What are the new findings?

By testing a large number of traditional (e.g., ARIMA, EWMA) and non-traditional (e.g., Random Forest, Count Regression) models, this forecasting study improved understanding of which model types were the most accurate and demonstrated a more robust ensemble prediction. The ensemble models developed by this forecasting challenge provided more accurate forecasts in general, when compared to most individual models.

What is the impact on readiness and force health protection?

Respiratory diseases represent a major impediment to military readiness and force health, including interruptions in duties caused by isolation or quarantine requirements as well as morbidity caused by illnesses themselves. Respiratory disease forecasting is a useful tool for senior leaders' preparations for illness surges.

Seasonal respiratory infections, including influenza and COVID-19, represent a major impediment to military readiness. Accurate forecasts of the burden of respiratory illness in the Department of Defense (DOD) population are crucial for allowing military leaders and public health practitioners to anticipate increases in disease activity and implement preventive measures.

Since 2013, the U.S. Centers for Disease Control and Prevention (CDC) has conducted an annual influenza forecasting challenge, inviting modelers to submit weekly forecasts of influenza-like illness (ILI) or confirmed influenza hospitalizations.[1] To produce more consistent and reliable forecasts across varying spatial resolutions, forecasting challenges often combine inputs from multiple models into one unified ensemble.[2]

Since 2019, the Integrated Biosurveillance (IB) Branch of the Armed Forces Health Surveillance Division (AFHSD),[3] part of the Defense Health Agency's Public Health Directorate, has conducted its own annual forecasting challenge during the influenza season, modeled after that of the CDC. The goal is to predict short-term (1-4 weeks ahead) respiratory disease activity among Military Health System (MHS) beneficiaries within collections of geographically-aligned military installations and medical facilities in the U.S. ("markets") to support timely decision-making by senior leaders. In addition to forecasting disease activity among MHS beneficiaries, AFHSD also forecasts activity among civilians living in counties within 30 miles of a market. This challenge is open to forecasts submitted by government, academic, and industry partners.

During influenza season, AFHSD-IB reports forecast data through weekly biosurveillance products emailed to more than 3,000 individuals. Stakeholders can access these data as needed to inform resource allocation and prevention activities via an interactive dashboard (by Common Access Card only) updated weekly by AFHSD-IB.[4] This dashboard includes summary information about respiratory illness in each market and DHA network, as well as maps and time series plots of 1- through 4-week ahead forecasts.

This report summarizes the results and lessons from AFHSD's forecasts for the 2022-2023 forecasting season.

Methods

Influenza seasons were defined as epidemiological weeks 40 through 20 according to CDC's Morbidity and Mortality Weekly Report (MMWR) epidemiological weeks.[5] The 2022-2023 influenza season began on October 2, 2022 and ended May

20, 2023. The 2022-2023 challenge focused on MHS and civilian COVID-19 cases, as well as MHS COVID-like illness (CLI), ILI, and COVID-19 outpatient encounters.

Weekly respiratory illness data from multiple sources were downloaded for the 2022-2023 influenza season. MHS COVID-19 cases were collected by AFHSD's Epidemiology & Analysis Branch using laboratory and reportable medical event (RME) data provided by the Defense Centers for Public Health (DCPH)–Portsmouth and DCPH–Aberdeen. The Armed Forces RME Guidelines and Case Definitions document defines 70 DOD RMEs, which closely mirror the nationally notifiable diseases monitored by CDC.[6,7] A confirmed case of COVID-19 in MHS beneficiaries was defined using laboratory, clinical, epidemiological, and death certificate data (Unpublished, **Supplementary Table 1**). Civilian COVID-19 cases, by county, were obtained from HHS Protect and defined according to CDC criteria.[8,9] MHS outpatient encounters were extracted from DOD's Electronic Surveillance System for the Early Notification of Community-based Epidemics (ESSENCE). CLI, ILI, and COVID-19 encounter case definitions were developed internally using International Classification of Diseases, 10th Revision, Clinical Modification (ICD-10-CM) diagnosis codes, and are provided in **Supplementary Table 1**.

Weekly case and encounter observed data were used to generate 1- through 4-week ahead forecasts of disease activity. Forecasts were generated using various models, including time series (including Autoregressive Integrated Moving Average [ARIMA], Error, Trend, Seasonal [ETS], Exponentially Weighted Moving Average [EWMA], and Vector Autoregressive [VAR]), machine learning (including Random Forest), and count regression (including Poisson, Negative Binomial, and Log-binomial) models. To create unified combinations of model inputs for evaluation across multiple spatial resolutions, 8 individual models were used to calculate the 3 ensemble models: 1) the average of the time series and machine learning models—ENSEMBLE, 2) the average of the 3 best-performing time series and machine learning models—ENSEMBLE_TOP, and 3) the average of the count regression models—ENSEMBLE_CNT.

The accuracy of forecasts compared to the observed activity for each model was evaluated by calculating a weighted interval score (WIS),[10] a metric also used by the CDC, that compares performance among models. A lower score indicates better model performance. All analyses were conducted using R software (version 4.1, The R Foundation for Statistical Computing, Vienna, Austria). The R packages "fable," "randomForest," and "tscount" were used to generate forecasts and the "evalcast" package to calculate the WIS.[11-14]

Results

Weekly observed counts of MHS and civilian COVID-19 cases by market were converted to population-adjusted rates, while weekly observed MHS outpatient encounters were converted to a percentage of total outpatient encounters for that week. Weekly 1- through 4-week ahead forecasts for each ensemble model were generally higher than observed data, especially during periods of peak activity (December through February), with peaks in forecasted activity occurring later than observed peaks **(Figure 1)**. The larger the forecasting horizon (i.e., 4 weeks ahead versus 1 week), the more pronounced the gap between forecasted peak and observed peak.

Forecasts of peak MHS COVID-19 case rates were mostly higher than observed, ranging from 44% higher for the ENSEMBLE_CNT model to 457% higher for the ENSEMBLE_TOP model **(Table 1)**. Peak civilian COVID-19 case rate forecasts were more accurate, ranging from 13% lower (ENSEMBLE_CNT) to 99% higher (ENSEMBLE). Peak encounter forecasts for the ENSEMBLE_CNT model were lower than observed peaks (16% and 9% lower for ILI and CLI, respectively) and equal to the observed peak for COVID-19 encounters. Peak encounter forecasts for the ENSEMBLE_TOP model were higher than observed peaks, including 24% higher for ILI, 27% higher for CLI, and 10% higher for COVID-19 encounters. Peak week forecasts tended to be 2 to 6 weeks later than observed for most ensemble models and forecast targets. The ENSEMBLE_CNT model accurately predicted forecasts of peak civilian COVID-19 cases and MHS ILI encounters, however.

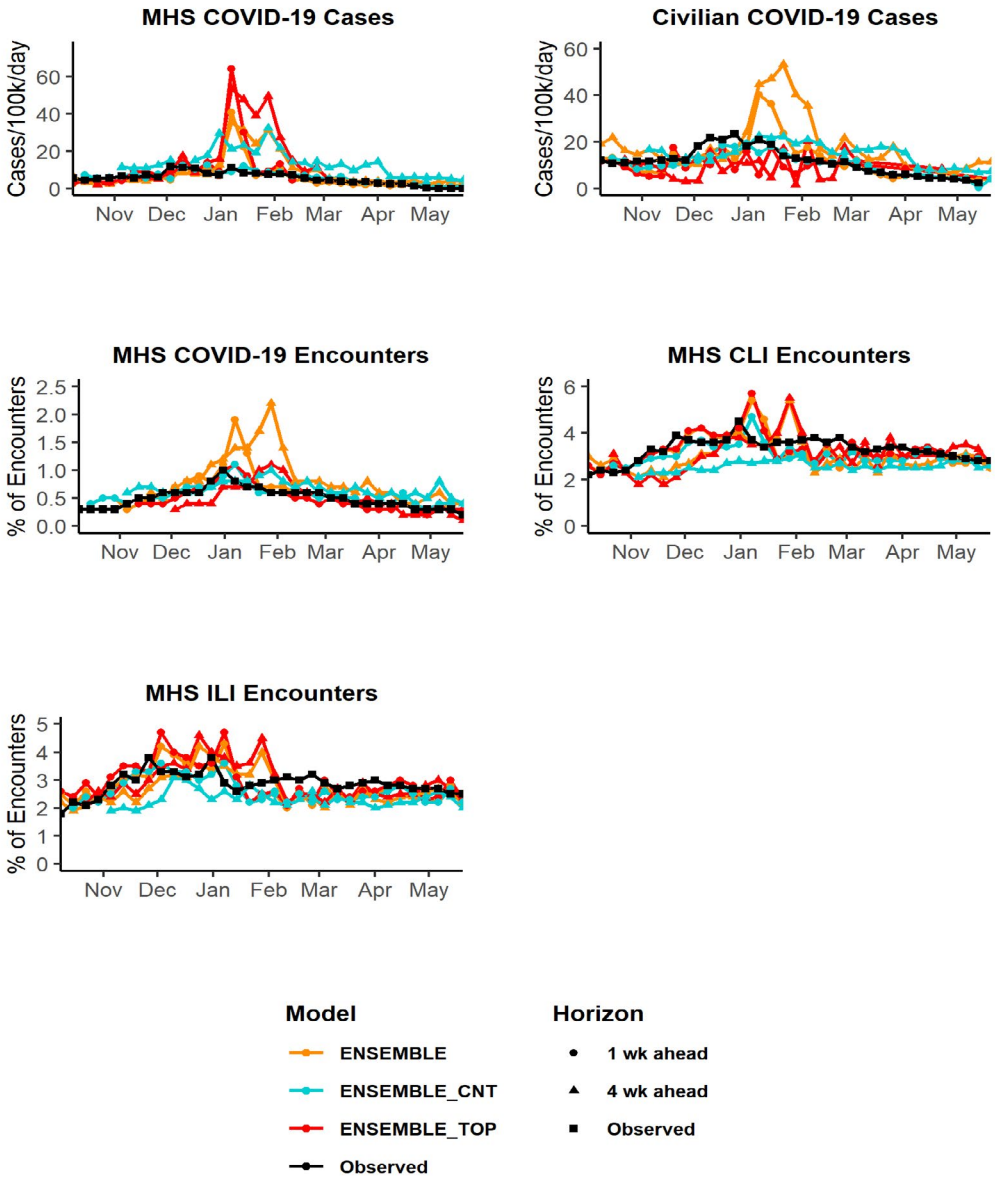
Overall, the ENSEMBLE_CNT model had the lowest WIS of all forecasting horizons, indicating the most accurate forecasts for civilian and MHS COVID-19 cases **(Figure 2)**. The ENSEMBLE_TOP model was the most accurate for COVID-19 encounter forecasts, while all 3 ensemble models performed similarly for CLI and ILI encounters. Model performance decreased as forecast horizons increased, with the median WIS for all 4-week ahead forecasts of the ensemble models increasing between 10% (MHS ILI encounters) and 98% (civilian COVID-19 cases) compared to 1-week ahead forecasts.

Discussion

This is the first published results from the AFHSD Respiratory Forecasting Challenge since it was begun in 2019. Respiratory disease forecasting was more challenging during the 2022-2023 influenza season, due in part to decreased COVID-19 activity compared to prior years and ILI resurgence **(Supplementary Table 2)**. Peak observed MHS and civilian COVID-19 case rates in 2022-2023 were 95% and 91% lower, respectively, compared to the 2021-2022 season, while peak observed MHS COVID-19 and CLI encounters were 76% and 26% lower, respectively, than the prior season. Conversely, peak observed MHS ILI encounters during the 2022-2023 season were 41% higher than during the 2021-2022 season and 111% higher than during the 2020-2021 season. Historical data for the previous 2 seasons were, therefore, not predictive of respiratory activity in 2022-2023.

Ensemble models generally provided more accurate forecasts, especially the ENSEMBLE_CNT and ENSEMBLE models, compared to most individual models **(Supplementary Figure)**. Although certain individual models outperformed ensemble models for specific forecasting targets,

FIGURE 1. Weekly Forecasts Versus Observed Data by Ensemble Model and Forecasting Horizon, All U.S. Surveillance Markets, October 2022–June 2023



Abbreviations: MHS, Military Health System; COVID-19, coronavirus disease 2019; CLI, COVID-like illness; ILI, influenza-like illness; AFHSD, Armed Forces Health Surveillance Division; IB, Integrated Biosurveillance.

including the Random Forest model for MHS COVID-19 case forecasts and the Poisson model for civilian COVID-19 case forecasts, each performed similarly when compared to the best-performing ensemble model. Model performance decreased as the forecasting horizon increased, with WIS scores ranging from 10% to 95% higher on average for 4-week ahead forecasts compared to 1-week ahead forecasts. These results are consistent with a previous publication of COVID-19 forecasts in the U.S. COVID-19 Forecast Hub that found that an ensemble model comprised of 27 individual models was consistently more accurate than the individual models, and that the accuracy of forecasting models decreased as forecast horizons increased.[15]

This forecasting study has several strengths. First, the forecasting results showed that several models accurately predicted COVID-19 cases and respiratory encounters with enough lead time for senior leaders to take action. Second, this forecasting study tested a large number of traditional (e.g., ARIMA, EWMA) and non-traditional (e.g., Random Forest, Count Regression) models, increasing our understanding of which types of models were most accurate and providing a more robust ensemble prediction.

The forecasting of the 2022-2023 season also showed several limitations that may have affected model accuracy. COVID-19 cases may have been generally under-reported due to the large number

TABLE 1. Comparison of Observed and Forecasted Activity by Forecast Target, All U.S. Surveillance Markets, 2-Week Forecasting Horizon

Forecast Target	Peak Activity				Peak Week			
	Observed Activity	Forecasted Activity			Observed Week	Difference Between Forecasted and Observed Week		
		ENSEMBLE	ENSEMBLE_TOP	ENSEMBLE_CNT		ENSEMBLE	ENSEMBLE_TOP	ENSEMBLE_CNT
MHS COVID-19 cases 100k/day	11.6	40.8	64.6	16.7	48	+6	+6	+2
Civilian COVID-19 cases 100k/day	23.3	46.3	18.9	20.3	51	+2	+3	0
MHS % ILI encounters	3.8%	4.2%	4.7%	3.2%	47	+2	+2	0
MHS % CLI encounters	4.5%	5.3%	5.7%	4.1%	52	+2	+2	+2
MHS % COVID-19 encounters	1.0%	2.0%	1.1%	1.0%	52	+2	+2	+2

Abbreviations: MHS, Military Health System; COVID-19, coronavirus disease 2019; k, 1,000; CLI, COVID-like illness; ILI, influenza-like illness.

COVID-19 case definition: Any positive laboratory result for SARS-CoV-2 or a confirmed COVID-19 reportable medical event

CLI encounter definition: Any of the following ICD-10 diagnosis codes in any diagnostic position: B34.2, B97.21, B97.29, J00, J06.9, J12.81, J12.89, J12.9, J16.8, J17, J18.0, J18.1, J18.8, J18.9, J20.8, J20.9, J40, J22, J80, R05, R50.9, R06.0, R06.00, R06.02, R06.03, R06.09, U07.1, R43.0, R43.2, J84.111

ILI encounter definition: Any of the following ICD-10 diagnosis codes in any diagnostic position: B97.89, H66.9, H66.90, H66.91, H66.92, H66.93, J00, J01.9, J01.90, J06.9, J09, J09.X, J09.X1, J09.X2, J09.X3, J09.X9, J10, J10.0, J10.00, J10.01, J10.08, J10.1, J10.2, J10.8, J10.81, J10.82, J10.83, J10.89, J11, J11.0, J11.00, J11.08, J11.1, J11.2, J11.8, J11.81, J11.82, J11.83, J11.89, J12.89, J12.9, J18, J18.1, J18.8, J18.9, J20.9, J22, J40, R05, R50.9

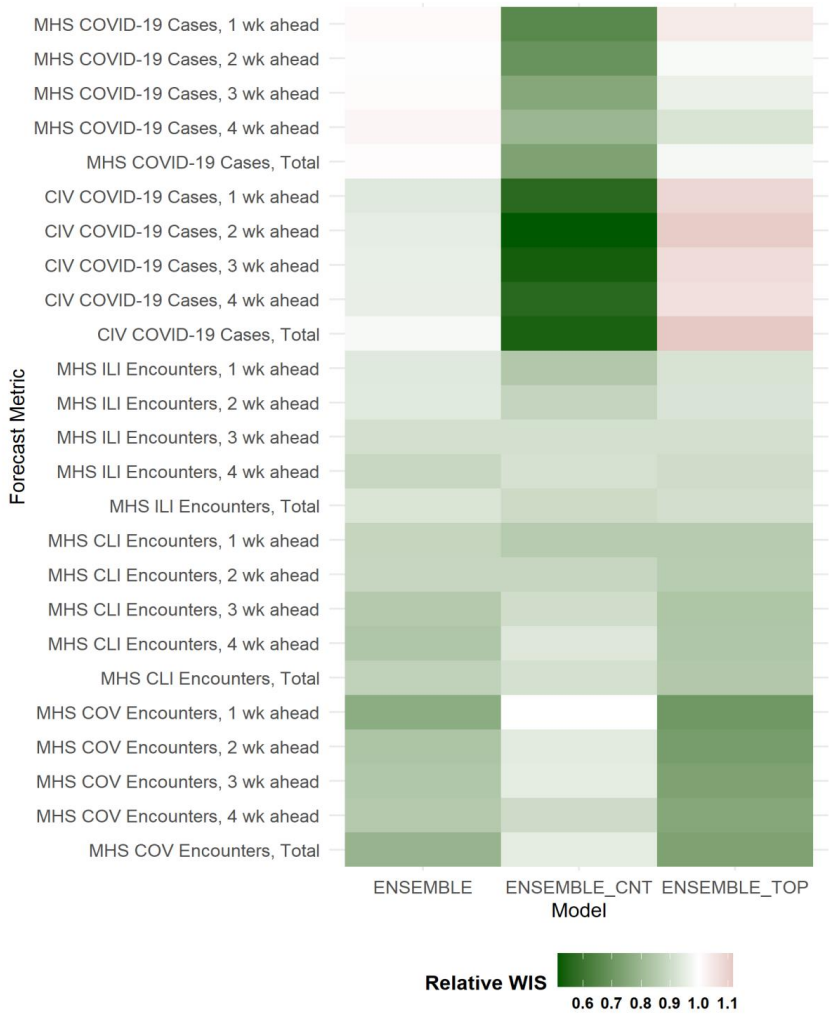
COVID-19 encounter definition: Any of the following ICD-9 or ICD-10 diagnosis codes in any diagnostic position: B97.29, U07.1, Z03.818, Z20.828, B34.2, J12.81, 079.82, 480.3, V01.82

of asymptomatic cases and use of at-home testing, both within DOD and civilian populations. Data reporting schedules, particularly for civilian COVID-19 cases, changed dramatically during the season after the May 11, 2023 end of the U.S. Public Health Emergency for COVID-19. This policy change disrupted county case reporting by CDC.[16] Many states and military treatment facilities also changed their COVID-19 case reporting schedules, from daily to weekly, monthly, or not at all. To abridge some of gaps in COVID-19 reporting, health encounter data from DOD ESSENCE could be utilized, but syndromic surveillance systems such as ESSENCE may suffer from inconsistent data quality between reporting sites and gaps in coverage.[17] In addition, these data can also lag by at least 4 days from the encounter date, leading to under-reporting of health encounters during the most recent week; these data present challenges for forecasting, as the observed value for this week may change significantly in subsequent weeks. During the 2022-2023 season, reported numbers of civilian and MHS COVID-19 cases for a given week increased by as much as 50% 1 month after an initial reporting date, as older cases were reported, while MHS encounter data ranged from a 40% decrease to a 40% increase as additional encounters populated the system. Efforts were made to account for potential backfill in each market for both case and encounter data prior to generating weekly forecasts, but forecasting analysis can be challenging due to unpredictable data processing schedules. Other limitations included the availability and usefulness of covariate data. Data that previously relied on for COVID-19 forecasting, including vaccination and case data, became less reliable or unavailable during the season.

Another limitation of this study is the relative usefulness and timeliness of the forecasts. As mentioned, forecast accuracy decreased as forecasting horizon increased. The data lags in ESSENCE, compounded by the time constraints of downloading and aggregating weekly data and generating weekly forecasts, meant that weekly forecasts were not available for senior leaders until nearly 1 week after the most recently observed data. This circumstance renders the 1-week ahead forecasts of disease activity mostly unusable, limiting senior leaders' response time to 2-week ahead forecasts. Although the 3- and 4-week ahead forecasts provide adequate time for senior leaders to make necessary preparations, their accuracy is greatly diminished compared to 1- and 2-week ahead forecasts. Efforts to improve the utility of 1- and 2-week ahead forecasts may be achieved by downloading data earlier each week and generating weekly forecasts more efficiently, but efforts for improving the more distant horizon forecasts and expanding beyond 4 weeks are current priorities.

Future AFHSD-IB respiratory forecasting challenges will consider additional

FIGURE 2. Assessment of Error in the Ensemble Models by Forecasting Target and Horizon Based on Median WIS, All U.S. Surveillance Markets



Abbreviation: wk, week; WIS, Weighted Interval Score; MHS, Military Health System; COVID-19, coronavirus disease 2019; CLI, COVID-like illness; ILI, influenza-like illness.

COVID-19 case definition: Any positive laboratory result for SARS-CoV-2 or a confirmed COVID-19 reportable medical event.

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ILI encounter definition: Any of the following ICD-10 discharge diagnosis codes in any diagnostic position: B97.89, H66.9, H66.90, H66.91, H66.92, H66.93, J00, J01.9, J01.90, J06.9, J09, J09.X, J09.X1, J09.X2, J09.X3, J09.X9, J10, J10.0, J10.00, J10.01, J10.08, J10.1, J10.2, J10.8, J10.81, J10.82, J10.83, J10.89, J11, J11.0, J11.00, J11.08, J11.1, J11.2, J11.8, J11.81, J11.82, J11.83, J11.89, J12.89, J12.9, J18, J18.1, J18.8, J18.9, J20.9, J22, J40, R05, R50.9

COVID-19 encounter definition: Any of the following ICD-9 or ICD-10 discharge diagnosis codes in any diagnostic position: B97.29, U07.1, Z03.818, Z20.828, B34.2, J12.81, 079.82, 480.3, V01.82

Relative WIS: The median WIS for that target, horizon, and model divided by the median WIS for that target and horizon, intended to show how well a model performed compared to the average, with green above average and red below average.

covariates, such as environmental data, and combine time series and count regression forecasts into a single ensemble model. The incorporation of new models, such as neural network models, machine learning models, and wavelet forecasting, will also be explored. More emphasis will be placed on non-pandemic seasons to lessen the impacts of changes in COVID-19 and influenza reporting. Forecasting will focus on more consistently available data sources for both DOD and civilian populations, including COVID-19 hospitalizations, influenza hospitalizations, and health encounter data. As the time elapsed since the initial years of the COVID-19 pandemic increases, historical data may become more reliable in predicting the volume and peak activity for COVID-19 and other respiratory diseases during upcoming influenza seasons.

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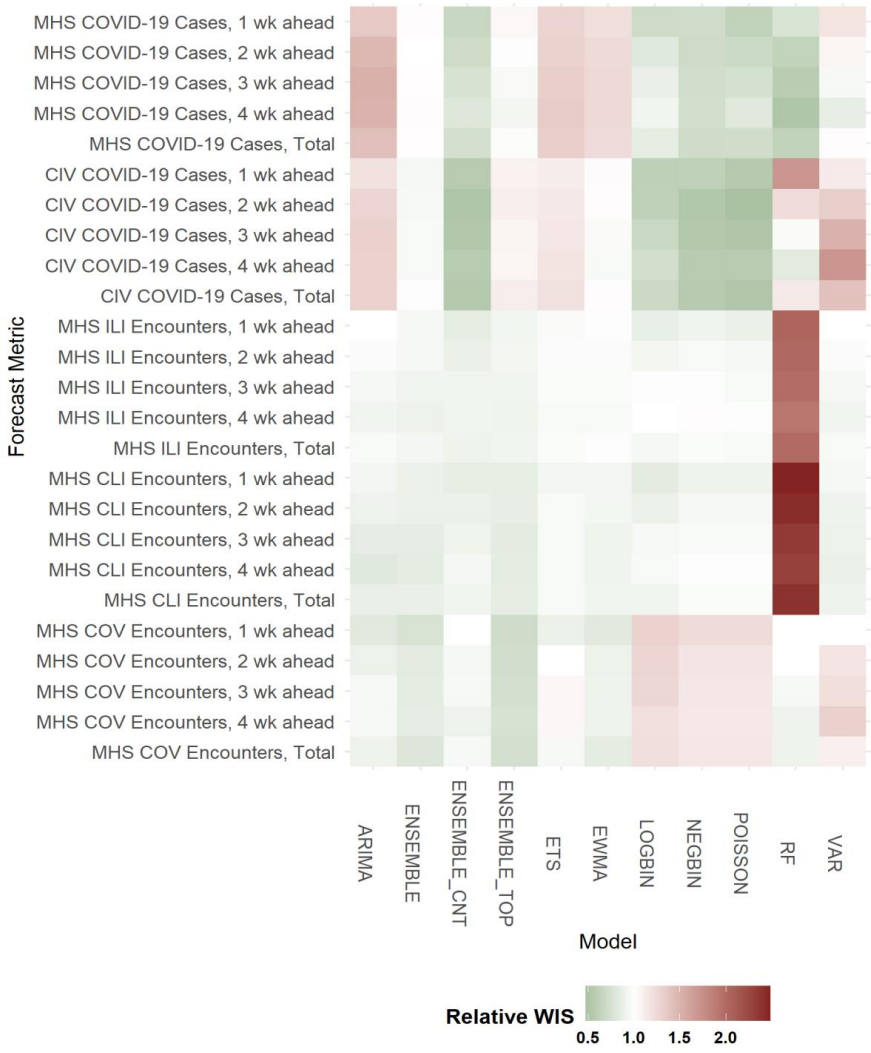
SUPPLEMENTARY FIGURE. Assessment of Error in Forecasting Models by Forecasting Target and Horizon Based on Relative Median WIS, All U.S. Surveillance Markets



Abbreviation: wk, week; WIS, Weighted Interval Score; MHS, Military Health System; COVID-19, Coronavirus disease 2019; CLI, COVID-like illness; ILI, influenza-like illness.

COVID-19 case definition: Any positive laboratory result for SARS-CoV-2 or a confirmed COVID-19 reportable medical event

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ILI encounter definition: Any of the following ICD-10 diagnosis codes in any diagnostic position: B97.89, H66.9, H66.90, H66.91, H66.92, H66.93, J00, J01.9, J01.90, J06.9, J09, J09.X, J09.X1, J09.X2, J09.X3, J09.X9, J10, J10.0, J10.00, J10.01, J10.08, J10.1, J10.2, J10.8, J10.81, J10.82, J10.83, J10.89, J11, J11.0, J11.00, J11.08, J11.1, J11.2, J11.8, J11.81, J11.82, J11.83, J11.89, J12.89, J12.9, J18, J18.1, J18.8, J18.9, J20.9, J22, J40, R05, R50.9

COVID-19 encounter definition: Any of the following ICD-9 or ICD-10 diagnosis codes in any diagnostic position: B97.29, U07.1, Z03.818, Z20.828, B34.2, J12.81, 079.82, 480.3, V01.82

Relative WIS: The Median WIS for that target, horizon, and model divided by the median WIS for that target and horizon, intended to show how well a model performed compared to the average, with green above average and red below average.

SUPPLEMENTARY TABLE 1. AFHSD Forecasting Target Definitions

Forecasting Target	Case Definition
MHS COVID-19 Case	Confirmed: Detection of SARS-CoV-2 nucleic acid (RNA) by molecular amplification from a clinical or autopsy specimen Probable: Meets any of the following criteria 1) Epidemiologically linked to another case of COVID-19 with no confirmatory COVID-19 laboratory testing and meets the following clinical description of a case: a. At least TWO of the following symptoms: fever, chills, rigors, myalgia, headache, sore throat, nausea or vomiting, diarrhea, fatigue, congestion or runny nose OR b. Any ONE of the following symptoms: cough, shortness of breath, difficulty breathing, new olfactory disorder, or new taste disorder OR c. Severe respiratory illness with at lease 1 of the following: clinical or radiographic evidence of pneumonia, or acute respiratory distress syndrome (ARDS) 2) Detection of SARS-CoV-2 antigen from a respiratory specimen 3) A death certificate that lists COVID-19 disease or SARS-CoV-2 as an underlying cause of death or a significant condition contributing to death with no confirmatory COVID-19 laboratory testing
MHS CLI Encounter	Any of the following ICD-10-CM diagnosis codes in any diagnostic position: B34.2, B97.21, B97.29, J00, J06.9, J12.81, J12.89, J12.9, J16.8, J17, J18.0, J18.1, J18.8, J18.9, J20.8, J20.9, J40, J22, J80, R05, R50.9, R06.0, R06.00, R06.02, R06.03, R06.09, U07.1, R43.0, R43.2, J84.111
MHS ILI Encounter	Any of the following ICD-10-CM diagnosis codes in any diagnostic position: B97.89, H66.9, H66.90, H66.91, H66.92, H66.93, J00, J01.9, J01.90, J06.9, J09, J09.X, J09.X1, J09.X2, J09.X3, J09.X9, J10, J10.0, J10.00, J10.01, J10.08, J10.1, J10.2, J10.8, J10.81, J10.82, J10.83, J10.89, J11, J11.0, J11.00, J11.08, J11.1, J11.2, J11.8, J11.81, J11.82, J11.83, J11.89, J12.89, J12.9, J18, J18.1, J18.8, J18.9, J20.9, J22, J40, R05, R50.9
MHS COVID-19 Encounter	Any of the following ICD-9-CM or ICD-10-CM diagnosis codes in any diagnostic position: B97.29, U07.1, Z03.818, Z20.828, B34.2, J12.81, 079.82, 480.3, V01.82

Abbreviations: MHS, Military Health System; COVID-19, coronavirus disease 2019; CLI, COVID-like illness; ILI, influenza-like illness.

SUPPLEMENTARY TABLE 2. Comparison of Observed Activity by Influenza Season, All U.S. Surveillance Markets

Forecast Target	Peak Activity				Peak Week			
	2022-2023	2021-2022	2020-2021	2019-2020	2022-2023	2021-2022	2020-2021	2019-2020
MHS COVID-19 cases	11.6	216.7	47.0	NA	48	1	1	NA
Civilian COVID-19 cases	23.3	264.0	79.4	NA	51	2	1	NA
MHS ILI encounters	3.8%	2.7%	1.8%	5.3%	47	52	46	52
MHS CLI encounters	4.5%	6.1%	3.6%	3.9%	52	52	52	1
MHS COVID-19 encounters	1.0%	4.2%	4.1%	NA	52	52	1	NA

COVID-19 case definition: Any positive laboratory result for SARS-CoV-2 or a confirmed COVID-19 reportable medical event

CLI encounter definition: Any of the following ICD-10 diagnosis codes in any diagnostic position: B34.2, B97.21, B97.29, J00, J06.9, J12.81, J12.89, J12.9, J16.8, J17, J18.0, J18.1, J18.8, J18.9, J20.8, J20.9, J40, J22, J80, R05, R50.9, R06.0, R06.00, R06.02, R06.03, R06.09, U07.1, R43.0, R43.2, J84.111

ILI encounter definition: Any of the following ICD-10 diagnosis codes in any diagnostic position: B97.89, H66.9, H66.90, H66.91, H66.92, H66.93, J00, J01.9, J01.90, J06.9, J09, J09.X, J09.X1, J09.X2, J09.X3, J09.X9, J10, J10.0, J10.00, J10.01, J10.08, J10.1, J10.2, J10.8, J10.81, J10.82, J10.83, J10.89, J11, J11.0, J11.00, J11.08, J11.1, J11.2, J11.8, J11.81, J11.82, J11.83, J11.89, J12.89, J12.9, J18, J18.1, J18.8, J18.9, J20.9, J22, J40, R05, R50.9

COVID-19 encounter definition: Any of the following ICD-9 or ICD-10 diagnosis codes in any diagnostic position: B97.29, U07.1, Z03.818, Z20.828, B34.2, J12.81, 079.82, 480.3, V01.82

Abbreviations: MHS, Military Health System; COVID-19, coronavirus disease 2019; CLI, COVID-like illness; ILI, influenza-like illness; NA, mot applicable.

Update

Malaria Among Members of the U.S. Armed Forces, 2023

MSMR publishes annual updates on the incidence of malaria among U.S. service members. Malaria infection remains a potential health threat to U.S. service members located in or near endemic areas due to duty assignment, participation in contingency operations, or personal travel. In 2023, a total of 39 active and reserve component service members were diagnosed with or reported to have malaria, an 8.3% increase from the 36 cases identified in 2022. Over half of the malaria cases in 2023 were caused by *Plasmodium falciparum* (53.8%; n=21) followed by unspecified types of malaria (35.9%; n=14) and *P vivax* and other *Plasmodia* (5.1%; n=2 each). Malaria cases were diagnosed or reported from 22 different medical facilities: 18 in the U.S., 2 in Germany, 1 in Africa, 1 in South Korea. Of the 33 cases with known locations of diagnoses, 6 (18.2%) were reported from or diagnosed outside the U.S.

What are the new findings?

Numbers of malaria cases began to increase after a low (n=20) in 2021, reaching 39 cases in 2023, mainly due to more from Africa as well as other or unspecified locations. Cases acquired in South Korea declined substantially in 2023.

What is the impact on readiness and force health protection?

Malaria poses a health risk not only for service members deployed to endemic regions but those traveling to such areas for personal reasons. The finding that *P falciparum malaria*, which carries a high risk of serious sequelae, including death, was diagnosed in more than half of malaria cases in 2023 emphasizes the need for continued emphasis on effective preventive measures against this most dangerous malaria strain.

Malaria is a life-threatening disease spread to humans through the bites of *Anopheles* mosquitoes, found mostly in tropical countries.[1] In 2022 the World Health Organization (WHO) reported that nearly half the world's population was at risk of malaria, with an estimated 249 million malaria cases and 608,000 malaria deaths in 85 countries across different continents that present tremendous heterogeneity in the incidence of malaria deaths. Africa bears a disproportionately high share of the global malaria burden, with the vast majority (95%) of global malaria cases occurring there each year.[1-3]

Malaria is caused by 5 species of protozoan parasite of the genus *Plasmodium: P falciparum*, *P vivax*, *P malariae*, *P ovale*, or *P knowlesi*, of which *P falciparum* is most likely to cause severe infections and, if not promptly treated, may lead to death.[4] While *P falciparum* is most prevalent in Africa, *P vivax* is the most widely geographically-distributed parasite species, with relatively high prevalence of infection in Southeast Asia, Western Pacific, and Eastern Mediterranean regions, as well as less densely populated areas of the Americas.[5]

Although malaria is not endemic in the United States, it is critical to monitor the incidence and trends of malaria among U.S. service members, due to potential health threats that may arise from being located in endemic areas due to duty assignments, participation in contingency operations, or personal travel.[6] The *MSMR*'s focus on malaria reflects both historical lessons about this mosquito-borne disease and the continuing threat it poses to military operations and service members' health.

The 2023 *MSMR* malaria update documented 12 individuals with exposures classified as deployment-related, of which 10 were classified as non-duty-related and 9 were considered acquired in Africa. Non-Hispanic Black service members accounted for 8 of those non-duty cases, and leisure travel to countries in Africa was documented in the reportable medical event (RME) records of 4 of these service members.[6]

Although malaria is a serious and potentially fatal disease, illness and death from malaria can be prevented by avoiding mosquito bites and proper use of malaria prophylaxis and standard preventive measures. The U.S. military has effective countermeasures against malaria, including chemoprophylactic drugs, permethrin-impregnated uniforms and bed nets, and DEET-containing insect repellents. Nevertheless, literature suggests that most malaria cases are associated with poor compliance with existing preventive measures.[7-9]

There is a need to identify gaps in existing approaches to more effectively combat malaria outbreaks and reflect changes in the incidence and trends of malaria infections among U.S. military personnel. This update describes the epidemiological patterns of malaria incidence among service members in the active and reserve components of the U.S. Armed Forces, using methods similar to those employed in previous analyses to explore factors for malaria prevention among this population.

Methods

The surveillance period for this report was January 1, 2014 through December 31, 2023. The surveillance population included service members of the U.S. Army, Navy, Air Force, Marine Corps, Space Force, and Coast Guard.

The records of the Defense Medical Surveillance System (DMSS) were searched to identify qualifying evidence of a malaria diagnosis from RMEs, hospitalizations, outpatient encounters (in military and non-military facilities), and laboratory results from military facilities. Case definition criteria included 1) an RME record of confirmed malaria, 2) a hospitalization record with a primary diagnosis of malaria, 3) a hospitalization record with a non-primary diagnosis of malaria due to a specific *Plasmodium* species, 4) a hospitalization record with a non-primary diagnosis of malaria plus a diagnosis of anemia, thrombocytopenia, and related conditions, or malaria-complicating pregnancy in any diagnostic position, 5) a hospitalization record with a non-primary diagnosis of malaria plus diagnoses of signs or symptoms consistent with malaria in each diagnostic position preceding malaria, or 6) a positive malaria antigen test plus an outpatient record with a diagnosis of malaria in any diagnostic position within 30 days of the specimen collection date. The relevant International Classification of Diseases, 9th and 10th Revision (ICD-9/ICD-10) codes used to identify cases are shown in **Table 1**.

This analysis restricted each service member to 1 episode of malaria per 365-day period. When multiple records documented a single episode, the date of the earliest record was considered the date of clinical onset. Records within 30 days of the clinical onset date were reviewed for evidence of a *Plasmodium* species.

Presumed locations of malaria acquisition were estimated using a hierarchical algorithm: 1) cases diagnosed in a malaria-endemic country were considered acquired in that country, 2) RMEs that listed exposures to malaria-endemic locations were considered acquired in those locations, 3) RMEs that did not list exposures to malaria-endemic locations but were reported from installations in malaria-endemic locations were considered acquired in those locations, 4) cases diagnosed among service members during or within 30 days of deployment or assignment to a malaria-endemic country were considered acquired in that country, and 5) cases diagnosed among service members who had been deployed or assigned to a malaria-endemic country within 2 years before diagnosis were considered acquired in those respective countries. All remaining cases were considered to have acquired malaria in unknown locations.

TABLE 1. ICD-9 and ICD-10 Diagnosis Codes Used in Defining Malaria Cases from the Records for Inpatient Encounters (Hospitalizations)

	ICD-9	ICD-10
Malaria (*Plasmodium* species)		
P falciparum	84.0	B50
P vivax	84.1	B51
P malariae	84.2	B52
P ovale	84.3	B53.0
Unspecified	84.4, 84.5, 84.6, 84.8, 84.9	B53.1, B53.8, B54
Anemia	280–285	D50–D53, D55–D64
Thrombocytopenia	287	D69
Malaria-complicating pregnancy	647.4	O98.6
Signs, symptoms, or other abnormalities consistent with malaria	276.2, 518.82, 584.9, 723.1, 724.2, 780.0, 780.01, 780.02, 780.03, 780.09, 780.1, 780.3, 780.31, 780.32, 780.33, 780.39, 780.6, 780.60, 780.61, 780.64, 780.65, 780.7, 780.71, 780.72, 780.79, 780.97, 782.4, 784.0, 786.05, 786.09, 786.2, 786.52, 786.59, 787.0, 787.01, 787.02, 787.03, 787.04, 789.2, 790.4	E87.2, J80, M54.2, M54.5, N17.9, R05, R06.0, R06.89, R07.1, R07.81, R07.82, R07.89, R11*, R16.1, R17, R40*, R41.0, R41.82, R44*, R50*, R51, G44.1, R53*, R56*, R68.0, R68.83, R74.0

Abbeviations: ICD-9, International Classification of Diseases, 9th Revision; ICD-10, International Classification of Diseases, 10th Revision; *P, plasmodium*.

Results

In 2023, a total of 39 U.S. service members were diagnosed with or reported to have malaria **(Table 2)**, resulting in a rate of 1.9 per 100,000 persons (data not shown). This total from 2023 represents an 8.3% increase from the 36 cases ascertained in 2022 **(Figure 1)**. Twenty-one of the 39 cases (53.8%) in 2023 were identified from inpatient data reported as RMEs, while the remaining 18 cases were identified from inpatient data without associated RMEs. Six cases from 2023 were identified from laboratory data in combination with an outpatient record of malaria.

As in previous years, the majority of U.S. military members diagnosed in 2023 with malaria were men (92.3%), members of the active component (76.9%), and in the Army (69.2%). No cases from the Space Force nor Coast Guard were reported. Non-Hispanic Black service members and those under age 30 accounted for the most cases of malaria (79.5% and 35.9%, respectively) in 2023 **(Table 2)**.

Of the 21 malaria cases reported as RMEs in 2023, all were male and 15 were in the Army. Of these 21 cases, 17 were categorized as non-duty-related travel, of which 16 were considered acquired

TABLE 2. Malaria Cases by *Plasmodium* Species and Selected Demographic Characteristics, U.S. Armed Forces, 2023

	P vivax	*P falciparum*	Other/ Unspecified	Total	% Total	DMSS AC Reference Population[a] (Oct. 2023)	
						n	%
Total	2	21	16	39	100.0	2,102,128	100.0
Gender							
Male	2	20	14	36	92.3	1,699,479	80.8
Female	0	1	2	3	7.7	402,649	19.2
Age group, y							
<20	0	0	0	0	0.0	104,910	5.0
20-24	2	1	1	4	10.3	561,785	26.7
25-29	0	5	5	10	25.6	464,652	22.1
30-34	0	8	3	11	28.2	352,482	16.8
35-39	0	1	5	6	15.4	288,559	13.7
40-44	0	2	2	4	10.3	180,611	8.6
45-49	0	1	0	1	2.6	80,027	3.8
50+	0	3	0	3	7.7	69,102	3.3
Race and ethnicity							
White, non-Hispanic	1	1	3	5	12.8	1,159,050	55.1
Black, non-Hispanic	0	18	13	31	79.5	330,805	15.7
Other	1	2	0	3	7.7	235,945	11.2
Component							
Active	1	19	10	30	76.9	1,316,971	62.6
Reserve / Guard	1	2	6	9	23.1	785,157	37.4
Service							
Army	2	14	11	27	69.2	974,507	46.4
Navy	0	4	4	8	20.5	383,716	18.3
Air Force / Space Force	0	1	0	1	2.6	496,825	23.6
Marine Corps	0	2	1	3	7.7	201,964	9.6

Abbreviations: *P, Plasmodium*; DMSS, Defense Medical Surveillance System; AC, all components; y years.

[a] Data Source: Defense Medical Surveillance System (DMSS) as of Feb. 14, 2024 prepared by the Defense Health Agency.

in Africa. Non-Hispanic Black service members accounted for 13 of those non-duty cases.

During the 2014-2023 surveillance period, malaria cases attributed to Africa accounted for the greatest number of cases (n=178; 44.4%), followed by other/unspecified locations (n=87; 21.7%), Korea (n=66; 16.5%), Afghanistan (n=64; 16%), and South and Central America (n=6; 1.5%) **(Figure 2)**. The annual percentages of cases associated with Africa had the greatest variability, ranging from 34.5% in 2020 to 60.0% in 2021. From 2022 to 2023, the number of cases associated with Korea decreased the most, from 8 to 3. There was no case in Afghanistan in 2023.

Malaria cases were diagnosed or reported in 2023 from 22 different medical facilities in the U.S., Germany, Africa, and South Korea **(Table 3)**.

Over half of the malaria cases in 2023 were caused by *P falciparum* (53.8%; n=21). Of the 18 cases not attributed to *P falciparum*, 2 (5.1%) cases each were caused by *P vivax* and other *Plasmodia*, while 14 were labeled as associated with other or unspecified types of malaria (35.9%) **(Figure 1)**. This result reflects historical data over a 10-year surveillance period, where malaria cases caused by *P falciparum* have accounted for the largest number of cases (n=195; 48.6%) followed by *P vivax* (n=98; 24.4%), unspecified species (n=95; 23.7%), and other *Plasmodium* species (n=13; 3.2%). The annual percentages of cases attributed to *P vivax* during the surveillance period showed the greatest variability, ranging from 11.1% in 2022 to 51.7% in 2020.

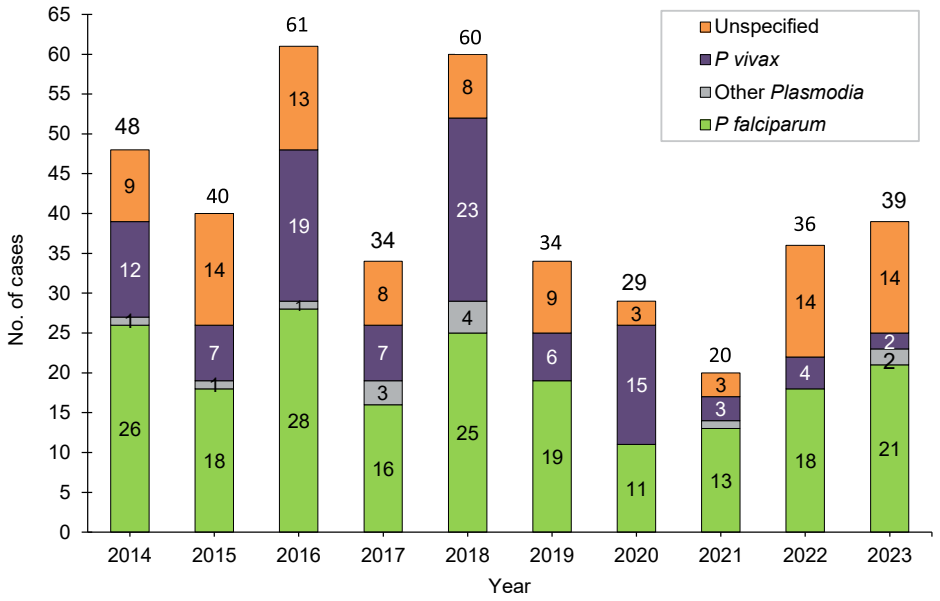
Most cases acquired in Africa were caused by *P falciparum* (65.0%; 13/20) **(Figure 3)**. Of the 20 malaria infections acquired in Africa in 2023, 3 each were linked to Djibouti and Sierra Leone; 2 were linked to Togo; 1 each were linked to Ghana, Côte d'Ivoire, and Nigeria; and 9 were associated with unknown African locations (data not shown).

Between 2014 and 2023, most non-*P vivax* malaria cases (67.1%) were diagnosed or reported during the 6 months from the Northern Hemisphere middle of spring through the middle of autumn (May–October) **(Figure 4)**. During the 10-year surveillance period, the proportions of non-*P vivax* malaria cases diagnosed or reported from May through October varied by region of acquisition: Korea (84.6%, 22/26), Afghanistan (84%, 21/25), Africa (67.8%, 116/171), and South and Central America (50.0%, 3/6) (data not shown).

Discussion

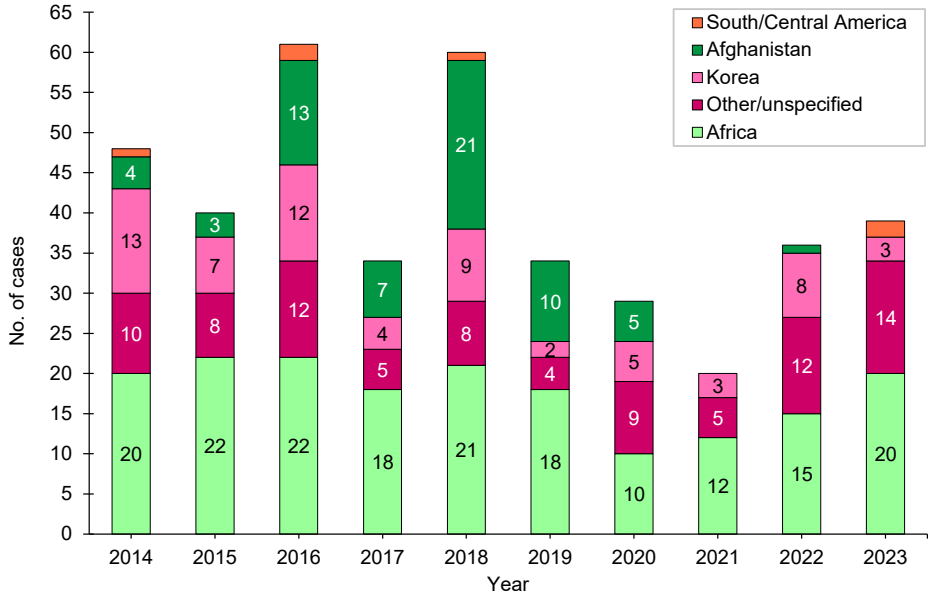
Malaria remains an important infectious disease threat to U.S. service members deployed to tropical and subtropical regions due to operational constraints it imposes, lack of compliance with currently available preventive measures, and continuing emergence of drug-resistant malarial parasites.[10] Although deployment-related exposures are targets for prevention, malaria poses a significant medical concern among service members who travel to malaria-endemic regions while on leave.[11,12]

FIGURE 1. Numbers of Malaria Cases by Species and Calendar Year of Diagnosis or Report, Active and Reserve Components, U.S. Armed Forces, 2014–2023



Abbreviations: *P, Plasmodium*; No., number.

FIGURE 2. Numbers of Malaria Cases by Location of Acquisition, Active and Reserve Components, U.S. Armed Forces, 2014–2023



Abbreviation: No., number.

In 2023 *P falciparum* was responsible for more than half of U.S. service member malaria cases, emphasizing the need for continued focus on prevention of the disease, given its potential severity and risk of death. Given that most RME-reported malaria infections occurred during non-duty-related activities and were acquired in Africa, it is important to effectively communicate malaria countermeasures to service members for both deployment and non-duty-related activities.

Several studies have reported low adherence with the recommended full course of prophylaxis and inadequate use of malaria chemoprophylaxis.[13-15] Among the information regarding malaria patients and adherence to chemoprophylaxis, premature discontinuation of recommended chemoprophylaxis regimen upon completion of travel was given as a reason for non-adherence.[8] Despite effective countermeasures against malaria and the success of mandatory chemoprophylaxis measures to prevent malaria, malaria infections will continue if service members do not adhere to the chemoprophylaxis necessary for its prevention. Completion of prophylaxis medication is necessary to prevent infection despite potential side effects. Efforts are needed to investigate side effects that may arise from these medications, for their effective mitigation, concurrent with efforts to identify factors that influence chemoprophylaxis adherence.

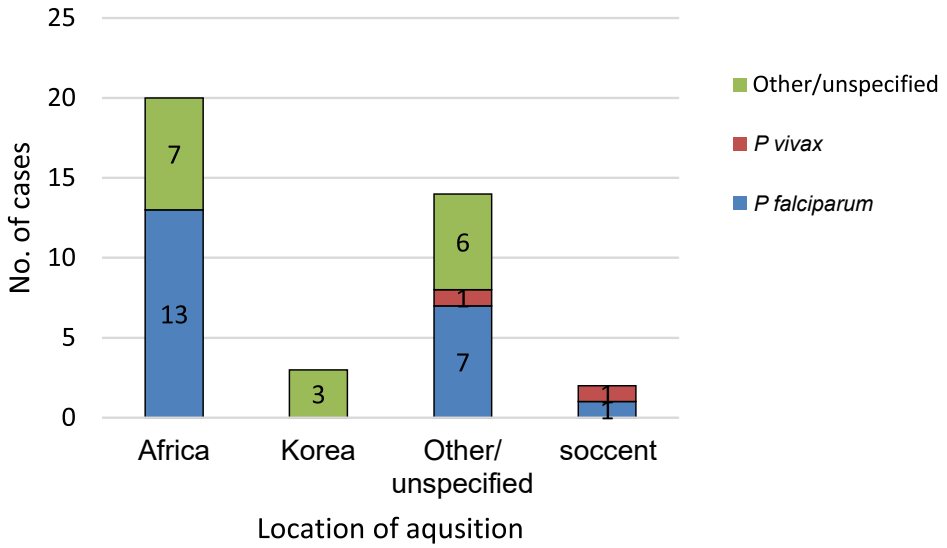
How risk management and prevention information is presented, and what specific or relevant information is provided, can have a greater impact on the knowledge, attitudes, and practices of deployed service members or travelers than basic information on what is prescribed.[8,16] It is also necessary to consider the perceived risk of malaria infection during travel so service members do not mistakenly believe they have residual or innate immunity because they are visiting relatives, or that malaria treatment is easier than its prophylaxis.[14] It is critical to explore more proactive approaches to assessing malaria risk and developing practical strategies according to identified risk factors to protect U.S. service members.[17]

Of particular concern is when foreign-born personnel travel on personal leave to their country of origin. A prior study demonstrated malaria rates 44 times greater for U.S. service members born in 7 western African countries than for those born in the U.S.[11] Leisure travel to certain African countries, as reported on notifiable medical event records, may account, at least in part, for the disproportionately high malaria rates observed among non-Hispanic Black service members in this report.

For service members visiting their birth countries in malaria-endemic regions, susceptibility due to loss of partial immunity from prior continuous exposure poses a substantial risk for infection and morbidity.[18]

Observations of seasonality in malaria diagnoses **(Figure 4)** indicate the need for more collaborative local and regional data collection efforts to quantify malaria seasonality and develop improved prevention strategies. Because *P falciparum* transmission is often seasonal, and a majority of non-*P vivax* malaria occurs during a 6-month period, from mid-spring to mid-autumn (May to October) in the Northern Hemisphere, accurate accounting of seasonality is important for informing efficient malaria control and treatment strategies.[19] Surveillance for elimination purposes demands integration of related data, for timely, targeted, and efficient resource

FIGURE 3. Numbers of Malaria Cases by Species Type and Location of Acquisition, Active and Reserve Components, U.S. Armed Forces, 2023



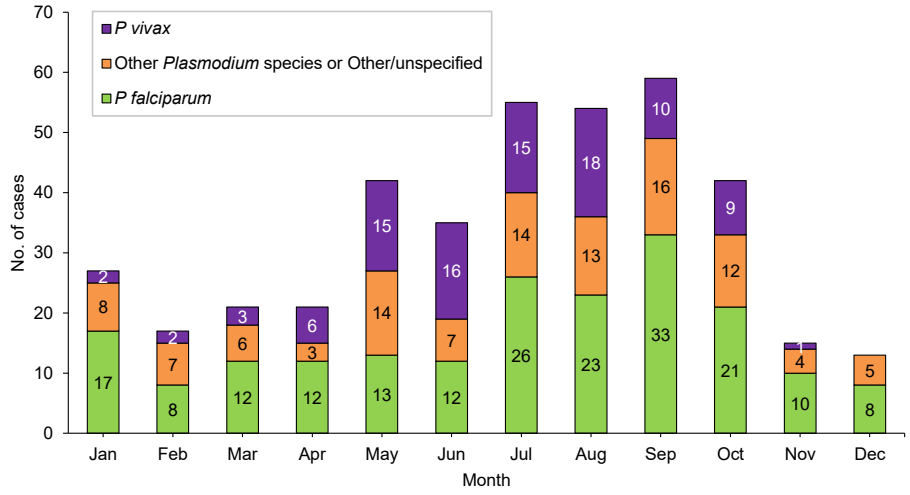
Abbreviations: No., number; *P, Plasmodium*; SOCCENT, Special Operations Command Central.

TABLE 3. Number of Malaria Cases by Geographic Location of Diagnosis or Report and Presumed Location of Acquisition, Active and Reserve Components, U.S. Armed Forces, 2023

Location Where Diagnosed or Reported	Korea	Afghanistan	Africa	South/ Central America	Other/ Unknown Location	Total	
	No.	No.	No.	No.	No.	No.	%
William Beaumont AMC, Fort Bliss, TX	3	0	2	0	0	5	12.8
Guthrie AHC, Fort Drum, NY	0	0	3	0	0	3	7.7
Womack AMC, Fort Liberty, NC	0	0	2	0	0	2	5.1
Carl R. Darnall AMC, Fort Cavazos, TX	0	0	2	0	0	2	5.1
NMC Portsmouth, VA	0	0	1	0	1	2	5.1
Lanstuhl Regional Medical Center, Germany	0	0	0	0	2	2	5.1
Expeditionary Medical Facility, Djibouti	0	0	2	0	0	2	5.1
Lyster AHC, Fort Novosel, AL	0	0	0	0	1	1	2.6
NMC San Diego, CA	0	0	1	0	0	1	2.6
Eisenhower AMC, GA	0	0	0	0	1	1	2.6
Martin ACH, Fort Moore, GA	0	0	0	1	0	1	2.6
Tripler AMC, HI	0	0	1	0	0	1	2.6
Walter Reed National MMC, MD	0	0	0	1	0	1	2.6
General Leonard Wood ACH, Fort Leonard Wood, MO	0	0	0	0	1	1	2.6
NMC Camp Lejeune, NC	0	0	1	0	0	1	2.6
Alexander T. Augusta MMC, Fort Belvoir, VA	0	0	0	0	1	1	2.6
Madigan AMC, Joint Base Lewis-McChord, WA	0	0	1	0	0	1	2.6
NHC Quantico, VA	0	0	1	0	0	1	2.6
Hohenfels AHC, Germany	0	0	1	0	0	1	2.6
DiRaimondo TMC, Fort Carson, CO	0	0	0	0	1	1	2.6
LaPointe AHC, Fort Campbell, KY	0	0	1	0	0	1	2.6
Henry L. Jenkins Medical Home, Camp Humphries, South Korea	0	0	1	0	0	1	2.6
Location not reported	0	0	0	0	6	6	15.4
Total	3	0	20	2	14	39	100

Abbreviations: No., number; AMC, Army Medical Center; AHC, Army Health Clinic; ACH, Army Community Hospital; NMC, Navy Medical Center; MMC, Military Medical Center; NHC, Naval Health Center; TMC, Troop Medical Center.

FIGURE 4. Cumulative Numbers of Malaria Cases by Species Type and Month of Clinical Presentation or Diagnosis, Active and Reserve Components, U.S. Armed Forces, 2014–2023



Abbreviations: *P, Plasmodium*; No., number.

deployment to prevent reintroduction of malaria to eliminated areas by mapping risk of receptivity and vulnerability.[20]

Limitations to this report should be considered when interpreting these findings. Malaria case documentation, especially for the reserve components as well as non-deployment-related exposures, is likely incomplete, leading to an underestimate of rates. Some cases treated in deployed or non-U.S. military medical facilities may not have been reported or otherwise ascertained at the time of this analysis. Malaria diagnoses recorded only in outpatient settings without confirmatory testing and not reported as notifiable events were not included. The geographic location where malaria was acquired was estimated from reported information; some cases had reported exposures in multiple malaria-endemic regions or areas, and others had no relevant exposure information. Personal travel or deployment within malaria-endemic countries was not accounted for unless specified in notifiable event reports. Limited information on species type in RME records reveals the need for greater attention on complete documentation of reportable conditions.

Military personnel frequently deploy to malaria-endemic regions, and most travel-related malaria cases occur due to non-compliance with preventive measures. Considering factors that can influence preventive measure compliance while promoting accurate awareness of malaria risk is critical. Positive perceptions of the necessity and efficacy of preventive measures, and appropriate reinforcement in relevant pretravel advice, are important elements for continued prevention of malaria transmission to U.S. service members.

Acknowledgments

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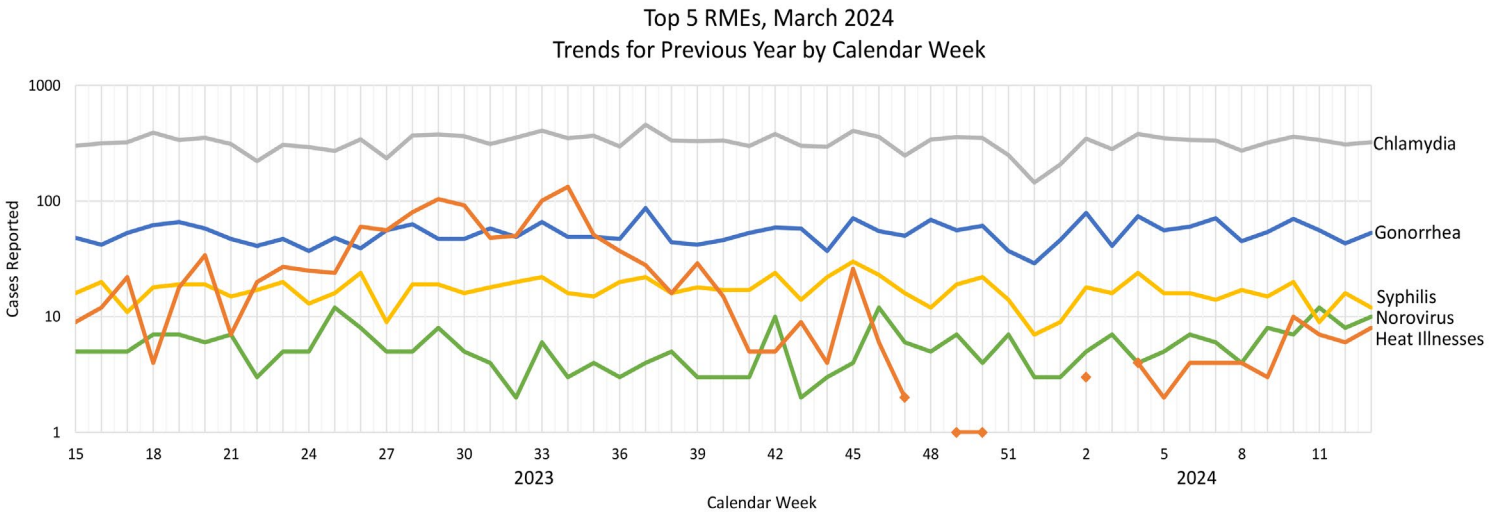
Reportable Medical Events at Military Health System Facilities Through Week 14, Ending April 6, 2024

Matthew W. R. Allman, MPH; Anthony R. Marquez, MPH; Katherine S. Kotas, MPH

TOP 5 REPORTABLE MEDICAL EVENTS BY CALENDAR WEEK, ACTIVE COMPONENT (APRIL 15, 2023 - APRIL 6, 2024)



Abbreviation: RMEs, reportable medical events.

Cases are shown on a logarithmic scale.

Note: There were 0 heat illness cases in the following weeks in 2023: 48, 51-52, and weeks 1 and 3 in 2024. Markers added to represent instances of heat illnesses that were not visible on the logarithmic scale graph.

Reportable Medical Events (RMEs) are documented in the Disease Reporting System internet (DRSi) by health care providers and public health officials throughout the Military Health System (MHS) for monitoring, controlling, and preventing the occurrence and spread of diseases of public health interest or readiness importance. These reports are reviewed by each service's public health surveillance hub. The DRSi collects reports on over 70 different RMEs, including infectious and non-infectious conditions, outbreak reports, STI risk surveys, and tuberculosis contact investigation reports. A complete list of RMEs is available in the *2022 Armed Forces Reportable Medical Events Guidelines and Case Definitions*.[1] Data reported in these tables are considered provisional and do not represent conclusive evidence until case reports are fully validated.

Total active component cases reported per week are displayed for the top 5 RMEs for the previous year. Each month, the graph is updated with the top 5 RMEs, and is presented with the current month's (March 2024) top 5 RMEs, which may differ from previous months. COVID-19 is excluded from these graphs due to changes in reporting and case definition updates in 2023.

For questions about this report, please contact the Disease Epidemiology Branch at the Defense Centers for Public Health–Aberdeen. Email: dha.apg.pub-health-a.mbx.disease-epidemiologyprogram13@health.mil

Authors' Affiliation: Defense Health Agency, Disease Epidemiology Branch, Defense Centers for Public Health–Aberdeen

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TABLE. Reportable Medical Events, Military Health System Facilities, Week Ending April 6, 2024 (Week 14)[a]

Reportable Medical Event[b]	Active Component[c]					MHS Beneficiaries[d]
	February 2024	March 2024	YTD 2024	YTD 2023	Total, 2023	March 2024
	no.	no.	no.	no.	no.	no.
Amebiasis	1	4	5	3	15	1
Arboviral diseases, neuroinvasive and non-neuroinvasive	0	0	0	0	2	0
COVID-19-associated hospitalization and death[e]	7	0	14	56	113	43
Campylobacteriosis	8	19	44	61	268	8
Chikungunya virus disease	0	0	0	1	2	0
Chlamydia trachomatis	1,347	1,397	4,162	4,786	17,496	211
Cholera	0	1	1	1	4	0
Coccidioidomycosis	8	5	19	8	36	1
Cold weather injury[f]	41	8	114	88	148	N/A
Cryptosporidiosis	15	3	22	18	67	1
Cyclosporiasis	0	0	0	0	15	0
Dengue virus infection	0	1	2	1	7	1
E. coli, Shiga toxin-producing	2	2	7	4	70	4
Ehrlichiosis/anaplasmosis	0	0	0	0	28	0
Giardiasis	4	10	26	15	79	3
Gonorrhea	241	234	750	728	2,761	35
Haemophilus influenzae, invasive	0	0	0	0	1	2
Hantavirus disease	0	0	0	0	2	0
Heat illness[f]	14	32	55	79	1,255	N/A
Hepatitis A	0	0	1	2	8	0
Hepatitis B, acute and chronic	13	5	29	47	154	14
Hepatitis C, acute andchronic	6	2	12	21	52	3
Influenza-associated hospitalization[g]	8	4	30	5	29	10
Lead poisoning, pediatric[h]	N/A	N/A	N/A	N/A	N/A	9
Legionellosis	3	0	3	1	5	0
Leishmaniasis	0	0	0	1	1	0
Leprosy	0	0	0	0	2	0
Leptospirosis	0	0	0	2	4	0
Lyme disease	2	3	12	15	70	2
Malaria	0	1	3	6	28	1
Meningococcal disease	0	0	0	1	4	0
Mpox	0	0	0	0	4	0
Mumps	0	0	0	0	0	1
Norovirus	25	41	87	208	419	61
Pertussis	1	2	5	1	15	0
Post-exposure prophylaxis against Rabies	34	38	127	134	598	27
Q fever	0	0	0	1	2	0
Rubella	0	0	0	2	2	0
Salmonellosis	6	6	20	14	129	12
Shigellosis	4	3	10	13	59	3
Spotted fever rickettsiosis	0	0	0	12	31	0
Syphilis (all)	69	60	202	259	945	13
Toxic Shock Syndrome	0	1	2	1	2	0
Trypanosomiasis	0	0	1	1	1	0
Tuberculosis	0	0	1	2	11	0
Tularemia	1	0	1	0	1	0
Typhoid fever	0	0	0	0	2	0
Typhus fever	0	0	1	1	3	1
Varicella	0	0	4	1	12	4
Zika virus infection	0	0	1	0	0	0
Total case counts	1,860	1,882	5,773	6,600	24,962	471

Abbreviations: MHS, Military Health System; YTD, year to date; no., number; N/A, not applicable; COVID-19, coronavirus disease 2019; E., Escherichia; RME, reportable medical event; DRSi, Disease Reporting System internet; AD, active duty; FMP, family member prefix.

[a] RMEs reported through the DRSi as of Apr. 30, 2024 are included in this report. RMEs were classified by date of diagnosis, or where unavailable, date of onset. Monthly comparisons are displayed for the period of Feb. 1, 2024-Feb. 29, 2024 and Mar. 1, 2024-Mar. 31, 2024. YTD comparison is displayed for the period Jan. 1, 2024-Mar. 31, 2024 for MHS facilities. Previous year counts are provided as the following: previous year YTD, Jan. 1, 2023-Mar. 31, 2023; total 2023, Jan. 1, 2023-Dec. 31, 2023.

[b] RME categories with 0 reported cases among active component service members and MHS beneficiaries for the periods covered were not included in this report.

[c] Services included in this report include Army, Navy, Air Force, Marine Corps, Space Force, and Coast Guard, including personnel classified as FMP 20 with duty status of AD, Recruit, or Cadet in DRSi.

[d] Beneficiaries included individuals classified as FMP 20 with duty status of Retired and individuals with all other FMPs except 98 and 99. Civilians, contractors, and foreign nationals were excluded from these counts.

[e] Only cases reported after case definition update on May 4, 2023. Includes only cases resulting in hospitalization or death. Does not include cases of hospitalization or death reported under the previous COVID-19 case definition.

[f] Only reportable for active component service members.

[g] Influenza-associated hospitalization is reportable only for individuals under 65 years of age.

[h] Pediatric lead poisoning is reportable only for children aged 6 years or younger.

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