MSMR

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30TH ANNIVERSARY ISSUE

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Medical Surveillance for Military Readiness

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The Medical Surveillance Monthly Report: The First 30 Years

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In April 1995 the inaugural issue of the *Medical Surveillance Monthly Report* declared, "If the *MSMR* is not useful to its readers, it will have no value."[1] Throughout its 30-year history, *MSMR* has continuously sought to improve its content with the ultimate goal of providing its readers with unbiased, scientifically rigorous, evidence-based information on the current status, trends, and determinants of the physical and mental health of U.S. military service members. Empowering military public health leaders with timely access to militarily relevant routine and specialized reports positions them to identify and contain outbreaks, understand disease burden, guide policy changes, and evaluate and improve prevention and control strategies. *MSMR*'s utmost priority is publishing articles and summary data directly relevant to the health, safety, well-being, and military operational fitness of the members of the U.S. military.

On the first page of the first issue of *MSMR*, executive editor John Brundage, MD, MPH, articulated the new journal's objectives as "medical surveillance information of broad interest…The ultimate goal…is to provide…information necessary to inform, motivate, and empower commanders, their surgeons, and medical staffs to design, implement, and resource programs that enhance health, fitness, and readiness."[1]

The need for a publication like *MSMR* was evident in the early 1990s due to the lack of dissemination of routine periodic medical surveillance in the U.S. military, exacerbated by the cessation of publication of service-specific surveillance reports including *Health of the Army* and *Statistics of Navy Medicine* in the late 1980s. In addition, at the time there were no ready nor centrally available sources of timely and reliable information on extant medical threats, and published insights on medical situational awareness were generally out of date, incomplete, and largely uninformative. In its formative years, one of *MSMR*'s core functions was to report routine monthly surveillance statistics not otherwise readily available to intended readership.

MSMR was also intended to emulate, for the U.S. military, the *Morbidity and Mortality Weekly Report (MMWR)* published by the U.S. Centers for Disease Control and Prevention (CDC). Like *MMWR*, *MSMR* is a mechanism to disseminate public health data and reports targeted principally to military public health professionals, in addition to military commanders, leaders and policy-makers, as well as the scientific and lay press. Dissemination is a core function of public health surveillance, defined by the CDC as "the ongoing, systematic collection, analysis, and interpretation of health data, essential to the planning, implementation and evaluation of public health practice, closely integrated to the dissemination of these data to those who need to know and linked to prevention and control."[2]

A key difference between civilian and military public health surveillance is the military's focus on force health protection and medical readiness, along with communication of health threats to military commanders.[3] This focus has driven *MSMR*'s desire to provide unbiased, scientifically rigorous, and evidence-based estimates of the incidence, distribution, impact and trends of illness, injury, and other health threats to the physical and mental health of U.S. military members, as well as drawing attention to conditions that are "high burden" for the military and have an associated effect on the health of the force.

MSMR represented one of the first and most widely visible products of the U.S. Army Center for Health Promotion and Preventive Medicine (USACHPPM). Initially, *MSMR* primarily reported Army-specific surveillance summaries of hospitalizations; notifiable diseases (i.e., reportable medical events); counts, rates, and trends of illnesses and injuries of surveillance interest (e.g., acute respiratory illness, sexually transmitted infections, heat and cold related injuries); and field reports of outbreaks and medical events of interest to military medical staffs and commanders. *MSMR*, however, rapidly grew and evolved prompted both by increases in the type and sources of data available for analyses, as well as a desire to provide more complex analyses to help interrogate threats to the health of the force.

During *MSMR*'s relatively short lifespan, the military health data infrastructure has grown in extraordinary ways. These three decades have produced remarkable advancements in comprehensive notifiable disease reporting, expansion of deployment-related health care, and more complete capture of health care provided to military service members and beneficiaries, including incorporation of prescription drug data, laboratory tests and results, immunizations, mortality data, and an extensive array of periodic and time-sensitive health assessments.

When *MSMR* began publishing in 1995, comprehensive and reliable health surveillance data for all services were not routinely transmitted nor stored in a centralized repository, as they were for the U.S. Army in USACHPPM's newly established Army Medical Surveillance Activity (AMSA). By the following year, however, AMSA had begun receiving monthly personnel rosters of all members of all services, retroactively to 1990. In 1997, this comprehensive database transitioned into the Defense Medical Surveillance System


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Data in the MSMR is provisional, based on reports and other sources of data available to the Medical Surveillance Activity. Notifiable conditions are reported by date of onset (or date of notification when date of onset is absent). Only cases submitted as confirmed are included.


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100TH ISSUE

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MEDICAL SURVEILLANCE MONTHLY REPORT

Annual Summary Issue

A publication of the Armed Forces Health Surveillance Center

(DMSS) and began routine receipt of health surveillance data from sources throughout the Department of Defense (DOD). These data were critical for ascertaining and calculating timely and accurate counts, rates and trends in illness and injury for all members of all services.

This evolution in health surveillance reporting led to the creation, in 2002, of the first *MSMR* report evaluating the morbidity burden of illnesses and injuries to the U.S. Armed Forces: "Relative Burdens of Selected Illnesses and Injuries, U.S. Armed Forces, 2001." Using a modification of the classification system developed by the Global Burden of Disease Study,[4] the report and its accompanying data tables provided a means of summarizing the annual numbers of medical encounters, hospital bed days, and unique individuals affected using the inpatient, outpatient, and personnel records available in the DMSS. This report evolved into *MSMR*'s annual issue that provides updated summaries of all hospitalizations, outpatient visits, medical evacuations, deployed medical care, and morbidity burdens of illnesses and injuries among members of the U.S. Armed Forces, as well as non-service member beneficiaries of the Military Health System (MHS).

The annual burden of health care issue highlights an example of *MSMR* analyses that presage issues of military medical importance. Well before post-traumatic stress disorder (PTSD) and traumatic brain injury (TBI) were recognized as "signature wounds" of the wars in Afghanistan and Iraq, *MSMR* was highlighting the importance of mental disorders, including mood disorders and adjustment reactions, and musculoskeletal injuries, including injuries of the head and neck, as major sources of morbidity, lost duty time, and health care use among military members.[5]

Like the rest of the U.S. military, *MSMR* was challenged to respond to the events of September 11, 2001, and the war that ensured over the following decade. In response, *MSMR* initiated reports documenting illnesses including heat and cold injuries, PTSD, malaria, and leishmaniasis, as well as injuries such as traumatic amputations and traumatic brain injuries associated with service in combat zones.

The February/March 2007 edition of *MSMR* marked its 100th issue, and through its initial 12 years of publication, *MSMR* had disseminated approximately 240 reports of surveillance findings and results of preventive interventions; 50 reports of outbreaks, of which approximately 80% were on infectious diseases; and 40 case and case series reports, of which approximately 85% were on infectious diseases.[6] The editorial leading the 100th issue milestone highlighted the "…steady stream of unimaginable events with profound military medical significance" since the publication of the first issue:

> …including the initiation and conduct of U.S. military operations in the Balkans; terrorist attacks on the United States (including the Pentagon) on 11 September 2001; the initiation and conduct of the global war on terrorism; widespread uses of vaccines for military-specific indications, including smallpox, anthrax, and tick-borne encephalitis; outbreaks of 'mysterious' illnesses with unknown causes among deploying/deployed U.S. troops; life-threatening hyponatremia from excessive water consumption in heat stressful conditions; the reemergence of vivax malaria along the demilitarized zone in Korea; the loss of vaccines against adenovirus types 4 and 7—and the reemergence of adenoviruses as significant causes of acute respiratory disease among military recruits; interrupted supplies of benzathine penicillin for preventing severe group A beta hemolytic streptococcal diseases among recruits; uses of the DOD

Serum Repository for health surveillance, policymaking, and medical research purposes; outbreaks of community-acquired methicillin-resistant *S. aureus* (MRSA), particularly among recruits; routine health assessments before and after overseas deployments; numerous combat casualties, illnesses, and non-battle injuries during service in Afghanistan and Iraq, including wounds from conventional and improvised munitions, accidents, and endemic and nosocomial infections (e.g., leishmaniasis, malaria, multiple drug resistant *Acinetobacter baumanii*); greater appreciation of the scopes and consequences of post-traumatic stress reactions and emerging infections; and many others.[6]

The 100th issue of *MSMR* also foreshadowed its coming evolution as the publication of record for the Armed Forces Health Surveillance Center (AFHSC), the precursor of today's Armed Forces Health Surveillance Division (AFHSD). The AFHSC was established by the Deputy Secretary of Defense in 2008[7] through the combination of the resources of legacy organizations AMSA, the DOD Global Emerging Infectious Disease Surveillance and Response System (DoD-GEIS), and the Global Health Surveillance Activity supporting the Force Health Protection Directorate in the Office of the Assistant Secretary of Defense for Health Affairs. AFHSC was charged with promoting, maintaining, and enhancing the health of U.S. military and military-associated populations, through relevant, timely, actionable, and comprehensive health surveillance information.[7] The establishment of the AFHSC represented a consolidation of DOD efforts to improve health surveillance capabilities throughout all services.

MSMR's rapid evolution during this time included a broader scope concurrent with its new emphasis on all services, while continuing to publish surveillance analyses on topics that were militarily important, timely, and relevant. Subject areas with high priority for *MSMR* attention included health threats associated with military training and operations; effects of force health protection measures; and other specific concerns of military members and their families, advocacy groups, politicians, the popular press, and others. *MSMR*'s focus on deployment health issues sharpened during periods of high operational tempo.

The creation of the AFHSC and the continued development of its extensive data warehouse, DMSS, with its broad analytic capabilities, facilitated *MSMR*'s ability to provide routine surveillance statistics regularly for a wide variety of health leaders and epidemiologists. *MSMR* content continued its expansion to include in-depth surveillance analyses pertaining to diverse populations, trends over multi-year periods, and risk factors for diseases and injuries of particular interest. Because readers and the combatant commands expressed interested in topics such as hospital-acquired infections, dental readiness, physical fitness data, for example, not able to be addressed using DMSS databases alone, *MSMR* encouraged more submissions from outside sources with access to other data sets or responsibility for disease and injury prevention research or epidemiological investigations. Additional changes included a new appearance, more widespread distribution, and improved accessibility via a new website.[6]

In 2011, *MSMR* applied and was accepted for indexing in MEDLINE, the principal online bibliographic citation database of the National Library of Medicine's MEDLARS® system. The acceptance of *MSMR* for indexing in MEDLINE validated its evolution and development as an evidence-based peer-reviewed journal. To be accepted to MEDLINE, *MSMR* was evaluated on its scientific policy and quality, and found to have sufficient merit for inclusion in the database. This independent designation formally distinguished *MSMR* content as fundamentally different from routine reports or *ad hoc* requests produced by AFHSD. It also further expanded the scope and reach of its content and increased the number and quality of external submissions to *MSMR*.

The establishment of the Defense Health Agency (DHA) in 2013 formally consolidated the medical services of all branches of the U.S. military, which included integration of all U.S. military public health surveillance activities. These integration efforts reinforced *MSMR*'s focus on reporting results for all service branches. As a result, *MSMR* established an editorial advisory board of leaders from all military services. The advisory board continues to be a key part of *MSMR*'s continuous quality improvement efforts and an important element of ensuring key stakeholder involvement and input.

Two years later, *MSMR*'s April 2015 issue marked its 20th anniversary. The editorial leading that issue highlighted several elements that were instrumental in its progress to that point, including "unprecedented support of military force health protection and health surveillance initiatives and unimaginable advances in telecommunications and information management/data warehousing technologies."[8]

Over the past decade, *MSMR* has continued to explore ways to expand and improve its content and make it more readily usable to readers. *MSMR* increased its production of thematic issues and made significant efforts to engage subject matter

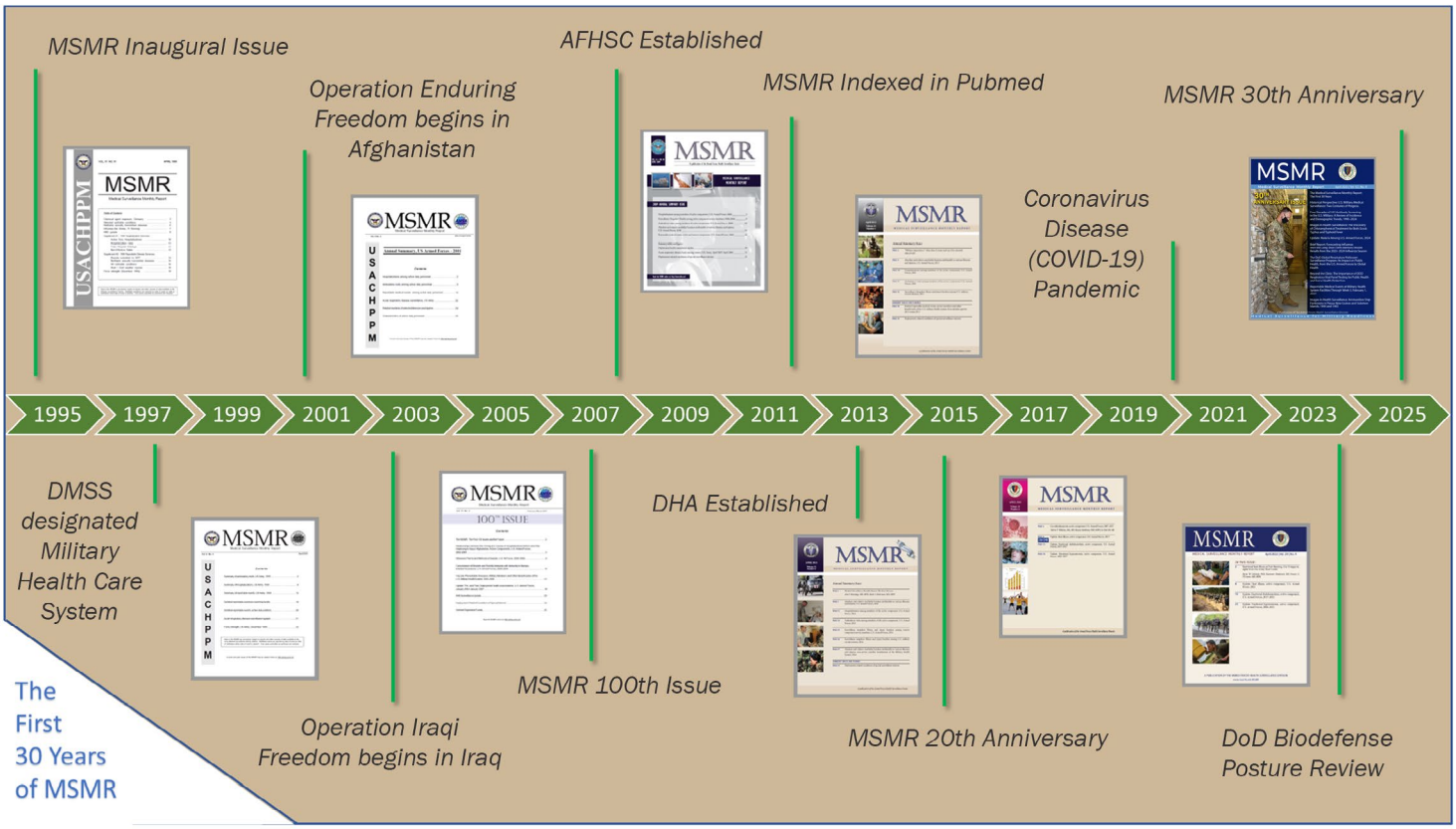
To emphasize the potential impacts of MSMR's published surveillance data and new findings on force health protection and readiness, MSMR reformatted its layout in November 2018, introducing new text boxes for full reports that briefly summarize their new findings—"What are the new findings?"—in addition to placing those findings in context—"What are the implications for force health protection?"—following the general abstract.

experts throughout the MHS, for submissions of reports on thematic issues in addition to invited editorials that contextualized surveillance findings. These thematic issues have focused on a wide range of subjects including women's health, mental and behavioral health, heat- and cold-related injuries and illnesses, sexually transmitted infections, gastrointestinal infections, vision-related conditions, and a Global Emerging Infections Surveillance (GEIS)-themed issue with surveillance reports from GEIS partners.

A review published in the January 2024 issue of *MSMR*[9] summarized the journal's content over the preceding 5 years and presented areas of interest for future *MSMR* submissions including, but not limited to, topics related to improving biodefense posture consistent with the 2023 DOD Biodefense Posture Review; submissions in the area of pharmacoepidemiology, utilizing the data from the Pharmacy Data Transaction Services (PDTS); and outbreak and field reports, primarily with significance beyond the setting in which they occurred. This review also lists the 10 most-read articles on the *MSMR* website during the 5-year period. Notably, 2 of the most-read articles—on heat injury and routine screening for antibodies to HIV—represent reports that were some of the earliest developed by *MSMR* and published annually. Also significant is that 3 of the articles were co-authored by military preventive medicine residents during their rotations at the AFHSD, highlighting a little known but valuable synergy with preventive medicine residency training at the Uniformed Services University for Health Sciences.

MSMR staff has contributed further significant value to the MHS in the development and dissemination of standardized case definitions for health surveillance. *MSMR* editorial staff, in consultation with other AFHSD epidemiologists and other MHS subject matter experts, has helped develop over 100 standardized case definitions designed for use with administrative health care data derived from the U.S. military electronic health record and contained in the DMSS and other available datasets. Many (although not all) of these case definitions are readily accessible to other public health and epidemiological researchers via the surveillance case definition website on the AFHSD Epidemiology and Analysis website.[10] Case definitions are regularly reviewed and updated by the Surveillance Methods and Standards (SMS) Working Group of the AFHSD. This provides a valuable resource that furthers the goal of increasing standardization in surveillance methods and practices throughout the DHA.

The future of *MSMR* will undoubtedly benefit from increasingly modernized public health data infrastructure and data analysis and integration capabilities. Unprecedented access to this extensive and expanding network of data, along with advanced forecasting and data analytics, will allow *MSMR* to continue its long-standing role in providing timely access to reports on population-based morbidity, risk assessments, vaccine adverse effects, emerging threats, deployment surveillance, policy effects, serological surveys, and



sero-epidemiological research.[11] *MSMR* analyses are regularly referenced in reports developed for and used by governmental agencies to inform policy-makers throughout the U.S. Government, including the Congressional Research Service[12-14] and the United State Government Accountability Office,[15] demonstrating *MSMR*'s utility and reach as a readily accessible, accurate, and useful source of health surveillance information.

As *MSMR* enters its 31st year, its editorial staff aims to continue its tradition of excellence while making its content more clinically relevant, continuing to increase collaboration with external agencies and individuals, publishing topics of military relevance, and making practical military-specific recommendations based on sound scientific evidence.

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Historical Perspective

U.S. Military Medical Surveillance: Two Centuries of Progress

Sanders Marble, PhD

The U.S. Army began coordinated medical surveillance over 200 years ago. The earliest records of the U.S. military medical corps are incomplete, in no small part due to the British burning of official buildings in Washington in 1814, but it is verifiable that regular reporting of medical information about Army personnel occurred at least as early as 1814.[1]

In 1818, following post-War of 1812 reorganization of the U.S. Army, its first official Surgeon General, Joseph Lovell, ordered all Army surgeons to regularly report on the diseases they treated. Those early medical reports ordered by Lovell were completed monthly, then compiled and sent quarterly to Washington, DC. With horses the fastest, but exhaustible, means of communication, there was no chance of prompt response to news of an outbreak in any remote area. Disease monitoring had severe limits, because treatment was limited by the communication technologies of the time. Even if information could be advanced relatively rapidly, sick patients transported over dirt roads to hospitals with no better diagnostic tools nor treatment methods would likely experience worse outcomes. Coastal forts and posts in the eastern seaboard would generally be properly provisioned, but resources for isolated garrisons in frontier areas were more limited.

Discerning patterns in disease incidence has direct utilitarian purpose for military forces, but in the nineteenth century officials were also looking to acquire as much information as they could about the vast expanse of continent across which the U.S. was expanding. In 1818 Louisiana was the only state that had been established west of the Mississippi River. In 1804 President Thomas Jefferson had dispatched Lewis and Clark to explore the Louisiana Purchase, with other expeditions exploring the west for decades. The medical reports compiled by the U.S. Army were part of this era of exploration. In addition to information on diagnoses, Surgeon General Lovell also required information on weather conditions from Army surgeons. "The influence of weather and climate upon diseases, especially epidemic, is perfectly well known," declared Lovell. Collation of meteorological data could potentially validate the current miasmatic theory of disease, but such data also provided valuable information about the greater continent. Lovell was already publishing meteorological data in 1826, with more data published in 1840.[2,3]

Monthly medical and meteorological reports continued to be required by the Army for decades in the nineteenth century. Compliance by surgeons seems high. Lovell's successor, Thomas Lawson, continued publishing health and meteorological data through 1860,[4,5] but routine reporting of weather data to Army headquarters was disrupted by the Civil War.

There was little need for redundant reports from units in the same place during the Civil War. Both health and weather condition reporting were often consolidated at a higher headquarters. A report, *Sickness and Mortality of the Army during the First Year of the War*, covering July 1861-June 1862, published by Surgeon General Joseph Barnes, mentions monthly reporting and strongly implies that medical officers were not being punctual nor accurate with their reports.[6] Recently volunteered doctors unfamiliar with U.S. Army reporting practices, lacking the discipline of regular officers to submit monthly reports, likely had lower compliance rates (George Wunderlich, email communication, Oct. 2024).

In the decades following the Civil War, Army reports on sickness could be both truthful and useless simultaneously. Before the acceptance of germ theory, few diseases could be differentiated. Regardless of diagnosis, there were few effective medicines, so an accurate or inaccurate diagnosis (in modern terms) made little impact on treatment or outcomes.

The Surgeon General's annual report to the Secretary of War, which was conveyed to Congress, would typically detail the number of admissions to hospital per thousand, as a broad indicator of force health. In 1884, diseases began to be grouped in the Surgeon General's report **(Figures 1a-1c)**.[7] During the ensuing decade, statistical comparisons became routine. In 1887 disease reports were further divided by geographic region. In 1888 diseases began being numbered—the predecessor of International Classification of Diseases codes—and by 1890 there was enough international agreement that the U.S. Army could compare its morbidity and mortality experience with foreign forces. By 1895, the Army was reporting its data based on the "diseases of the international nosological table."[8]

By the close of the nineteenth century, the electric telegraph and railroads were widespread, allowing not only information but material to flow quickly. Patients as well as extra medical personnel could be moved, if necessary. A degree of local surveillance of conditions occurred, with alarming data rapidly reported to the Surgeon General's Office in Washington.

The Spanish-American War (April-December 1898) was the first major conflict fought by the U.S. in the era of germ theory. Disease was a significant problem during the war, with outbreaks of typhoid within the U.S. and malaria and yellow fever infecting troops in the Caribbean and South Pacific. By that time, the essentials of public health practice were being taught at the Army Medical School, now the Walter Reed Army Institute of Research, which was established in 1893.

FIGURE 1a. The Army interrogated its data to determine rates of incidence over time, regional rates, any racial differences, and establish international comparisons.

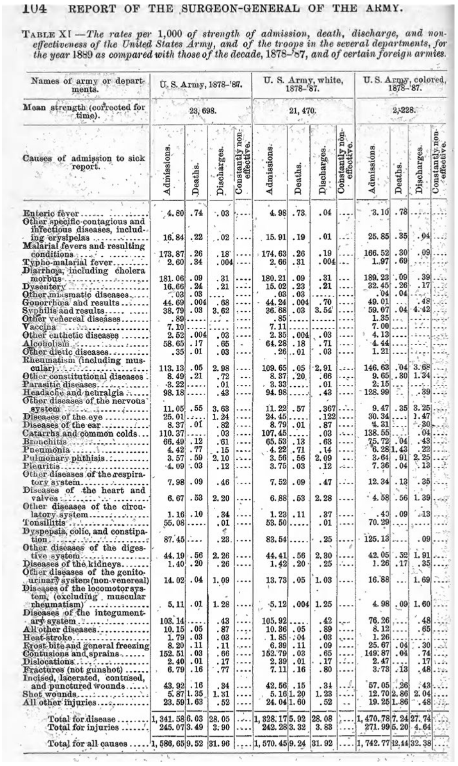


FIGURE 1b. The Army further stratified its data to understand seasonal patterns in disease incidence and severity, for the force as a whole and regionally (not shown).

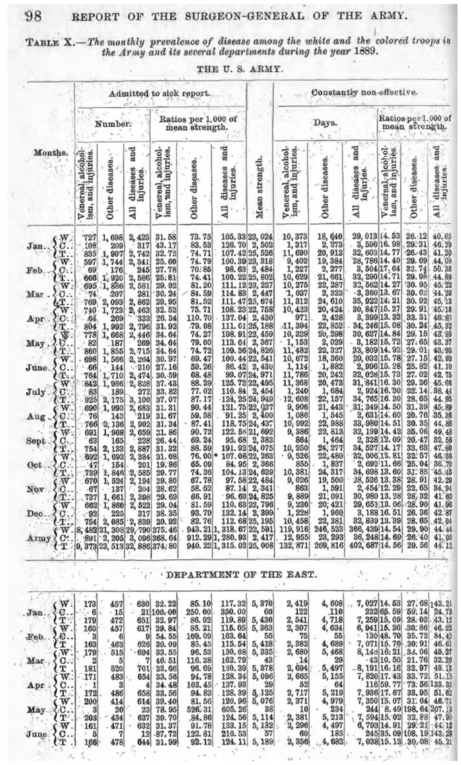
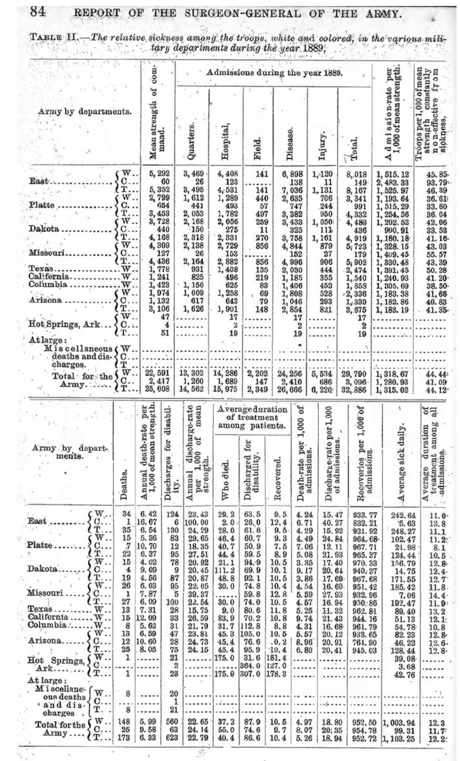


FIGURE 1c. The Army also examined its data to evaluate disease burden quantity and severity by U.S. region.



Typhoid was endemic in the U.S. but became a scandal due to outbreaks at numerous Army encampments. A typhoid outbreak at Camp Thomas, outside Chattanooga, Tennessee, in 1898, was serious enough for Surgeon General George M. Sternberg to send a research team—of Walter Reed, Victor Vaughan, and Edward Shakespeare—to investigate it. Neither the groundbreaking scientific research by that trio, nor the statistics of the outbreak were published quickly: Statistics were still published within annual reporting, and the team's research was not published until 6 years later, in 1904, after Reed's and Shakespeare's deaths.[9]

From 1913 until 1918, the Army Medical Department published a medical bulletin at uneven intervals, with 11 issues published in 6 years, apparently more a means of publishing research that was too long to be published in article form. By early 1918 the bulletin was focused solely on reconstruction, the term during that period for rehabilitation, anticipating wounded American soldiers' departure from the military hospital system and return to civilian life.[10] The 1918 iteration of the Army bulletin lasted only 4 issues, ending in late May, after which the Army apparently only published annual reports, either for internal or external audiences.

The following year, in December 1919 a twice-monthly newsletter, *Medico-Military Review*, began disseminating "information bearing upon the problems of disease control."[11] Produced by the Division of Laboratories and Infectious Diseases, the *Review* was intended for internal audiences but was mailed to civilians who requested it. In the wake of the influenza pandemic, disease was a more salient topic for the Army, and the Military Intelligence Division of the General Staff was in close contact with the Surgeon General's Office about epidemics, and the Chief of Staff of the Army was briefed weekly on communicable diseases.[12]

The *Medico-Military Review* published for over 2 years, until the advent of the *Army Medical Bulletin* in 1922. While there was mention of a "Medico-Military Review Section" of the *Bulletin*, there is no evidence such a section manifested.[13] For the next 2 decades, until World War II, surveillance data were available internally for outbreak responses, and annual data were published, but with no greater frequency.

After the first full year of combat in World War II, in 1943 the Army began publishing the *Monthly Progress Report*, which included a medical section. The medical section soon became lengthy enough that it was published separately, although still titled as part of the *Monthly Progress Report*. The medical section of the *Report* included surveillance information in addition to short articles on medical experiences in particular battles and campaigns, as well as particular diseases. In wartime this medical information had a security classification, albeit the second lowest.

After the war, the *Monthly Progress Report* transitioned to *Health of the Army*, and continued publishing monthly **(Figure 2a)**. It is unclear what element of the Surgeon General's Office produced this post-war reporting, which amalgamated data

reported to, and analyzed by, several sections. In the early 1950s the report ceased publishing articles that provided medical analysis, other than occasional "diseases of special interest," and *Health of the Army* published purely surveillance data, overseen by the Patient Administration Systems and Biostatistics Activity. *Health of the Army* ceased publication at the end of 1988, but its last analytical article had appeared decades earlier, and it had evolved into a proto-dashboard of data—but published monthly, printed, and mailed.

During the 20th century the U.S. Navy published some medical data in annual reports and published a monthly *Naval Medical Bulletin*, from 1907 to 1949, which was replaced by *Statistics of Navy Medicine*, from 1945 until 1989 **(Figure 2b)** (Andre Sobocinski, email communication, Oct. 2024). The U.S. Air Force published some medical data in annual reports, in addition to internal disease surveillance (Joseph Frechette, email communication, Oct. 2024).

The nature of medical surveillance changes continuously, but the value in gathering, analyzing, and disseminating available data is constant. Different types and forms of data have been useful during different time cycles, whether for responding to a particular outbreak or investigating disease patterns over years. Throughout history, publishing and distribution patterns have been dictated by the relative rapidity of available data transmission. Whatever the limitations of current medical understanding, data collection and analysis, and available publishing and distribution, the U.S. military has consistently utilized the best data it could collect, analyze, and disseminate, to not only protect the health and lives of its personnel, but to improve current medical knowledge and practice, in addition to advancing scientific discovery.

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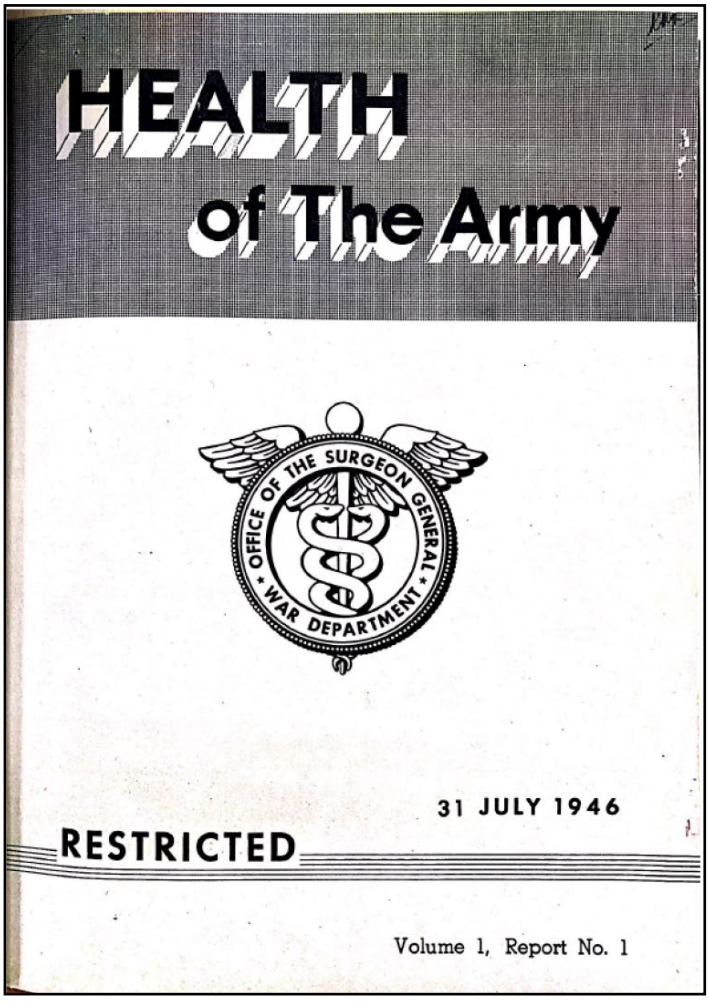
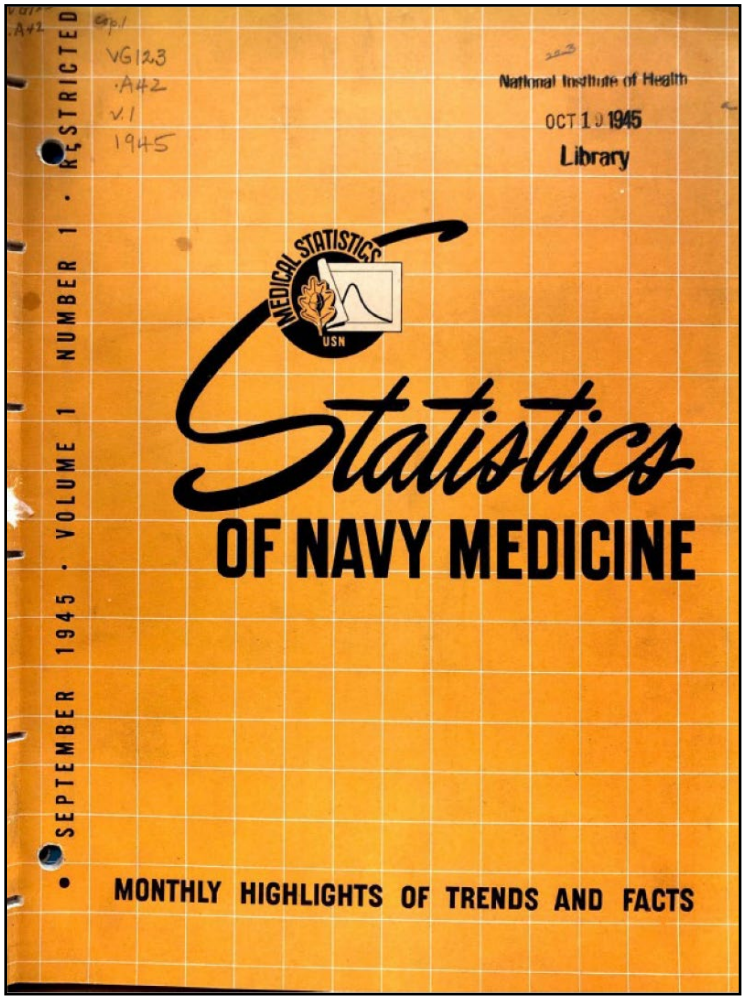
FIGURES 2a and **2b**. Inaugural Issues of and *Health of the Army* (1946) and *Statistics of Navy Medicine* (1945)





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Four Decades of HIV Antibody Screening in the U.S. Military: A Review of Incidence and Demographic Trends, 1990–2024

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Since 1985 the U.S. military has conducted mandatory HIV antibody screening of active and reserve members of the Armed Forces.[1,2] By 1990, all service members had been tested at least once, and routine screening primarily detected recent HIV infections.[3] *MSMR* began publishing summaries of HIV rates and trends in the U.S. military 10 years after screening began, in 1995.[4]

In the initial years, routine screening detected both prevalent and incident HIV infections, with the rate of new HIV diagnoses among active duty U.S. Army members reported as high as 283 cases per 100,000 persons tested in 1985-1986.[4] With Department of Defense (DOD) policies barring HIV-positive individuals from entering or serving in the military, initial control efforts led to a precipitous drop in the rate of new HIV diagnoses in the active component, to approximately 30 cases per 100,000 individuals during the 1990s.[3,5] By the 2000s, overall rates of new HIV diagnoses continued to decline, albeit slowly, subsequently stabilizing during the following 2 decades, within a range of 20-25 new cases per 100,000 individuals tested, or approximately 350 to 400 new infections annually.[6] This marked decline and stabilization within a decade and a half evidences the success of the U.S. military HIV program in controlling HIV spread and maintaining low rates of infections within its ranks.[5,6]

In 2004, the DOD adjusted the standard HIV testing interval from annual to biennial.[7] Reflecting evolving screening practices and shifts in the epidemiological profile of HIV cases, in 2005 *MSMR* began summarizing HIV rates and trends starting from 1990. In 2011, *MSMR* shifted to reporting summary HIV rates for the most recent 5.5 years, reflecting the stabilization of seropositivity rates and advancements in HIV treatment that established HIV as a chronic, manageable condition.[7,8]

Despite significant efforts to further reduce HIV incidence, including the introduction and scaling of pre-exposure prophylaxis (PrEP) in 2012, the repeal of the "Don't Ask, Don't Tell" (DADT) policy in 2011, and test-and-treat initiatives aligned with the 2019 "Ending the HIV Epidemic" initiative, annual rates have continued to show little to no annual declines. To better understand the nature of new infections in the U.S. military, this retrospective analysis examined cases and trends in greater depth to 1) identify and describe total HIV antibody seropositivity rates from 1990 to 2024, with stratification by demographic characteristics, and 2) identify and characterize potential shifts in the epidemiological profile of HIV cases during the course of the evolving HIV epidemic.

What are the new findings?

From 1990 through 2024, over 46 million tests for HIV antibodies were conducted among active, Guard, and reserve members of the U.S. Armed Forces, and 11,280 (24.3 per 100,000 persons tested) were diagnosed with HIV. Male service members comprised 96.3% of all HIV infections. The total rate of new HIV diagnoses declined over the period of surveillance, with the steepest decline in the first decade. Overall rates stabilized in 1997, but differences persist between different age and racial and ethnic population groups. New HIV diagnoses have risen among male service members under age 30 years, with non-Hispanic Black service members bearing the highest burden, while Hispanic service members demonstrating the largest relative increases. Since 1997, rates in all racial and ethnic groups have more than doubled for those under age 25 years; for Hispanic service members, the increase was nearly 10-fold.

What is the impact on readiness and force health protection?

Rising HIV infection rates among male U.S. service members under age 30 years underscores the need for targeted and enhanced prevention efforts to sustain progress and mitigate marked and increasing differences between specific populations and age groups. Given the impact of HIV on force readiness, optimization of screening strategies, including indications-based testing after service entry, could improve the effectiveness and value of current screening efforts. The HIV-antibody screening program remains an important element of force health protection.

Methods

The population of interest for this study included all individuals screened for HIV antibodies while serving in the active, reserve and National Guard components of the U.S. Army, Navy, Air Force, Marine Corps, and Coast Guard. The surveillance period covered January 1, 1990 through December 31, 2024. Data analysis followed the case definition and incidence rules established by the Armed Forces of Health Surveillance Division (AFHSD) for HIV surveillance in the U.S. military. Laboratory testing methods and decision-making algorithms for identifying HIV infection are standardized and have been described in detail previously.[1,6]

All individuals tested through U.S. military medical testing programs were ascertained from the Department of Defense Serum Repository (DODSR) specimens accessioned to the Defense Medical Surveillance System (DMSS). Annual HIV diagnosis rates reflect new infections identified among service members tested each calendar year, calculated as the number of HIV antibody seropositive cases per 100,000 persons. An individual was counted once per calendar year if that

person was tested for HIV during that year. Due to incomplete or unavailable specimen and HIV testing results for the Coast Guard before 1996 and Air Force prior to 2006, these years were excluded from the relevant analyses.

For the descriptive characterization of HIV cases, distributions by demographic and military factors, such as age, race, service branch, and occupation, were examined. To facilitate identification and characterization of changes in the epidemiological profile of HIV cases within the evolving HIV epidemic, the 35-year surveillance period was divided into distinct phases. Key events and historical milestones that shaped the efforts to control HIV both nationally and within the U.S. military over the course of HIV surveillance were considered according to 4 phases: 1) the early epidemic, 1990-1995, 2) implementation of highly active antiretroviral therapy (HAART), 1996-2005, 3) expanded testing and prevention, 2005-2013, and 4) the modern era: "Ending the HIV Epidemic," 2014-present **(Table 1)**.

HIV rate analyses of age-related trends for male service members were restricted to 1997-2024, as male rates stabilized after 1997. This restriction minimized the influence of early surveillance fluctuations. Since rates for the female population followed a more consistent trajectory, no such restriction was applied. In addition, due to low female case counts, female data were aggregated into 10-year age groups, to improve graphic interpretation. Where appropriate, further aggregation was applied to charting both male and female data if no notable variations were observed between grouped categories.

Results

Total, branch of service, and component seropositivity rates

From January 1990 through December 2024, a total of 46,409,929 annual tests for HIV antibodies were conducted among active, Guard, and reserve service members of the U.S. Armed Forces. During this 35-year surveillance period, 11,280 service members were diagnosed with HIV, yielding a crude total seropositivity rate of 24.3 per 100,000 persons tested **(Table 2)**. Among the service branches, the Navy had the highest overall rate, at 30.3 cases per 100,000 persons tested, followed by the Army, at 26.3 cases per 100,000 persons tested, while the Marine Corps, Air Force, and Coast Guard had lower rates, averaging about 15 new cases per 100,000 persons tested **(Figure 1)**. After the initial decline during the earliest phase of the epidemic, rates of new HIV diagnoses in the Army and Marine Corps gradually increased during subsequent phases. Rates were relatively similar in the early stages of the epidemic but diverged by the current Ending the HIV Epidemic phase. The highest rates were in the reserve component, followed by the Guard, with lowest rates in the active component **(Table 2)**.

Sex-stratified seropositivity rates

Male service members constituted an overwhelming majority, 96.3% (n=10,865), of all cases of HIV-antibody seropositivity documented during the surveillance period, with the total trend for the U.S. Armed Forces closely paralleling that observed for male service members **(Figure 2)**. The incidence rate among service men was highest in 1990, at 76.4 per 100,000 persons tested, before dropping to 14.5 (around 81% decline) in 1995, the lowest recorded in any year during the 35-year observation period. With the exception of a small spike in 1996, rates subsequently stabilized, averaging 25.7 new infections per year per 100,000 persons tested from 1997 through 2024. This average rate is much lower than the peak, but still higher than the recorded minimum.

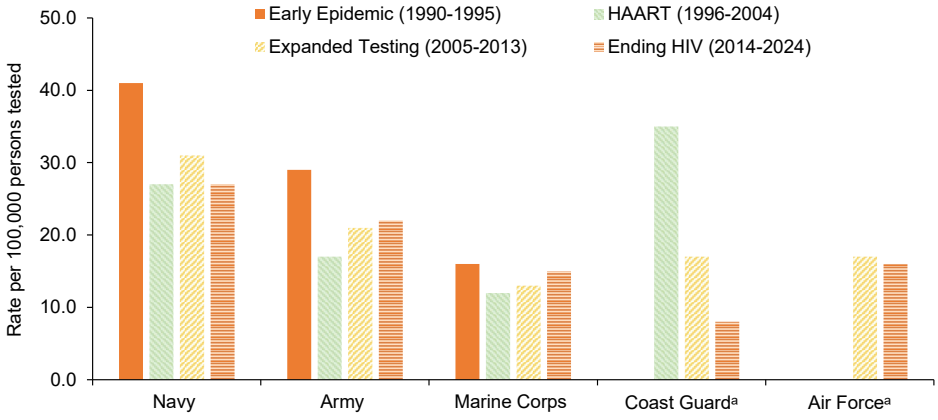
Seropositivity rates among female service members were much lower. The peak rate among women was observed in 1991, at 19.1 new infections per 100,000 tested persons, which declined sharply to 4.9 (74.4% decline) in 1993. Rates were relatively stable in subsequent years, fluctuating within a range of 6.7 to 12.7 per 100,000 tested persons until 2002, averaging 11.2 new cases per year. Starting in 2003, rates for

TABLE 1. Phases of the HIV Epidemic, 1990–Present

Phase	Time Period	Description
Early Epidemic	1990–1995	This period is characterized by growing recognition of the HIV epidemic, streamlining of HIV testing and screening algorithms, early prevention efforts, and limited treatment options and effectiveness.
HAART	1996–2005	This period is distinguished by the introduction and widespread availability of highly active antiretroviral therapy (HAART) in 1996, and transformed HIV from a fatal disease to a manageable chronic condition.
Expanded Testing and Prevention	2005–2013	This period followed DOD adjustment of mandatory screening frequency to biennial in 2004, CDC expansion of routine testing guidelines in 2006 to include all adults, introduction of PrEP in 2012, and repeal of "Don't Ask, Don't Tell" policy in 2011.
Modern Era: *Ending the HIV Epidemic*	2014–Present	This period is marked by the launch of the "Ending the HIV Epidemic" initiative in 2019 and focuses on PrEP to support "Undetectable=Untransmittable" (U=U) principle.

Abbreviations: HIV, human immunodeficiency virus; HAART, highly active antiretroviral therapy; DOD, Department of Defense; CDC, Centers for Disease Control and Prevention; PrEP, pre-exposure prophylaxis.

FIGURE 1. HIV Seropositivity by Service and Epidemic Phase, Active Component, U.S. Armed Forces, 1990–2024



[a] Due to incomplete or unavailable specimen and HIV testing results, data for Coast Guard are not available prior to 1996, nor for Air Force prior to 2006.

FIGURE 2. Total and Sex-Stratified HIV Antibody Seropositivity Rates, U.S. Armed Forces, 1990–2024

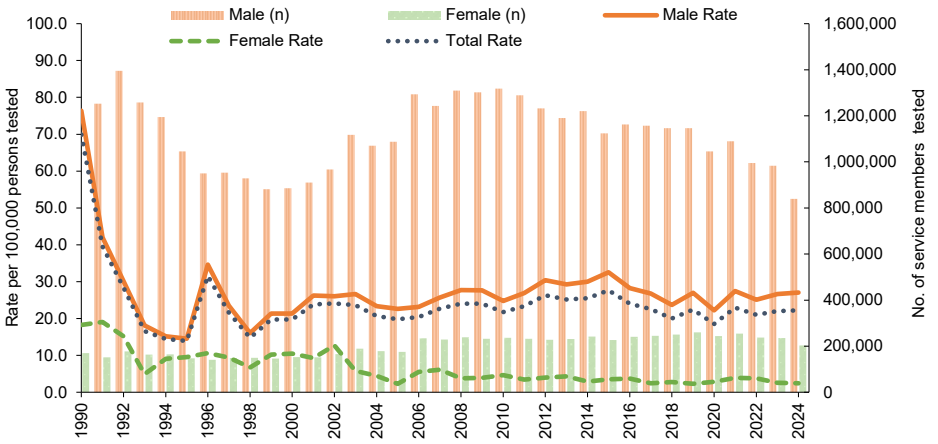
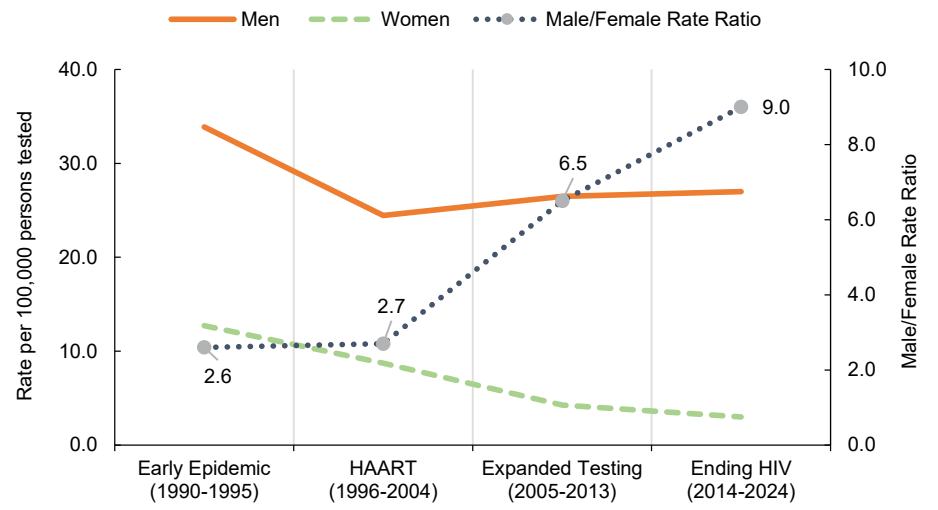


FIGURE 3. HIV Antibody Seropositivity Rates by Sex and Epidemic Phase



women slowly but progressively declined, ultimately reaching one of their lowest levels, 2.5 cases per 100,000 persons tested (an approximately 87% decline), in 2024. The growing divergence between the sexes is further illustrated by the male-to-female rate ratios, which rose from a 3-fold difference during the earlier 2 phases to a 9-fold difference in the current phase **(Figure 3)**.

Aggregated rates of HIV seropositivity for the differentiated phases of the epidemic broadly reflect the annual rates. The highest seropositivity rate, 31.4 per 100,000 persons tested (n=2,665), was observed during the earliest phase of the HIV epidemic, which was followed by a 29.3% decline to 22.2 per 100,000 persons tested (n=2,242) in the second phase, defined by the introduction of HAART. The rate of decline slowed in subsequent phases, even increasing to 23.1 per 100,000 persons tested (n=3,072, 3.9% increase) in the third phase, which was characterized by expanded testing and prevention efforts, before decreasing slightly to 22.7 per 100,000 persons tested in the current phase (n=3,301), marked by the launch of Ending the HIV Epidemic initiative **(Table 2)**.

Age and race-stratified seropositivity rates

Over 90% of HIV infections occurred among individuals under age 40 years **(Table 2)**. The lowest rate (10.0 per 100,000 persons tested) was observed in the youngest age group, under age 20 years, while the highest (31.7 per 100,000 persons tested) was among those in the 25-29-year age group. The trajectory of HIV seropositivity rates by age group also revealed diverging trends. Among individuals over age 30 years, rates steadily declined, ultimately decreasing by half during the past decade **(Table 2)**. While incidence rates among service members under age 30 years initially declined along with other age groups, the trend was not sustained, and in the current phase, aggregated rates for those under age 30 years either mimicked or exceeded those observed in the earliest phase.

Age-stratified, annual trends for men show the lowest rates among the youngest age groups, with 4.0 cases per 100,000 persons tested in 1997 for those under age 20 years and 15.4 cases per 100,000 persons

TABLE 2. Epidemiological Profiles of Incident HIV Cases, U.S. Armed Forces, 1990–2024

Characteristics	Overall 1990-2024			Early Epidemic 1990-1995			HAART 1996-2004		
	Persons Tested (n)	HIV+ Cases (n)	Rate[a]	Persons Tested (n)	HIV+ Cases (n)	Rate[a]	Persons Tested (n)	HIV+ Cases (n)	Rate[a]
Total	46,409,929	11,280	24.3	8,474,969	2,665	31.4	10,085,560	2,242	22.2
Sex									
Male	39,336,799	10,865	27.6	7,499,865	2,541	33.9	8,662,379	2,118	24.5
Female	7,073,130	415	5.9	975,104	124	12.7	1,423,181	124	8.7
Age group, y									
< 20	5,465,222	548	10.0	1,051,461	95	9.0	1,405,051	95	6.8
20–24	14,368,318	3,787	26.4	2,769,793	810	29.2	3,184,365	612	19.2
25–29	9,277,994	2,944	31.7	1,625,310	777	47.8	1,813,500	477	26.3
30–34	6,415,196	1,789	27.9	1,158,514	487	42.0	1,354,238	456	33.7
35–39	5,041,910	1,188	23.6	851,094	276	32.4	1,156,359	352	30.4
≥ 40	5,841,289	1,024	17.5	1,018,797	220	21.6	1,172,047	250	21.3
Race and ethnicity									
White, non-Hispanic	28,777,369	3,419	11.9	5,752,788	1,059	18.4	6,240,806	667	10.7
Black, non-Hispanic	7,883,708	5,822	73.8	1,638,605	1,385	84.5	1,867,116	1,185	63.5
Hispanic	5,270,878	1,172	22.2	438,325	111	25.3	964,904	176	18.2
Other / unknown	4,477,974	867	19.4	645,251	110	17.0	1,012,734	214	21.1
Education level									
High school or less	32,362,591	8,883	27.4	6,579,109	2,279	34.6	7,685,461	1,841	24.0
Some college	4,455,128	920	20.7	365,225	87	23.8	558,327	114	20.4
Bachelor's or advanced degree	7,936,394	1,141	14.4	1,140,036	185	16.2	1,443,666	213	14.8
Other / unknown	1,655,816	336	20.3	390,599	114	29.2	398,106	74	18.6
Marital status									
Single, never married	22,508,360	7,554	33.6	4,071,124	1,717	42.2	5,061,705	1,461	28.9
Married	21,853,133	3,165	14.5	4,099,908	834	20.3	4,677,935	666	14.2
Other / unknown	2,048,436	561	27.4	303,937	114	37.5	345,920	115	33.2
Rank, grade									
Junior enlisted (E1–E4)	22,993,670	6,066	26.4	4,363,368	1,391	31.9	5,307,776	1,141	21.5
Senior enlisted (E5–E9)	16,691,404	4,432	26.6	3,010,732	1,135	37.7	3,436,665	939	27.3
Junior officer (O1–O3)	3,549,499	459	12.9	606,147	77	12.7	680,264	94	13.8
Senior officer (O4–O10)	2,539,134	273	10.8	379,670	52	13.7	517,698	59	11.4
Warrant officer (W01–W05)	636,222	50	7.9	115,052	10	8.7	143,157	9	6.3
Military occupation									
Combat-specific (Infantry / artillery / combat engineering / armor)	5,940,291	972	16.4	903,850	200	22.1	1,333,144	181	13.6
Motor transport	1,736,637	504	29.0	234,803	103	43.9	464,875	79	17.0
Pilot / air crew	1,505,453	112	7.4	199,079	16	8.0	318,645	28	8.8
Repair / engineering	10,821,213	2,166	20.0	1,575,310	362	23.0	2,295,425	397	17.3
Communications / intelligence	8,457,040	3,019	35.7	1,110,753	597	53.7	1,676,142	580	34.6
Health care	3,183,230	1,061	33.3	409,468	180	44.0	638,918	199	31.1
Other	14,766,065	3,446	23.3	4,041,706	1,207	29.9	3,358,411	778	23.2
Service branch									
Army	22,558,658	5,924	26.3	4,487,647	1,426	31.8	4,937,643	1,096	22.2
Marine Corps	6,087,759	879	14.4	1,143,998	174	15.2	1,662,547	201	12.1
Navy	11,472,225	3,479	30.3	2,839,304	1,065	37.5	3,393,677	916	27.0
Air Force[b]	5,743,352	917	16.0	—	—	—	—	—	—
Coast Guard[b]	547,935	81	14.8	4,020	—	—	91,693	29	31.6
Component									
Active	31,922,686	7,183	22.5	5,582,275	1,764	31.6	7,356,912	1,477	20.1
Guard	7,316,696	1,889	25.8	1,253,170	372	29.7	1,140,838	308	27.0
Reserve	7,170,547	2,208	30.8	1,639,524	529	32.3	1,587,810	457	28.8

Abbreviations: HIV, human immunodeficiency virus; HAART, highly active antiretroviral therapy; n, number; HIV+, HIV-positive; y, years; E, enlisted; O, officer.
[a] Rate per 100,000 persons tested.
[b] Due to incomplete or unavailable specimen and HIV testing results, data for Coast Guard are not available prior to 1996, nor for Air Force prior to 2006.

TABLE 2 cont. Epidemiological Profiles of Incident HIV Cases, U.S. Armed Forces, 1990–2024

Characteristics	Expanded Testing and Prevention 2005-2013			Modern Era: *Ending the HIV Epidemic* 2014-2024		
	Persons Tested (n)	HIV+ Cases (n)	Rate[a]	Persons Tested (n)	HIV+ Cases (n)	Rate[a]
Total	13,300,592	3,072	23.1	14,548,808	3,301	22.7
Sex						
Male	11,265,323	2,985	26.5	11,909,232	3,221	27.0
Female	2,035,269	87	4.3	2,639,576	80	3.0
Age group, y						
<20	1,391,009	178	12.8	1,617,701	180	11.1
20–24	4,142,734	1,080	26.1	4,271,426	1,285	30.1
25–29	2,778,136	751	27.0	3,061,048	939	30.7
30–34	1,735,649	367	21.1	2,166,795	479	22.1
35–39	1,429,227	322	22.5	1,605,230	238	14.8
≥40	1,823,837	374	20.5	1,826,608	180	9.9
Race and ethnicity						
White, non-Hispanic	8,466,968	903	10.7	8,316,807	790	9.5
Black, non-Hispanic	2,056,084	1,574	76.6	2,321,903	1,678	72.3
Hispanic	1,515,221	354	23.4	2,352,428	531	22.6
Other/unknown	1,262,319	241	19.1	1,557,670	302	19.4
Education level						
High school or less	9,149,428	2,349	25.7	8,948,593	2,414	27.0
Some college	1,534,288	299	19.5	1,997,288	420	21.0
Bachelor's or advanced degree	2,253,703	370	16.4	3,098,989	373	12.0
Other/unknown	363,173	54	14.9	503,938	94	18.7
Marital status						
Single, never married	6,101,069	2,115	34.7	7,274,462	2,261	31.1
Married	6,546,514	786	12.0	6,528,776	879	13.5
Other/unknown	653,009	171	26.2	745,570	161	21.6
Rank, grade						
Junior enlisted (E1–E4)	6,415,240	1,599	24.9	6,907,286	1,935	28.0
Senior enlisted (E5–E9)	4,927,008	1,215	24.7	5,316,999	1,143	21.5
Junior officer (O1–O3)	1,013,281	131	12.9	1,249,807	157	12.6
Senior officer (O4–O10)	774,314	108	13.9	867,452	54	6.2
Warrant officer (W01–W05)	170,749	19	11.1	207,264	12	5.8
Military occupation						
Combat-specific (infantry/artillery/combat engineering/armor)	1,908,942	256	13.4	1,794,355	335	18.7
Motor transport	504,772	114	22.6	532,187	208	39.1
Pilot/air crew	493,510	36	7.3	494,219	32	6.5
Repair/engineering	3,318,343	622	18.7	3,632,135	785	21.6
Communications/ intelligence	2,728,240	955	35.0	2,941,905	887	30.2
Health care	999,519	380	38.0	1,135,325	302	26.6
Other	3,347,266	709	21.2	4,018,682	752	18.7
Service branch						
Army	6,264,925	1,558	24.9	6,868,443	1,844	26.8
Marine Corps	1,641,934	238	14.5	1,639,280	266	16.2
Navy	2,614,522	797	30.5	2,624,722	701	26.7
Air Force	2,572,276	447	17.4	3,171,076	470	14.8
Coast Guard[b]	206,935	32	15.5	245,287	20	8.2
Component						
Active	9,322,536	1,984	21.3	9,660,963	1,958	20.3
Guard	2,139,806	478	22.3	2,782,882	731	26.3
Reserve	1,838,250	610	33.2	2,104,963	612	29.1

Abbreviations: HIV, human immunodeficiency virus; HAART, highly active antiretroviral therapy; n, number; HIV+, HIV-positive; y, years; E, enlisted; O, officer.
[a] Rate per 100,000 persons tested.
[b] Due to incomplete or unavailable specimen and HIV testing results, data for Coast Guard are not available prior to 1996, nor for Air Force prior to 2006.

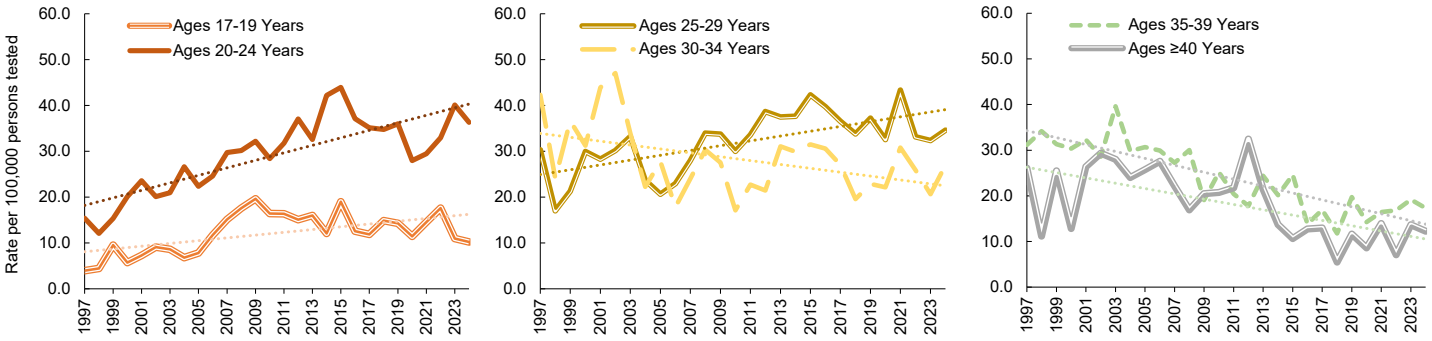
among those aged 20-24 years; by 2024, the rates for those age groups more than doubled, reaching 10.2 and 36.3 cases per 100,000 persons tested, respectively **(Figures 4a–4c)**. The older age groups (35-39, 40+) of male service members started at much higher levels, at rates of 31.2 and 26.1 per 100,000 persons tested, respectively, and their rates steadily declined over time, nearly halving to 17.3 and 12.2 per 100,000 persons tested, respectively, by 2024. The trends for the 2 intermediate age groups (25-29, 30-34) were less pronounced and overlapped, with consistently high rates for both groups throughout the period. The male 25-29-year age group evinced a weak upward trend, while the male 30-34-year age group started at the highest observed rate, 42.3 cases per 100,000 persons tested, in 1997 and decreased to 27.0 cases per 100,000 persons tested by 2024.

Despite representing 17.0% of those tested, non-Hispanic Black individuals accounted for more than half of all positive cases, with an overall rate of 73.8 per 100,000 persons tested **(Table 2)**. Non-Hispanic White individuals comprised 62.0% of all persons tested but had the lowest rate, 11.9 per 100,000 persons tested.

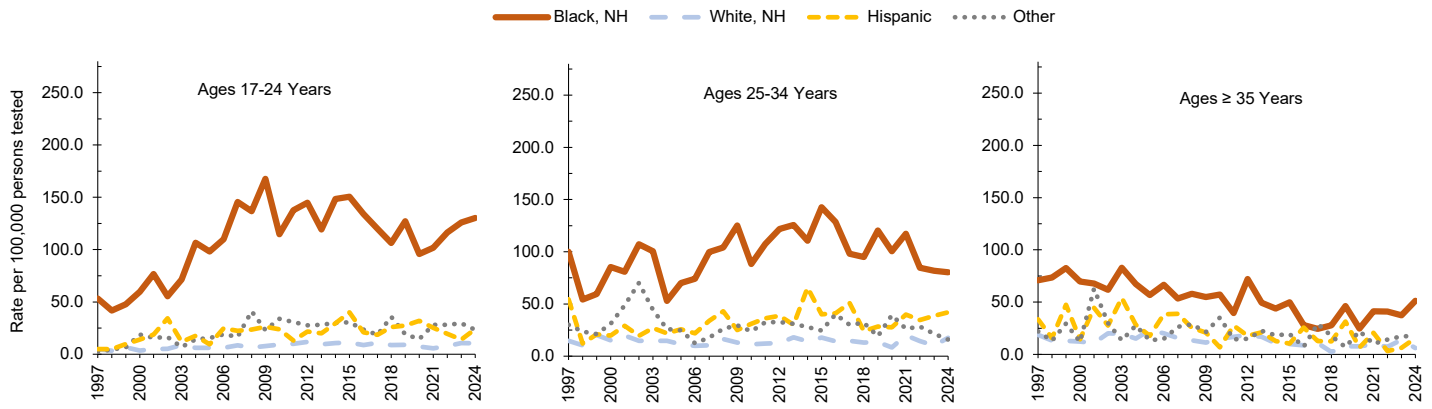
New diagnoses among non-Hispanic White service members steadily declined, from 18.4 in the earliest phase to 10.7 per 100,000 persons tested during the second and third phases, reaching a low of 9.5 per 100,000 persons tested in the last decade, a nearly 50% reduction **(Table 2)**. In contrast, the decline among non-Hispanic Black service members was less pronounced and consistent. Rates among Hispanic and Other or Unknown race and ethnicity categories remained largely unchanged.

HIV infection rates among male service members under age 25 years have risen among all ethnic and racial groups since 1997. **Figures 5a–5c** present annual HIV trends for male service members stratified by age as well as ethnic and racial group. The sharpest rise was observed

FIGURES 4a–4c. HIV Antibody Seropositivity Rates Among Male U.S. Service Members by Age Group and Year, 1997–2024

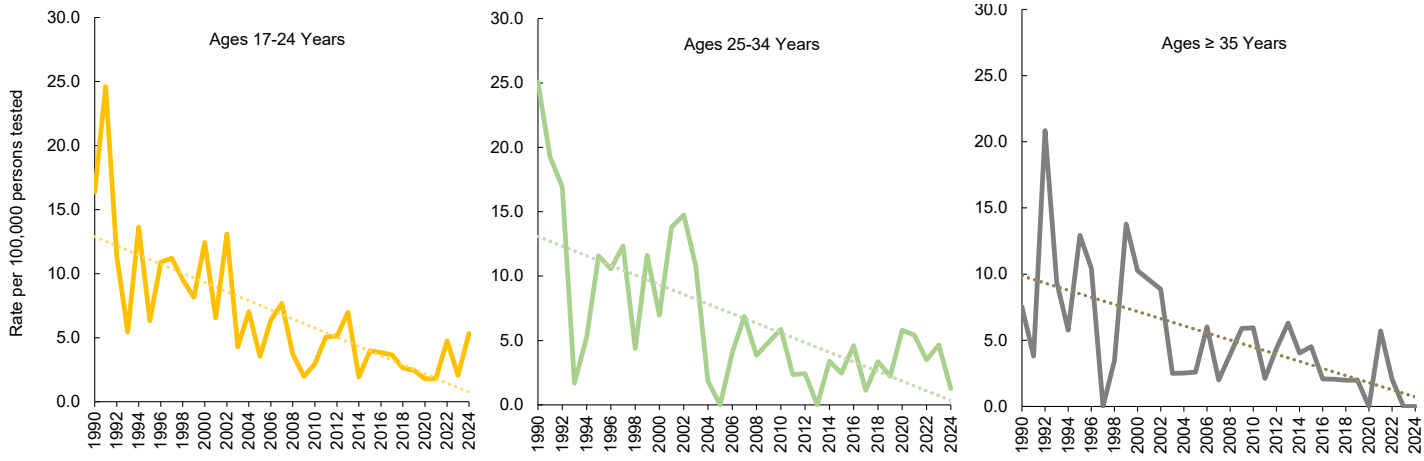


FIGURES 5a–5c. HIV Antibody Seropositivity Rates Among Male U.S. Service Members by Age Group, Race and Ethnicity, and Year, 1997–2024



Abbreviation: NH, non-Hispanic.

FIGURES 6a–6c. HIV Antibody Seropositivity Rates Among Female U.S. Service Members by Age Group and Year, 1990–2024



among Hispanic men, with rates increasing from 2.4 in 1997 to 23.5 per 100,000 persons tested in 2024, a nearly 10-fold increase. Rates among non-Hispanic Black and White male service members under age 25 years more than doubled. Among non-Hispanic Black male service members, rates rose from 53.2 persons tested in 1997 to 130.3 in 2024, with a peak of 167.6 per 100,000 persons tested in 2009. Rates for non-Hispanic White male service members rose from 4.7 per 100,000 persons tested in 1997 to 10.4 in 2024, with a peak rate of 11.8 in 2012. Among those in the Other or Unknown race category, rates increased nearly 5-fold.

Due to low case numbers, annual female rate variability was high during the entire surveillance period, but there was an overall trend of consistent decline among all age groups. **Figures 6a–6c** present age-stratified, annual trends for female service members. In the earliest years of the surveillance period, female rates reached as high as 25 cases per 100,000 persons tested but gradually declined to about 5 cases or less per 100,000 persons tested among those under age 35 years. In recent years, no cases have been reported among service women over age 35 years. Similar to trends observed among their male counterparts, non-Hispanic Black female service members, overall, had the highest HV rates throughout the surveillance period and among all age groups (data not shown).

Socio-economic and military characteristics

Service members with high school education or less comprised nearly 80% of HIV-positive cases. Although married individuals represented roughly half (47.1%) of all tested persons, they accounted for only 28.1% of positive cases **(Table 2)**. Enlisted service members had approximately twice the positivity rate of officers. Case distribution among occupational categories reflected, in general, that of the overall population, but personnel in communications/intelligence, health care, and motor transport exhibited higher rates of HIV seropositivity during all epidemic phases, at approximately 30 cases per 100,000 tested persons.

Discussion

This report presents the results of HIV screening programs in the U.S. military from 1990 to 2024 within the broader context of the evolving HIV epidemic. Given the uniformity of care standards, robust screening protocols, and medical fitness requirements, this analysis of a 35-year surveillance period offers new insights into the current trajectory of HIV incidence among U.S. military personnel.[1,9] Recent policy changes, including the 2022 DOD policy affirming medically fit HIV-positive individuals' right to serve[10] and the 2024 court ruling[11] allowing accession by HIV-positive applicants, necessitate provision of the most up-to-date evidence to address the implications of these policies for HIV transmission and ensure HIV care and treatment programs are well adapted to support service members living with HIV.

Stratified analysis revealed significant differences in HIV-antibody seropositivity, by age, sex, and race, within the U.S. Armed Forces. New HIV diagnoses among male service members under age 30 years have steadily increased, with the greatest burden among non-Hispanic Black men and highest rise among Hispanic men. Although non-Hispanic White service members have the lowest recorded rates of new HIV diagnoses, rates for both non-Hispanic White and Black male service members under age 25 years more than doubled in 2024 compared to 1997.

Among Hispanic male service members men under age 25 years, the increase in HIV diagnoses was nearly 10-fold. This increase among Hispanic service members generally corresponds with national 2010-2022 data that show a 24% increase in HIV among the Hispanic population, during a period when the national HIV rate decreased by 12% overall.[12-14] The sharp rise in the number of HIV cases among Hispanic service members reflects both a growing share of Hispanics within the U.S. military and actual increases in infection rates that could be driven by behavioral and structural factors.

A recent study by Goodreau et al. that analyzed data from the American Men's Internet Survey found declining condom use and rise in condom-less sex among HIV-negative MSM not using PrEP, with the most substantial increase noted among Hispanic men aged 15-24 years.[15] This finding suggests that high-risk behavioral factors may be playing role in rising infection rates in Hispanic service members, as well as those of other racial and ethnic groups. Although DMSS does not explicitly collect data on same-sex behavior, studies assessing sexual risk behaviors among service members have shown that MSM represent a significant proportion of the population at high risk for HIV infection within the armed forces.[16-18]

Geographic disparities appear to further influence HIV risk among men of color. The CDC reports that Hispanic or Latino individuals accounted for up 42% of new infections in the southern U.S., a region with historically higher HIV burden.[14,19] Similar trends were found in urban centers, with a multi-city study reporting increased HIV prevalence among MSM ages 23-29 years, from 10.2% in 1994-1999 to 16.7% in 2005-2011, with prevalence among MSM ages 18-22 years in Baltimore city nearly doubling, from 4.8% to 9.3%, during the same periods.[20] These findings emphasize the dynamic nature of HIV among young men in specific geographic areas and suggest that military HIV prevention programs should consider regional variations when designing prevention strategies.

The results of this study indicate increasing vulnerability of young male U.S. service members to HIV and suggest need for intensive and improved prevention strategies for this specific demographic, including condom use and healthy sexual behavior promotion. Shifting perceptions of HIV risk, including fading fear of HIV, reduced condom use, greater reliance on biomedical prevention such as PrEP, and "Undetectable=Untransmittable" messaging have been reported as factors potentially driving a rise in HIV among young adults in the general population.[12,13,19] These factors are likely contributing to rising infection rates among young male service members as well.

HIV PrEP has become a critical tool in HIV prevention, particularly among young men in the U.S. Studies show increased PrEP use among young men

both nationally and within the military.[21,22] Reported PrEP usage disparities persist, however, with lower use among non-Hispanic Black and Hispanic men.[23] A 2023 National HIV Behavioral Surveillance (NHBS) report found that less than half of non-Hispanic Black and Hispanic MSM reported current PrEP use, which has been attributed to systemic and structural inequities, including barriers to health care access and cultural constraints.[12,13,24]

The evolving dynamics of HIV antibody positivity rates in the U.S. military emphasize the need for continuous adaptation of prevention and screening strategies. While the overall trend shows a decline in HIV incidence, with the steepest drop occurring in the first decade of the screening program, total rates have plateaued since 1997. Increasing rates of HIV-antibody seropositivity among young, particularly under 25 years of age, male service members evidence a critical gap in HIV prevention efforts. By addressing behavioral shifts, improving PrEP accessibility, and incorporating demographic and regional risk factors into the design of intervention strategies, the U.S. military can strengthen its HIV prevention strategy and program, and safeguard the health and readiness of the force.

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Images in Health Surveillance

The Discovery of Chloramphenicol Treatment for Both Scrub Typhus and Typhoid Fever

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Today, the U.S. and its allies collaborate on missions throughout the globe, able to deploy in tropical regions without the massive disease casualties of 20th century conflicts. During World War II, at the dawn of the antibiotic era, thousands of Allied soldiers in the Pacific died of an untreatable illness, *tsutsugamushi*, or scrub typhus, a rickettsial infection endemic to Southeast Asia. An additional tens of thousands suffered non-fatal infections, often incapacitated for months.[1]

When the U.S. Typhus Commission was formed in 1942, its focus was epidemic typhus in Europe, but it came to include scrub typhus in the Pacific. Research to find an effective treatment for scrub typhus was a military priority, and Dr. Joseph Smadel, Chief of the Department of Virus and Rickettsial Diseases at the Walter Reed Army Institute of Research (WRAIR), was focused on these efforts.

Trials initiated by Dr. Smadel in partnership with scientists in the then-British colony of Malay, now Malaysia, resulted in the serendipitous discovery of treatment for 2 major infectious diseases. The U.S. Army Medical Research Unit–Malaysia resulted from initially informal collaborations between Dr. Smadel and WRAIR researchers and British scientists at the Institute for Medical Research in Kuala Lumpur.

Within a year of chloramphenicol's discovery in 1947, Dr. Smadel had collected most of the existing stock—it would not be fully synthesized until 1949—for field trials in Malaysia. Smadel first tested the drug in rickettsial laboratory cultures and then progressed to field trials in naturally infected rubber plantation workers in Malaysia.[2]

Within 6 weeks, in early 1948, 25 scrub typhus patients had been successfully treated with chloramphenicol. Patient fevers cleared in an average of 31 hours, despite total treatment duration as brief as a single day. This victory against disease was considered noteworthy enough to warrant an editorial cartoon, printed in a Malaysian English language newspaper, evoking the U.S. Marines on Iwo Jima **(Figure)**.

FIGURE. Cartoon in *The Malay Post*, ca. 1948, of the Joint Civil-Military Medical Team that Discovered Chloramphenicol Treatment for Lethal Rickettsial Infection of Scrub Typhus

Inadvertently, some initially mis-diagnosed typhoid fever patients were treated along with scrub typhus patients, and were found to be cured equally well. Ten typhoid cases received chloramphenicol, with fever clearance in 3.5 days; only 2 relapsed within 16 days, but subsequently responded well to re-treatment.[3]

In only a few months, definitive treatments to 2 lethal, infectious diseases had been discovered by clinical trials by a U.S. Army medical research team from WRAIR, working collaboratively with local partners. These dual achievements were recognized in 1962 by the Lasker Clinical Award, which was awarded to Dr. Smadel.

The scale and speed of the discovery of scrub typhus and typhoid treatment were unique, but important later discoveries were made at other WRAIR laboratories. Since World War II, WRAIR has operated more than a dozen laboratories overseas. Japanese encephalitis and hepatitis A vaccines were field-tested at the Armed Forces Research Institute of Medical Sciences (AFRIMS) in Thailand, and mefloquine and tafenoquine were tested for malaria at AFRIMS and U.S. Army Medical Research Unit-Kenya.[4,5] With often no perceived pharmaceutical profit potential in Western nations for new treatments for exotic diseases, the research and development by WRAIR laboratories and their partners are of even greater importance.

Disclaimer

The opinions expressed are those of the author and do not necessarily reflect those of the Australian Defence Force nor Department of Foreign Affairs and Trade.

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Update

Malaria Among Members of the U.S. Armed Forces, 2024

Malaria infection remains a potential health threat to U.S. service members located in or near endemic areas due to duty assignments, participation in contingency operations, or personal travel. In 2024, a total of 30 active and reserve component service members were diagnosed with or reported to have malaria, a 23.1% decrease from the 39 cases identified in 2023. Over half of U.S. service member malaria cases in 2024 were caused by *Plasmodium falciparum* (56.7%, n=17), followed by unspecified types of malaria (33.3%, n=10) and *P. vivax* (10.0%, n=3). Malaria cases were diagnosed or reported from 18 different medical facilities in the U.S., Germany, Africa, Japan, Middle East, and South Korea. Of the 27 cases with a known location of diagnosis, 11 (40.7%) were reported or diagnosed outside the U.S.

What are the new findings?

This report documents a total of 30 malaria cases in 2024, a 23.1% decrease from 39 cases in 2023, mainly due to declines in Africa and other or unspecified locations. As in 2023, *Plasmodium falciparum* continues to constitute over half of new malaria cases (n=17, 56.7%) among active and reserve component U.S. service members.

What is the impact on readiness and force health protection?

Malaria poses a risk for service members deployed to endemic regions or during travel to such areas for personal reasons. *P. falciparum*, the most dangerous malaria strain, with a high risk of serious sequelae, including death, was diagnosed in more than half of cases in 2024. This finding emphasizes the need for continued preventive measures and heightened awareness of potential diagnostic challenges, particularly in areas where *P. falciparum* is endemic.

Malaria, a life-threatening disease spread to humans through the bite of *Anopheles* mosquitoes, is transmitted mostly in tropical countries.[1] The World Health Organization (WHO) estimated 263 million malaria cases (incidence rate of 60.4 cases per 1,000 population at risk) in 2023 and 597,000 deaths (mortality rate of 13.7 per 100,000) within 83 endemic countries. Of those 83 countries with known malaria cases, 29 countries accounted for nearly 95% of cases and 96% of deaths.[2] The 5 countries with the greatest estimated burdens of malaria are Nigeria (26%), Democratic Republic of the Congo (13%), Uganda (5%), Ethiopia (4%), and Mozambique (4%).[2]

Four species of *Plasmodium* account for the most significant burdens of malaria disease in humans: *P. falciparum*, *P. vivax*, *P. malariae*, and *P. ovale*. *P. falciparum* is the most dangerous form of malaria, accounting for over 90% of malaria-related deaths.[3] While *P. falciparum* is most prevalent in Africa, *P. vivax* is the most widely distributed parasite species geographically, with relatively high prevalences of infection in the regions of Southeast Asia, the western Pacific, and eastern Mediterranean, as well as less densely populated areas of the Americas.[4]

Malaria is not endemic in the U.S. but remains a significant threat to its military service members deployed to tropical and subtropical regions. This risk to U.S. service members is due to operational constraints, lack of compliance with available preventive measures, in addition to continuing emergence of drug-resistant malarial parasites.[5] The U.S. Armed Forces have long maintained policies and prescribed measures effective against vector-borne diseases such as malaria, including chemoprophylactic drugs, permethrin-impregnated uniforms and bed nets, and topical insect repellents. During planning for overseas military operations, geographically-associated presence or absence of malaria risk is usually known and can be anticipated, but implementation of preventive measures can be complex and dependent upon individual adherence to personal protective measures. When cases and outbreaks of malaria occur, they are generally due to poor adherence to chemoprophylaxis and other personal preventive measures.[6-9]

Since 1999, *MSMR* has published regular updates on malaria incidence among U.S. service members. *MSMR*'s sustained focus on malaria reflects both historical trends about this mosquito-borne disease and the continuing threat it poses to military readiness and service member health. This update describes the epidemiological patterns of malaria incidence among service members in the active and reserve components of the U.S. Armed Forces from 2015 through 2024.

Methods

The surveillance population for this report includes service members of the U.S. Army, Navy, Air Force, Marine Corps, Space Force, and Coast Guard. The surveillance period was January 1, 2015 through December 31, 2024. Records from the Defense Medical Surveillance System (DMSS) were searched to identify qualifying evidence of a malaria diagnosis from reportable medical events (RMEs), hospitalizations, outpatient encounters (in military and non-military facilities), and laboratory results from military facilities.

Case definition criteria for malaria included either 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.[10] 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 with 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 not listing 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 deployed or assigned to a malaria-endemic country within 2 years before diagnosis were considered acquired in those countries. All remaining cases were considered to have acquired malaria in unknown locations.

Results

In 2024, a total of 30 U.S. service members were diagnosed with, or reported to have, malaria **(Table 2)**, resulting in a rate of 1.5 per 100,000 persons (data not shown). The annual total for 2024 represents a 23.1% decrease in malaria cases from the 39 cases reported in 2023 **(Figure 1)**.

Fifteen (50.0%) of the 30 cases in 2024 were identified from RME records. The remaining 15 cases were identified through additional case definition criteria: 11 cases from hospitalization records and 4 cases from a positive malaria antigen test plus an outpatient record with a diagnosis of malaria in any diagnostic position within 30 days of specimen collection date.

TABLE 1. ICD-9 and ICD-10 Diagnosis Codes Used to Define Malaria Cases from 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

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

As in previous years, the majority of U.S. military members diagnosed with malaria in 2024 were men (96.7%), members of the active component (86.7%), and in the Army (56.7%). No cases were reported in the Space Force or Coast Guard. Non-Hispanic Black service members and those aged 30-34 years accounted for the most cases of malaria (56.7% and 40.0%, respectively) **(Table 2)**.

Examination of the 15 malaria case records reported as RMEs revealed that 6 of the case exposures were classified as deployment-related, 6 as non-duty-related, 2 as duty-related but not deployment-related, and 1 case was missing exposure classification. All of the 6 non-duty exposure cases were considered to have been acquired in Africa (data not shown).

During the 2015-2024 surveillance period, malaria cases acquired in Africa (n=171, 44.6%) and other or unspecified locations (n=89, 23.2%) accounted for the largest numbers, followed by Korea (n=61, 15.9%), Afghanistan (n=60, 11.7%), and South and Central America (n=2, 0.5%) **(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. Malaria cases were diagnosed or reported in 2024 from 18 different medical facilities in the U.S. (n=12), Germany (n=2), Africa (n=1), Japan (n=1), Middle East (n=1), and South Korea (n=1) **(Table 3)**.

Over half of U.S. service member malaria cases in 2024 were caused by *P. falciparum* (56.7%, n=17). Of the 13 cases not attributed to *P. falciparum*, 3 (10.0%) were caused by *P. vivax*, while 10 were associated with other or unspecified types of malaria (33.3%) **(Figure 3)**.

In 2024, most cases acquired in Africa (n=13) were caused by *P. falciparum* (76.9%, n=10) **(Figure 3)**. The 13 malaria cases acquired in Africa were linked to several countries, including Djibouti (n=3), Cameroon (n=2), Nigeria (n=2), Chad (n=1), Gabon (n=1), Ghana (n=1), Senegal (n=1), and Uganda (n=1); 1 case was associated with an unknown African location (data not shown).

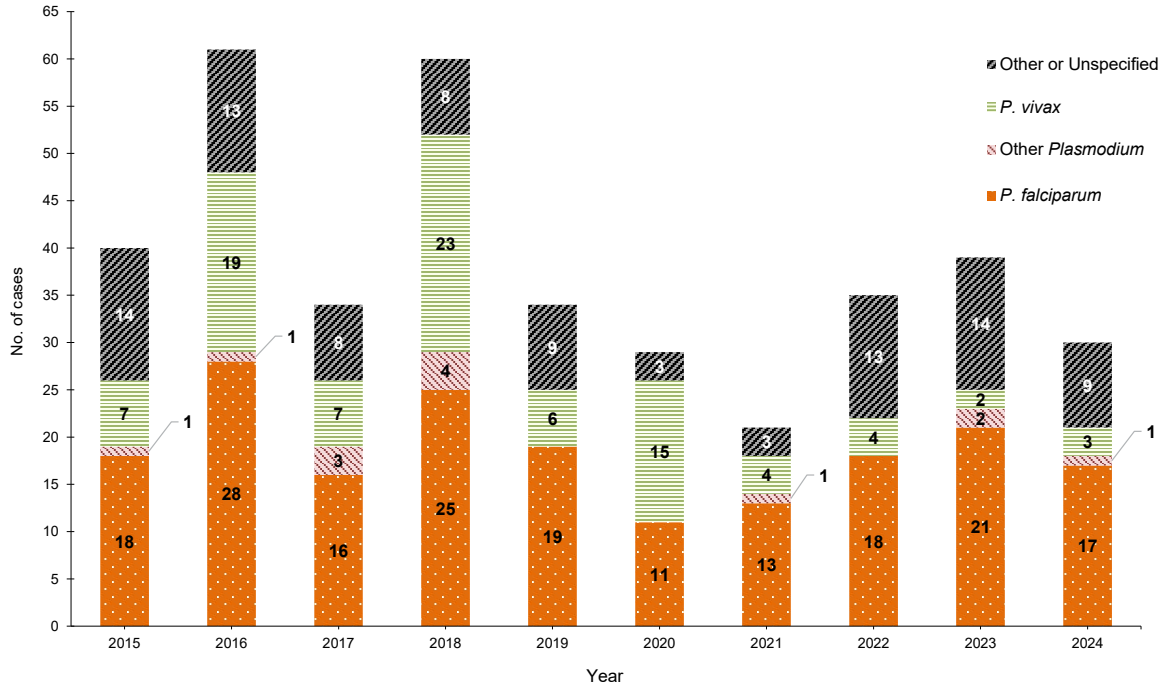
Over the past 10 years, malaria caused by *P. falciparum* has accounted for the largest number of cases (n=186, 48.6%) followed by other or unspecified species (n=94, 24.5%), *P. vivax* (n=90, 23.5%),

TABLE 2. Malaria Cases by *Plasmodium* Species and Selected Demographic Characteristics, U.S. Armed Forces, 2024

	P. vivax	*P. falciparum*	Other or Unspecified	Total		DMSS AC Reference Population[a]	
	No.	No.	No.	No.	%	No.	%
Total	3	17	10	30	100.0	2,055,342	100.0
Sex							
Male	2	17	10	29	96.7	1,656,109	80.6
Female	1	0	0	1	3.3	399,233	19.4
Age group, y							
<20	0	0	0	0	0.0	124,545	6.1
20–24	1	3	3	7	23.3	556,300	27.1
25–29	0	1	1	2	6.7	447,423	21.8
30–34	1	7	4	12	40.0	341,310	16.6
35–39	1	5	2	8	26.7	281,151	13.7
40–44	0	0	0	0	0.0	171,209	8.3
45–49	0	1	0	1	3.3	74,255	3.6
50+	0	0	0	0	0.0	59,149	2.9
Race and ethnicity							
White, non-Hispanic	1	3	7	11	36.7	1,101,662	53.6
Black, non-Hispanic	1	13	3	17	56.7	331,528	16.1
Hispanic	0	0	0	0	0.0	387,682	18.9
Other	1	1	0	2	6.7	234,470	11.4
Component							
Active	3	14	9	26	86.7	1,294,111	63.0
Reserve/Guard	0	3	1	4	13.3	761,231	37.0
Service							
Army	1	12	4	17	56.7	938,452	45.7
Navy	0	2	3	5	16.7	379,580	18.5
Air Force	0	2	0	2	6.7	481,381	23.4
Marine Corps	2	1	3	6	20.0	200,621	9.8
Coast Guard	0	0	0	0	0	45,940	2.2
Space Force	0	0	0	0	0	9,368	0.5

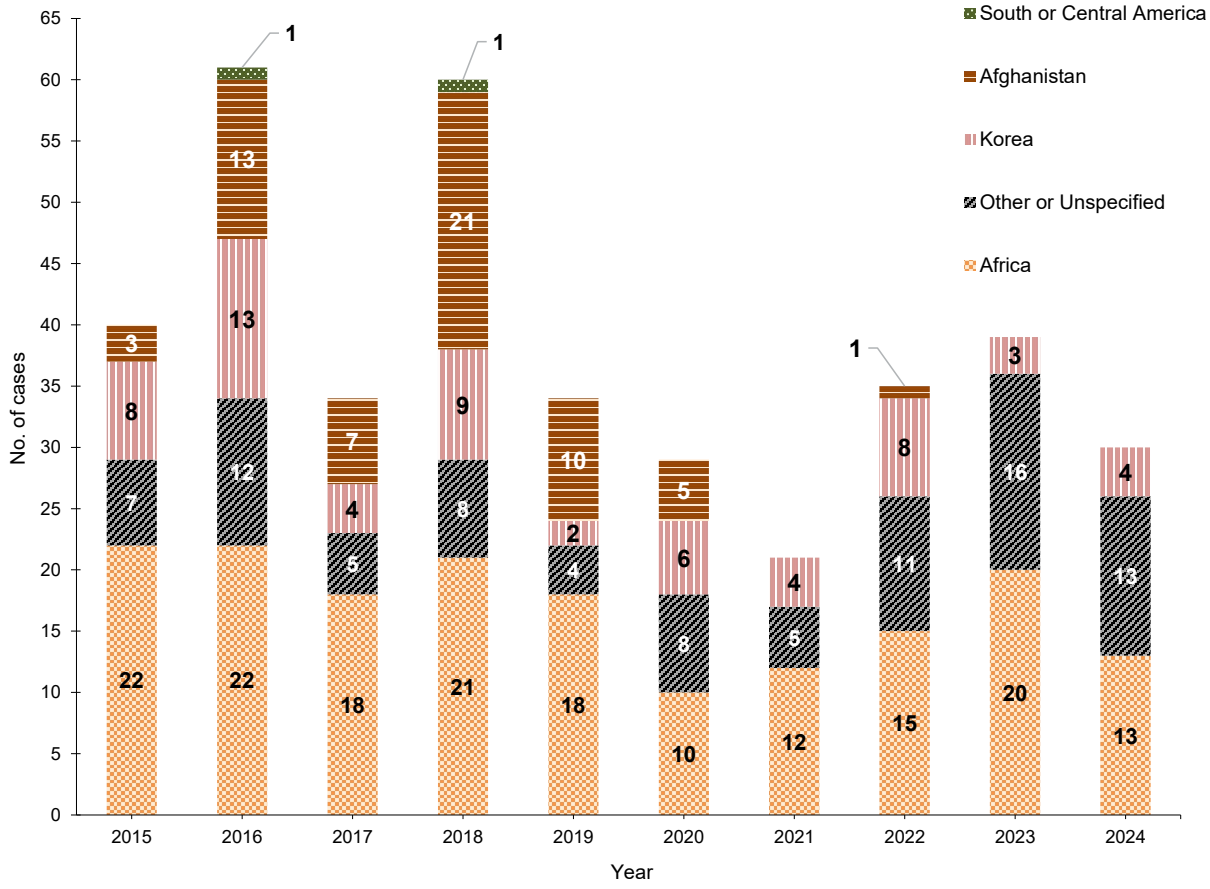
Abbreviations: *P., Plasmodium*; DMSS, Defense Medical Surveillance System; AC, all components; y, years.
[a] Data Source: Defense Medical Surveillance System (DMSS) as of Feb. 19, 2025 prepared by the Defense Health Agency.

FIGURE 1. Numbers of Malaria Cases by Species and Calendar Year of Diagnosis or Report, Active and Reserve Components, U.S. Armed Forces, 2015–2024



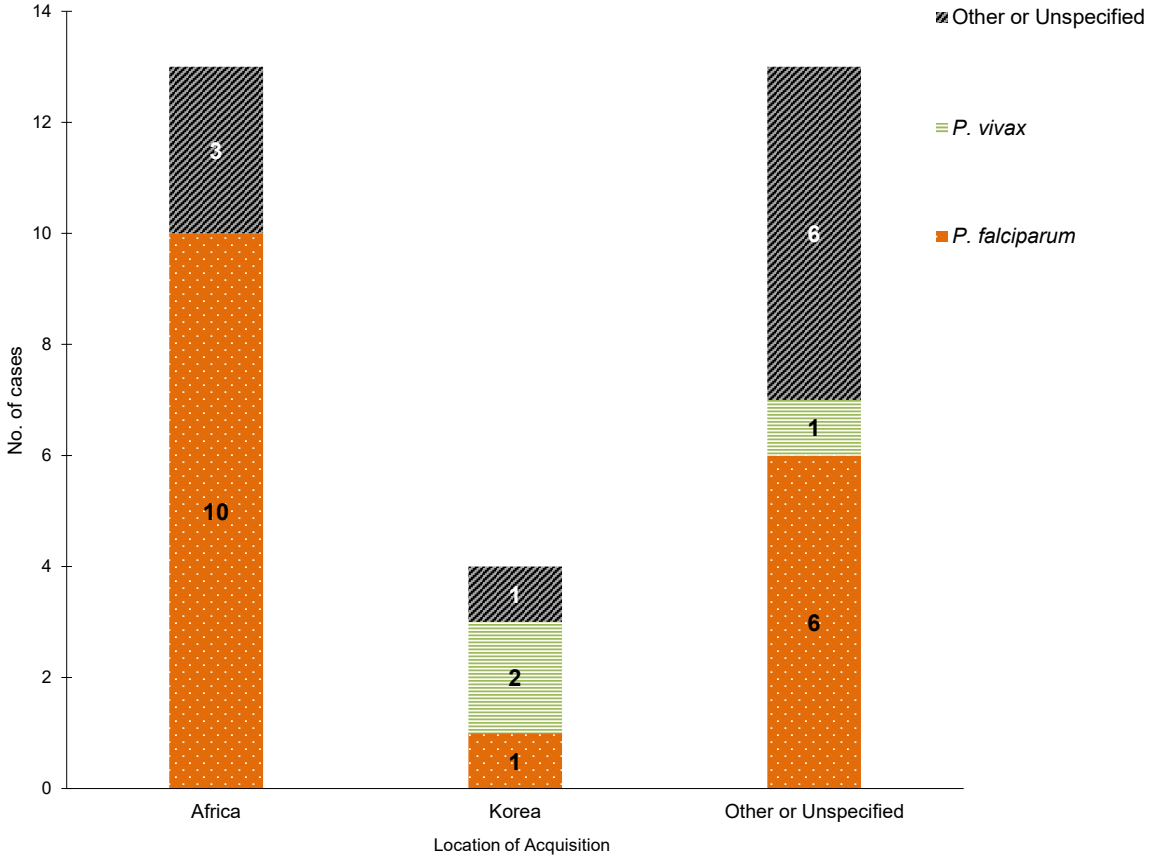
Abbreviations: *P, Plasmodium*; No., number.

FIGURE 2. Numbers of Malaria Cases by Location of Acquisition, Active and Reserve Components, U.S. Armed Forces, 2015–2024



Abbreviation: No., number.

FIGURE 3. Numbers of Malaria Cases by Species Type and Location of Acquisition, Active and Reserve Components, U.S. Armed Forces, 2024



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

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, 2024

Location Where Diagnosed or Reported	Korea	Africa	South or Central America	Other or Unknown Location	Total	
	No.	No.	No.	No.	No.	%
William Beaumont AMC, Fort Bliss, TX	0	1	0	3	4	13.3
NH Okinawa, Japan	1	0	0	3	4	13.3
Darnall AMC, Fort Cavazos, TX	0	2	0	0	2	6.7
Expeditionary Medical Facility, Djibouti	0	2	0	0	2	6.7
Brian D. Allgood ACH, Pyeongtaek, South Korea	1	1	0	0	2	6.7
NH Camp Pendleton, CA	0	1	0	0	1	3.3
NMC San Diego, CA	0	1	0	0	1	3.3
Evans Carson ACH, Fort Carson, CO	0	0	0	1	1	3.3
96th Medical Group, Eglin AFB, FL	0	0	0	1	1	3.3
Winn ACH, Fort Stewart, GA	0	1	0	0	1	3.3
Walter Reed National Military Medical Center, MD	0	0	0	1	1	3.3
Fort Meade Medical Department, MD	0	0	0	1	1	3.3
Reynolds AHC, Fort Sill, OK	1	0	0	0	1	3.3
Madigan AMC, Fort Lewis, WA	1	0	0	0	1	3.3
Naval Station Norfolk Branch Health Clinic, VA	0	0	0	1	1	3.3
Landstuhl Regional Medical Center, Germany	0	1	0	0	1	3.3
86th Medical Group, Ramstein Air Base, Germany	0	1	0	0	1	3.3
NBHC Naval Support Activity, Bahrain	0	1	0	0	1	3.3
Location not reported	0	1	0	2	3	10.0
Total	4	13	0	13	30	100

Abbreviations: No., number; AMC, Army Medical Center; ACH, Army Community Hospital; AHC, Army Health Clinic; AMC, Army Medical Center; AFB, Air Force Base; NH, Naval Hospital; NMC, Naval Medical Center.

and other *Plasmodium* species (n=13, 3.8%). The annual percentages of cases attributed to *P. vivax* from 2015 through 2024 showed the greatest variability, ranging from 5.1% in 2023 to 51.7% in 2020 (data not shown).

Between 2015 and 2024, most non-*P. vivax* malaria cases (66.1%) were diagnosed or reported during the 6 months from the Northern Hemisphere middle of spring through the middle of autumn (i.e., 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: Afghanistan (86.4%, n=19/22), Korea (79.2%, n=19/24), Africa (68.5%, n=113/165), and South and Central America (50.0%, n=1/2) (data not shown).

Discussion

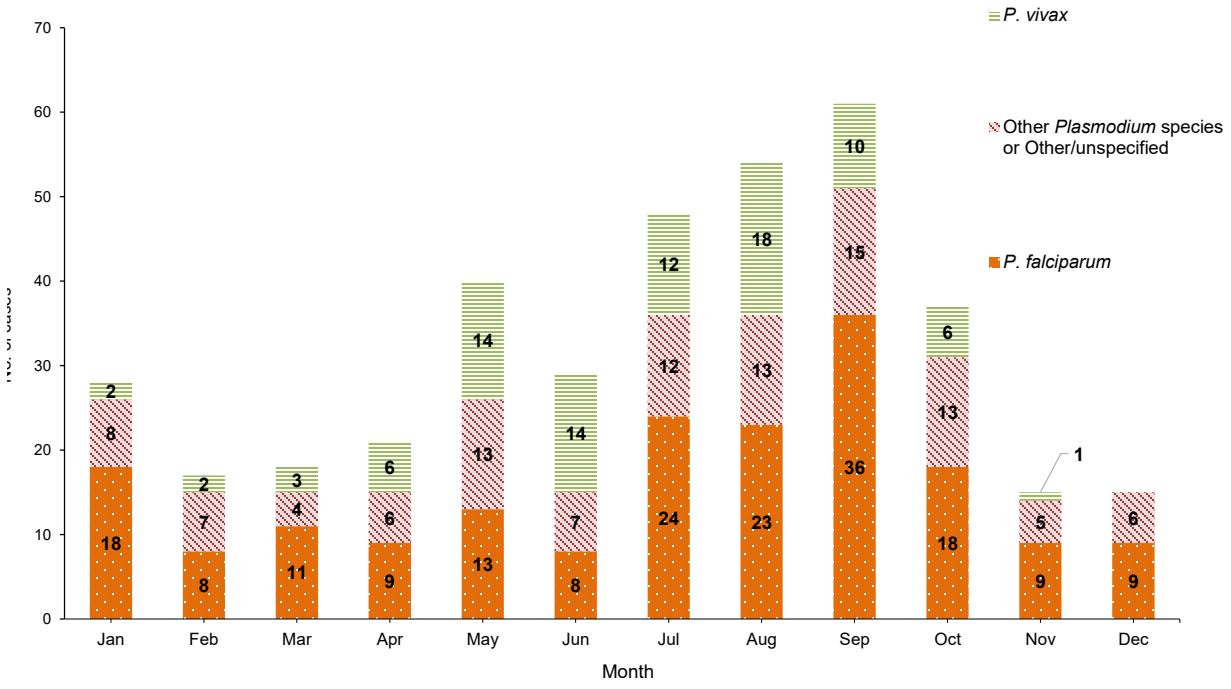
The 30 active and reserve component service members diagnosed with or reported to have malaria in 2024 represent a 23.1% decrease from the 39 cases reported in 2023. This decline may be attributed to effective countermeasures such as chemoprophylaxis and insecticide-treated uniforms or decreased risk of U.S. military personnel in areas of high malaria transmission. The most substantial decline in malaria cases reported from 2020 through 2021 may be attributed to progressive withdrawal of U.S. personnel from Afghanistan, along with restrictions on international travel due to the COVID-19 pandemic.

In 2024, *P. falciparum* persisted in more than half of U.S. service member malaria cases, demonstrating the need for continued focus on disease prevention, given its severity and mortality. The persistent burden of *falciparum* malaria acquired in Africa also emphasizes the importance of timely diagnostics for service members in deployed settings. The possibility of false negative results for *P. falciparum* on rapid diagnostic tests (RDTs) favored by units in resource-limited or austere locations was noted in 2019.[11] Since then, the emerging prevalence of mutant pfhrp2/3-deleted *P. falciparum* parasites has been described in parts of U.S. Southern Command (SOUTHCOM) and Africa Command (AFRICOM), highlighting the risk of hrp2-based rapid diagnostic tests as an unsuitable diagnostic tool for malaria in many countries.[12] In 2019, WHO outlined new recommendations to use non-HRP2-based RDTs when the prevalence of pfhrp2/3 deletions that cause false-negative results exceeds 5% in the specified geographic area for malaria risk.[13] These recommendations present a need for continued surveillance on the frequency and distribution of these mutant parasites where service members may deploy, as well as the development of alternative RDTs.[14]

Malaria continues to present a medical concern for service members traveling to endemic regions while on leave, as 40% of malaria cases in RMEs in 2024 occurred during non-duty travel. For service members traveling to malaria-endemic regions, pre-travel chemoprophylaxis should be emphasized; however, prescribing practices vary among Military Health System (MHS) and civilian health care providers.[14] While force health protection policy plays a major role in standardizing chemoprophylaxis regimens that may be indicated for a mission plan,[15] solutions are needed to extend risk management and prevention policies beyond large-scale deployment conditions.[14]

This report does not assess prescribed chemoprophylaxis adherence, but several

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, 2015–2024



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

studies document low adherence and inadequate chemoprophylaxis during periods of deployment or travel to endemic regioms.[16,17] In 2018, the CDC assessed 38 U.S. military personnel malaria cases using the National Malaria Surveillance System (NMSS) and National Notifiable Diseases Surveillance System (NNDSS), finding that 25 (65.8%) personnel members received any form of prophylaxis; of those, 7 (28.0%) took all doses of a correct regimen.[18] Only half of the malaria cases among active and reserve component U.S. service members in 2024 identified in this report were from RME records, hindering full assessment of chemoprophylaxis use and adherence.

Seasonality patterns should be considered in force health protection plans for optimal vector control and drug-based intervention strategies.[19] Non-*P. vivax* malaria case seasonality in this report is compatible with a presumption of greatest risk of malaria acquisition from May through October in temperate, climatic zones of the Northern Hemisphere. Rainfall and temperature are also significant factors for malaria seasonality; rainfall postpones onset of malaria transmission only in areas with high seasonal precipitation from September through November, as in sub-Saharan Africa; otherwise, malaria may be transmitted all year.[20]

Limitations to this report should be considered when interpreting its findings. Malaria case reporting, especially for reserve components and non-deployment exposures, is likely incomplete, contributing to under-estimation of rates; some cases treated in deployed or non-U.S. military medical facilities may not have been reported or otherwise ascertained at time of analysis. Malaria diagnoses documented only in outpatient settings without confirmatory testing and not reported as RMEs were not included in this report. Geographic location of malaria acquisition was estimated from reported information, with some cases reporting exposures in multiple malaria-endemic areas and others with no relevant exposure information. Personal travel or deployment to malaria-endemic countries was not documented unless specified in RMEs. Limited information on species type in RME records emphasizes the need for more complete attention to documentation of reportable conditions.

MSMR annually publishes malaria cases identified through comprehensive surveillance—evaluation of RMEs, hospitalization records, and laboratory results generated from the MHS—to inform force health protection policy. Malaria infection remains a potential health threat to U.S. service members within or near endemic areas due to duty assignment, contingency operations, or personal travel.

Acknowledgments

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Brief Report

Forecasting Influenza with the Long Short-Term Memory Model: Results from the 2023-2024 Influenza Season

Sneha P. Cherukuri, MS; Mark L. Bova, MPH; Shaylee P. Mehta, MPH; Christian T. Bautista, PhD

Timely detection of infectious diseases and health threats is of increasing importance, particularly for U.S. military service members. Existing surveillance systems are hindered, however, by a 1- to 2-week delay between actual disease outbreaks and release of surveillance data.[1] To address this challenge, since 2019 the Integrated Biosurveillance (IB) Branch of the Armed Forces Health Surveillance Division has conducted forecasting activities during influenza season to provide early warning and increased awareness of potential health risks to the Department of Defense (DOD) enterprise.[2] At the end of each influenza season, IB evaluates the performance of the individual forecasting models and assesses potential integration of new algorithms to improve forecasting capabilities for the next influenza season.

The Long Short-Term Memory (LSTM) model is a machine-learning method with potential to improve forecasting accuracy for respiratory disease surveillance.[3] The LSTM model is a recurrent neural network model that can be used in almost all modeling fields. LSTM has the capacity to selectively add new information and forget previously accumulated information. While LSTM models are well-established, their performance in forecasting influenza encounters utilizing DOD surveillance data has not been studied. This report assesses the performance of the LSTM model for possible inclusion in future DOD influenza forecasting analyses.

Methods

Influenza encounters were defined as outpatient visits with an International Classification of Diseases, 10th Revision (ICD-10) discharge diagnosis code, with codes J09 through J11 selected and identified for influenza encounters. Outpatient influenza encounter data from Military Health System (MHS) beneficiaries were collected weekly during the 2023-2024 influenza season from all U.S. military hospitals and clinics. Total outpatient encounter data were obtained from the DOD's Electronic Surveillance System for the Early Notification of Community-based Epidemics (ESSENCE). The percentage of outpatient influenza encounters was calculated as the weekly percentage of total outpatient encounters.

Short-term, 1-2-week forecasts were previously generated by the IB Branch each week during the influenza season for the U.S., including all military hospitals and clinics for 2023 epidemiological week (EW) 40 through 2024 EW 20. Forecasts were generated weekly using various time series and machine learning models, including autoregressive integrated moving average (ARIMA), error-trend-seasonality (ETS), exponentially weighted moving average (EWMA), naïve (NAÏVE), neural network (NNET), poisson (POISSON), prophet (PROPHET), random forest (RF), time series linear model (TSLM), and vector autoregressive (VAR) model. An ensemble model (ENSEMBLE) was created as an average of all the forecasting models used.

Short-term, 1-2-week LSTM model forecasts were generated for percentages of MHS influenza encounters for each week of the 2023-2024 influenza season by utilizing training data from the previous influenza season (2022 EW 40 through 2023 EW 20). Forecast horizons, the timeframe for which a forecast is made, were defined for 1 week, 2 weeks, and 1-2 weeks ahead. To validate the model, the data were separated into training and testing sets for each EW of evaluation. Training loss was calculated using mean squared error (MSE). Key hyper-parameters including number of hidden units (50), dropout rate (0.2), and an adaptive retrospective period were used to improve model performance.

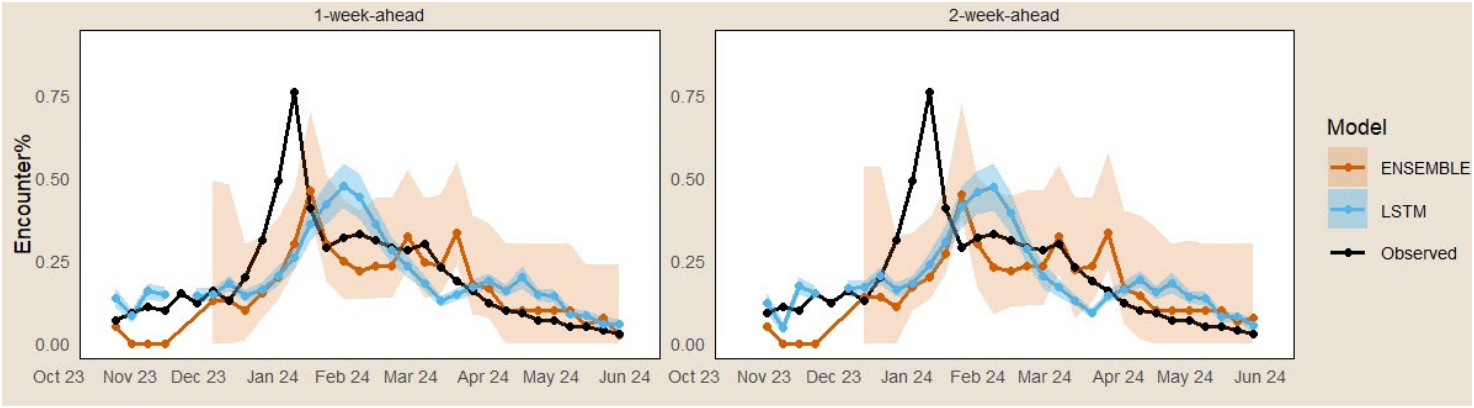
Weekly forecasts were then compared with observed values from each EW using the weighted interval score (WIS)[4] and absolute percentage error (APE). Scores from the LSTM model were then combined with all previously generated model scores to assess model performance.

All analyses and data processing used R version 4.4.2. LSTM models were created using the "torch" package in R, an open-source machine learning framework based on PyTorch.[5]

Results

WIS, log-transformed WIS, and APE were calculated for 1,924 total forecasts. The average training loss per evaluation week for the LSTM model was 0.5. Median log-transformed WIS and median APE are shown in the **Table** for each model as well as 1-week, 2-week, and combined 1-2-week forecasts. The LSTM model had the lowest median log-transformed WIS for all forecasting horizons: 1 week (0.3), 2 weeks (0.4), and combined 1-2 weeks (0.4). The VAR model had the lowest median APE for all forecasting horizons (37.5%). **Figure 1a** presents forecasts with 95% confidence interval (CI) bands for the LSTM and ENSEMBLE models over the study period. During 2023 EWs 51 and 52, observed influenza encounter percentages peaked at 0.5% and 0.8%, respectively. The LSTM and ENSEMBLE models under-predicted values, however, with estimates ranging from 0.17% to 0.2% during this period. **Figure 1b** displays a grouped boxplot of log WIS for each forecast target for all models,

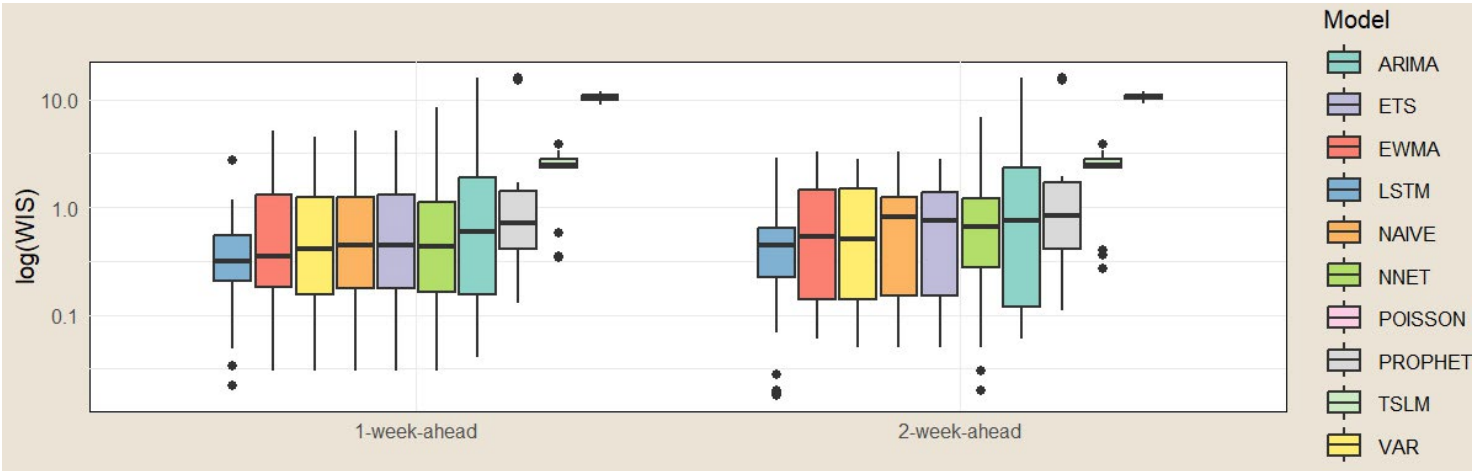
FIGURE 1a. Influenza Encounter Percentage by Forecast Target, Military Health System, November 2023–June 2024



Abbreviations: LSTM, long short-term memory; EW, epidemiological week.

[a] 95% Confidence intervals are represented in shaded area. LSTM values for EW 45 in the 1-week ahead target and EW 46 in the 2-week ahead target exceed values of 3.5 and are therefore not depicted.

FIGURE 1b. Weighted Interval Score by Forecast Target



Abbreviations: WIS, weighed interval score; ARIMA, autoregressive integrated moving average; ETS, error-trend-seasonality; EWMA, exponentially weighted moving average; LSTM, long short-term memory; NNET, neural network; TSLM, time series linear model; VAR, vector autoregressive.

ranked by median log WIS. The LSTM model had the lowest log WIS, while the POISSON model had the highest.

Discussion

Our analyses indicate that LSTM had the lowest log WIS among the individual models for all forecasting horizons, resulting in more accurate forecasts. These findings align with previous studies that successfully used LSTM models to forecast influenza-like illness and influenza hospitalizations.[6,7] Neither the LSTM nor ENSEMBLE models accurately predicted the peak period, 2023 EWs 51-52 (December 17-30), however. This could be due to the utilization of 2022-2023 influenza season data for the training data, as recent seasonal influenza patterns have exhibited significantly higher peaks earlier in the season compared to influenza seasons prior to the COVID-19 pandemic.[8,9] To improve influenza peak period forecasts, training data may need to include multiple years, before and after the COVID-19 pandemic, as part of further analysis.

This study had some limitations. First, this study did not employ a formal cross-validation method to optimize hyper-parameters and construct the best-performing LSTM model, which may have contributed to poor predictions, particularly in the early weeks of the study period. Further research is needed to optimize the LSTM model for influenza encounter predictions. Second, some WIS values were found to be 0, indicating that the estimated value was an exact match to the observed value. Scores equal to 0 should be interpreted with caution, as those values may be due to overconfidence and result in an undefined log-transformed WIS.[10] Consequently, WIS values equal to 0 were excluded from the calculation of log-transformed WIS, but this may have introduced bias by excluding forecasts that were very close to actual values. Third, it is not possible to state with confidence that these results are generalizable to other respiratory diseases or related metrics such as hospitalizations, admission rates, or case rates. Lastly, this analysis does not reflect changes after the 2023-2024 influenza season to improve forecasting, such as the removal of the ETS, EWMA, PROPHET,

TABLE. Median Weighted Interval Score (WIS) and Median Absolute Percent Error for Outpatient Influenza Encounter Forecasts in the Military Health System Population

	1 Week Ahead		2 Weeks Ahead		1-2 Weeks Ahead	
Model	Median Log (WIS)	Median Absolute Percent Error (%)	Median Log (WIS)	Median Absolute Percent Error (%)	Median Log (WIS)	Median Absolute Percent Error (%)
LSTM	0.3	45.9	0.4	43.7	0.4	45.2
EWMA	0.4	37.5	0.5	42.9	0.4	37.5
VAR	0.4	37.5	0.5	37.5	0.4	37.5
NAIVE	0.4	37.5	0.8	42.9	0.5	37.5
ETS	0.4	37.5	0.8	42.9	0.6	37.5
NNET	0.4	41.2	0.7	45.2	0.6	42.9
ARIMA	0.6	42.9	0.8	42.9	0.7	42.9
PROPHET	0.7	42.9	0.8	38.5	0.7	39.4
TSLM	2.4	65.5	2.4	65.5	2.4	65.5
POISSON	10.3	64.9	10.7	64.9	10.5	64.3
RF	NA*	39.2	NA	46.5	NA	42.9

Abbreviations: NA, not available; MHS, Military Health System.

and TSLM models. Although the LSTM model outperformed several models included in the ENSEMBLE model, it is likely the ENSEMBLE model will perform better for the 2024-2025 influenza season.

The findings of this study demonstrate that the addition of the LSTM model improves the short-term forecasting performance of the ENSEMBLE model for outpatient influenza encounter data, which is commonly used to assess the activity intensity of this respiratory disease within the MHS population. Further research is recommended to determine the performance of the LSTM model for other respiratory infections, including COVID-19.

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Guest Editorial

The Department of Defense Global Respiratory Pathogen Surveillance Program: Its Impact on Public Health, from the U.S. Armed Forces to Global Health

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The U.S. Department of Defense Global Respiratory Pathogen Surveillance Program (DoDGRPSP) has supported the prevention of respiratory illness in the U.S. Armed Forces since 1976, supported by the Armed Forces Health Surveillance Division Global Emerging Infections Surveillance (AFHSD-GEIS) branch of the Defense Health Agency (DHA) since 1997. DoDGRPSP utilizes a global network of sentinel sites and partner laboratories to collect respiratory surveillance data and share its findings with the U.S. Department of Defense (DOD) and installation stakeholders. Several significant findings have resulted from the program in the last decade, including novel influenza detections, outbreak characterizations, and early detection of SARS-CoV-2 variants. The program collaborates with other DOD and government entities to inform public health decisions, including vaccine effectiveness estimates, phylogenetic analyses, and antigenic characterizations to the U.S. Food and Drug Administration to aid selection of influenza strains for subsequent U.S. vaccines. DoDGRPSP adapts to changes in emerging pathogens, evolution of known pathogens, advancements in respiratory pathogen testing assays and instruments, new analytical methods, and new sequencing technologies. The program continues to provide continuous respiratory pathogen surveillance data, vaccine effectiveness estimates, and sequence data analyses in reports and peer-reviewed publications to DOD, government, and global partners.

The U.S. military plays a crucial role in combatting global respiratory illnesses. The close quarter, high stress environments of training stations that house recruits from a wide range of geographic areas constitute ideal situations for the introduction, spread, and mutation of respiratory pathogens. Conditions are similar at deployed locations, but with added risk of service member exposure to novel pathogens not encountered in the U.S. The regular movement of military personnel through deployments and routine changes of station facilitates wide diffusion of pathogens across an enormous geographic range and makes isolation of emergent pathogens extremely difficult.

The global network of U.S. military installations, in addition to providing locations of deployment and coordination with foreign military units, also afford extraordinary capacity for identifying and characterizing respiratory illnesses. The U.S. Department of Defense Global Respiratory Pathogen Surveillance Program (DoDGRPSP), currently based at Wright-Patterson Air Force Base (AFB) in Dayton, Ohio, is a cornerstone of U.S. Department of Defense (DOD) respiratory disease surveillance. DoDGRPSP currently relies upon a surveillance network of 115 active sentinel sites in addition to other participating sites, deployed locations, and partner laboratories.

DoDGRPSP was established in 1976 as part of the U.S. Air Force School of Aerospace Medicine (USAFSAM) at Brooks AFB in San Antonio, Texas. Then known as "Project Gargle," the program initially collected specimens from Lackland AFB, which conducted Air Force basic training. Over time, the program expanded its specimen collection from military and Coast Guard sites within the contiguous U.S. (CONUS) as well as outside the contiguous U.S. (OCONUS). Twenty years after the program was founded, the 1996 Presidential Decision Directive, National Science and Technology Council-7, tasked the DOD with enhancing its mission by increasing global surveillance for emerging infectious disease, improving research and training, engaging with international partners, and strengthening public outreach to address emerging infectious diseases. In response to this directive, the following year the DOD Global Emerging Infections Surveillance (DOD-GEIS) program was established.

In the years after DOD-GEIS was established, OCONUS DOD laboratories expanded their reach, capability, and coordination with CONUS surveillance systems, which at the time primarily comprised

USAFSAM and the Naval Health Research Center (NHRC) in San Diego, California. By 2006, the 2 programs had expanded to include all DOD services, with increased surveillance networks and standardized force health protection communications to CONUS and OCONUS facilities. In 2011, DOD-GEIS was transferred to the (now) Armed Forces Health Surveillance Division (AFHSD), and USAFSAM was relocated to Wright-Patterson AFB.[1] More recent DHA reorganization shifted DoDGRPSP authority to the Defense Centers for Public Health–Dayton (DCPH-D).

Year-round data collection from respiratory testing at USAFSAM / DCPH-D allows DoDGRPSP to create seasonal epidemiological curves for influenza, SARS-CoV-2, and numerous other respiratory pathogens. These curves encompass cumulative, regional, or installation-specific data, allowing leadership, health care providers, or public health employees within participating sites, Combatant Commands (COCOMs), or the DOD to determine risk levels, causative agents of respiratory illness, or mount appropriate public health measures.

Collaborations

DoDGRPSP collaborates with other DOD as well as non-DOD government agencies to ensure that surveillance data collected are efficacious for force health protection. The program routinely communicates with government partners to maintain up-to-date testing and sequencing assays, assess currently circulating strains and analyses, evaluate naming conventions, and share data or specimens that may be unique or propitious. These consultations occur with regularity throughout the year but intensify in the months preceding the annual World Health Organization (WHO) and Vaccines and Related Biological Products Advisory Committee (VRBPAC) meetings for the Northern Hemisphere and U.S. influenza strain recommendations, respectively.

One of the signal functions of DoDGRPSP is the preparation and presentation of the surveillance data for U.S. influenza vaccine strain recommendations. Each year, the U.S. Food and Drug Administration (FDA) VRBPAC[2] meets to discuss the annual influenza vaccine. In addition to the Centers for Disease Control and Prevention (CDC), a DOD representative presents mid-season surveillance results, vaccine effectiveness (VE) estimates, phylogenetic data, and antigenic cartography information to the committee, which then votes to accept or reject strain recommendations made by WHO based on season-to-date VE of current strains, subtype dynamics, and changes to circulating influenza virus clades.[3]

For antigenic characterization data, DoDGRPSP partners with the Navy Medical Research Command (NMRC) in Silver Spring, Maryland, to share specimens and data that are relevant to diverse strains of circulating influenza and SARS-CoV-2. Antibodies raised against current and candidate vaccine strains are tested against circulating strains to comparatively test levels of inhibition and determine which strains could provide broadest protection. These data are visually modeled using antigenic cartography and then presented to VRBPAC.

DoDGRPSP also collaborates with agencies such as the National Center for Biotechnology Information (NCBI), the Walter Reed Army Institute of Research (WRAIR), and the Infectious Disease Clinical Research Program (IDCRP) on, for example, database nomenclature consultation,[4] influenza vaccine breakthrough sieve analysis studies (ongoing, unpublished), the ARIA (Acute Respiratory Illness at Academies) study (ongoing, unpublished), and the PAIVED (Pragmatic Assessment of Influenza Vaccine Effectiveness in the DOD) study.[5]

Surveillance Network

A crucial part of any successful surveillance program is a robust network of collection sites and personnel not only capable but willing to participate. The DoDGRPSP team relies on a program network of sentinel, participating, deployed, and partner sites in multiple ways. Any breaks in a surveillance network risk missed important surveillance data, skewed data analyses, and a distorted picture, in scale or scope, of an emerging outbreak or seasonal trends.

At the beginning of each season, an approved program memorandum outlines site participation criteria and lists the sentinel sites selected to submit samples for the season. The list of sites is for broad, evenly distributed geographic coverage, while taking into consideration installation populations, capabilities, tri-service coverage, and past program participation. Sentinel sites may be removed from the list if they lack the resources to participate (e.g., freezers, facilities, personnel), or conversely, can be added based on ability and willingness to participate. OCONUS partner laboratories, which generate their own data through sample collection, testing, and sequencing, can help mitigate geographic gaps in surveillance data.

Sites participating in DoDGRPSP are asked to submit 6 to 10 respiratory specimens per week from patients meeting an influenza-like or COVID-19-like illness case definition (i.e., fever at or above 100.4°F and cough or sore throat[6]) or 1 or more symptoms associated with influenza or COVID-19, although clinical suspicion of respiratory illness also qualifies for submission. In response to the 2024 increase in cattle and human cases of avian influenza A(H5N1), conjunctivitis with known exposure to agricultural animals or humans infected with influenza A(H5N1) was added as a symptom category.[7] Participating sites are also asked to have personnel submit a questionnaire that collects patient demographic, symptomatic, and vaccination history information. These questionnaires allow the program to perform VE analysis, as well as reporting or conducting studies based on cumulative patient demographic or symptomology associated with laboratory results.

Education and training are vital components of maintaining a surveillance network. At the beginning of each season, online training sessions are conducted for the surveillance sites, at multiple times and dates to accommodate schedules and global time zones. Each training is followed by a question-and-answer session. DoDGRPSP team members also conduct selected site visits each year, which provide direct interactions whereby team members can learn about the processes and workflows of individual installations

while providing potential solutions to barriers of participation, often based on experiences from other sites. These in-person meetings lead to closer relationships with points of contact that can help bolster participation. The DoDGRPSP team reaches out to sites with low participation as a reminder of compliance and to help mitigate any problems that may be hindering sample submission such as collection kit supplies or MHS GENESIS ordering issues.

Specimen Testing

Specimens collected through the DoDGRPSP surveillance network are clinically tested in the College of American Pathologists (CAP)-accredited Epidemiology Laboratory in the Public Health department at USAFSAM/DCPH-D. Prior to 2018, specimens were initially tested using CDC influenza A/B and A subtype RT-PCR assays,[8] with influenza-negative specimens tested on the BioFire FilmArray Respiratory Panel (RP),[9] which tests for additional pathogens listed in **Table 1**. If an influenza A specimen could not be subtyped on either assay, then CDC influenza A/H5 and A/H7 subtype assays were performed. A positive A/H5 or A/H7 would be sent to the CDC for confirmation, although to date no positives have been identified. Selected specimens undergo viral culture to grow isolates and characterize pathogens **(Table 1)**. Sanger sequencing was performed on isolates from influenza-positive specimens for the hemagglutinin (HA), neuraminidase (NA), and matrix protein (MP) genes.

Beginning in 2018, the Luminex NxTag Respiratory Pathogen Panel (RPP) was adopted, and the testing algorithm was adjusted to perform RPP first, then CDC influenza A/B and A subtype RT-PCR on un-subtyped influenza specimens. The NxTag RPP allows high throughput testing for the pathogens listed in **Table 1**. Next-Generation Sequencing (NGS) was also adopted in 2018, allowing whole genome sequencing of influenza-positive specimens using an original specimen rather than cultured isolates. When the COVID-19 pandemic began, SARS-CoV-2 PCR was adopted, as well as whole genome sequencing of other selected respiratory-positive specimens.

An average of 5,760 (range 4,915–6,338) specimens were tested each season from 2014 until 2018, when the CDC influenza assays were the primary testing procedure, followed by FilmArray RP. During the same period, the average number of influenza-positive specimens sequenced was 1,363 (range 1,080–1,698), using Sanger sequencing.

After changing the primary testing method to the NxTag RPP, the number of specimens tested increased to 12,305 in the 2018-2019 season. The average number of specimens increased in the following seasons, but those numbers were skewed by the sheer number of SARS-CoV-2 tests performed during the 2020-2021 and 2021-2022 seasons. With implementation of NGS in 2019, the number of influenza-positive specimens sequenced increased to 3,059, for the 2018-2019 season.

Due to the COVID-19 pandemic, the number of influenza specimens sequenced each season has varied widely. The average number of SARS-CoV-2 positives sequenced per season from 2020 to 2024 was 5,574 (range 1,361–12,118) **(Table 2)**.

In addition to testing at USAFSAM/DCPH-Dayton, DoDGRPSP imputes surveillance data through data pulls and questionnaires from Landstuhl Regional Medical Center (LRMC) in Germany, Incirlik Air Base in Turkey, as well as Brooke Army Medical Center (BAMC) in Texas. Additional influenza sequence data have been supplemented through partnerships with global GEIS network partner laboratories (which are listed in the Acknowledgments).

TABLE 1. Respiratory Panel Testing at USAFSAM/DCPH-D Epidemiology Laboratory, 2014–Present

Pathogen	Type of Testing		
	BioFire FilmArray Respiratory Panel 2014-2018	Luminex NxTag Respiratory Pathogen Panel 2018-Present	Viral Culture
Viral			
adenovirus	✓	✓	✓
human coronavirus 229E	✓	✓	
human coronavirus HKU1	✓	✓	
human coronavirus NL63	✓	✓	
human coronavirus OC43	✓	✓	
influenza A H1	✓	✓	✓
influenza A H1-2009	✓	✓	✓
influenza A H3	✓	✓	✓
influenza B	✓	✓	✓
human metapneumovirus	✓	✓	
parainfluenza 1-3	✓	✓	✓
respiratory syncytial virus (A, B)	✓	✓	✓
rhinovirus/enterovirus	✓	✓	✓
human bocavirus		✓	
Bacterial			
Bordetella pertussis	✓		
Chlamydophila pneumoniae	✓	✓	
Mycoplasma pneumoniae	✓	✓	

Abbreviations: USAFSAM, U.S. Air Force School of Aerospace Medicine; DCPH-D, Defense Centers for Public Health–Dayton.

In-Depth Pathogen Characterization

When respiratory infections are abnormally high at an installation, within a geographic region, or when a site notifies DCPH-D about an outbreak, DoDGRPSP performs additional testing and characterization. While the collection of laboratory testing data along with demographic, syndromic, and vaccination data from questionnaires are essential, even the most complete data sets do not tell a complete story. Influenza type and subtype data alone do not provide insights into how strains may be mutating, how closely they are related to the current vaccine strain, or what strains would work best in the next vaccine formulation. Sequencing can answer many of these questions.

Each of the 8 influenza gene segments can provide some information about how a particular virus may respond to vaccine-induced antibodies, antiviral therapeutics, or the host immune system. Because they are the 2 surface proteins that interact with cellular receptors and antibodies, hemagglutinin (HA) and neuraminidase (NA) are the primary targets for determining vaccine coverage and are utilized to assign an influenza virus to a genetic grouping, or clade **(Figure 1)**. Influenza viruses in the same clade are often alike antigenically, therefore differences in circulating clades can provide insights into potential vaccine protection. Specific mutations to antigenic sites, the receptor binding site, or glycosylation motifs may alter vaccine effectiveness,[10] antiviral efficacy,[11] testing capabilities,[12] and the course of disease.[13] Additionally, mutations occurring in the remaining 6 gene segments have been known to affect antiviral resistance[11] and virulence.[13]

Epidemiologists at DCPH-D calculate influenza VE at both mid-season and end of season **(Figure 2)** by comparing vaccinated and unvaccinated patients in a case-control study, in which laboratory-confirmed influenza-positive specimens serve as cases and laboratory-confirmed influenza-negative specimens serve as controls. Crude and adjusted odds ratios (ORs) are calculated using logistic regression, and VE is calculated as (1 - OR)*100. When case numbers are high enough to yield statistically significant results, comparisons can be made among age groups, influenza subtypes, or in rare instances, genetic clades.

With the expansion to multiplex PCR testing, the program expanded its sequencing efforts to other respiratory pathogens, including SARS-CoV-2 viruses, to monitor for emerging variants, changes to variant proportions, and mutations posing possible threats to public health, either through host immune evasion, decreased response to vaccine-induced antibodies, or decreased effectiveness of therapeutic measures.

Impacts on Public Health

DoDGRPSP has detected and reported several significant findings over the past decade, including influenza clades linked to vaccine mis-matches, influenza swine variants, early detection of SARS-CoV-2 lineages, and in-depth characterizations of respiratory pathogen outbreaks.

DoDGRPSP surveillance findings are reported through the program's Common Access Card (CAC)-enabled dashboard,[14] which includes routine weekly and cumulative season reports. These reports contain summaries, trends, visualizations and interpretations of results, specimen submissions by site, and symptomatic, immunization, demographic, and sequencing data. Weekly reports are published on the dashboard as well as emailed to DOD, network partners, and entities and individuals who requested entry in the distribution list.

The program dashboard provides aggregated results for all data and regions, while sentinel sites can view their specific surveillance results along with sample and questionnaire submission numbers. Influenza and SARS-CoV-2 sequencing results were recently added to the dashboard, offering more detailed insight on circulating strains. An electronic questionnaire developed through the program dashboard[14] now allows more seamless pairing of questionnaire data to surveillance specimens;

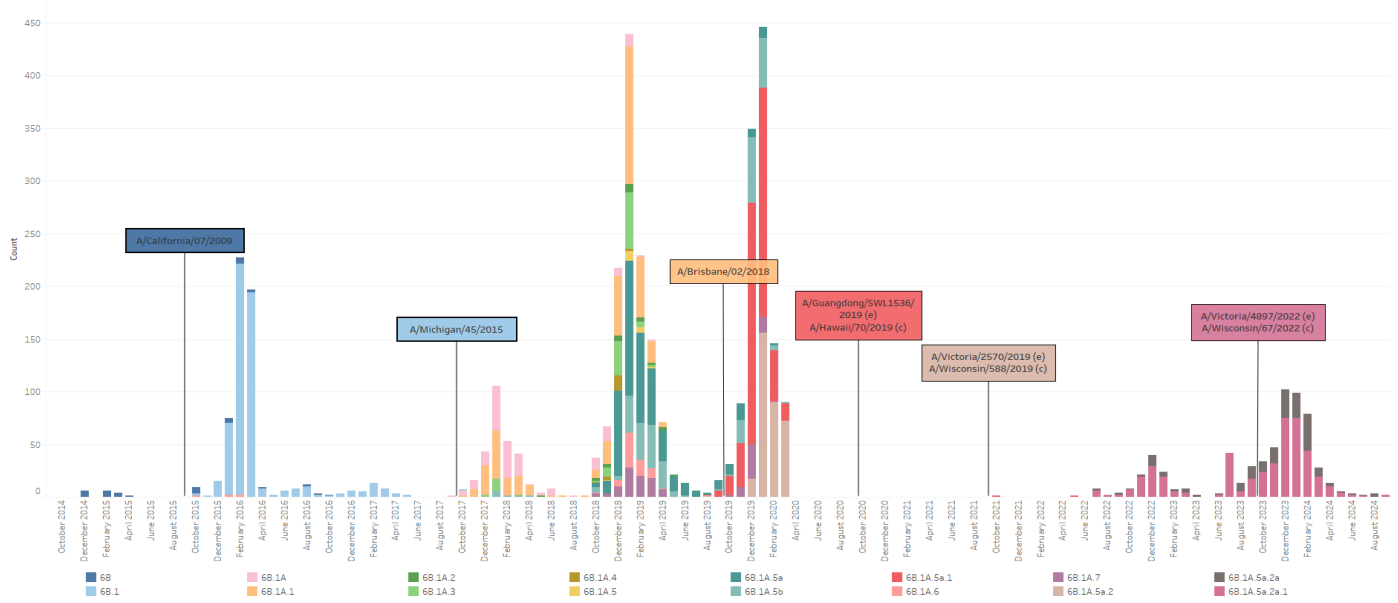
TABLE 2. Testing Data Processed at DoDGRPSP per Influenza Season, 2014–2024

	Season									
	2014–2015	2015–2016	2016–2017	2017–2018	2018–2019	2019–2020	2020–2021	2021–2022	2022–2023	2023–2024
Clinical Site										
Tested at USAFSAM/DCPH-D	6,338	4,915	6,027	9,987	12,305	24,788	60,323	30,085	6,831	9,197
Data from LRMC/EUCOM	2,445	1,439	1,617	2,451	2,119	2,345	37,800	37,370	15,903	3,379
Data from Incirlik	—	—	—	—	—	—	32	1,830	929	449
Data from BAMC	—	—	—	—	1,156	1,710	—	—	—	—
Sequencing										
Influenza sequenced	1,080	1,312	1,698	2,363	3,059	3,070	21	1,485	975	1,269
SARS sequenced	—	—	—	—	—	—	7,199	12,118	1,361	1,617

Abbreviations: DoDGRPSP, Department of Defense Global Respiratory Pathogen Surveillance Program; USAFSAM, U.S. Air Force School of Aerospace Medicine; DCPH-D, Defense Centers for Public Health–Dayton; LRMC, Landstuhl Regional Medical Center; EUCOM, European Command; BAMC, Brooke Army Medical Center; SARS, severe acute respiratory syndrome.

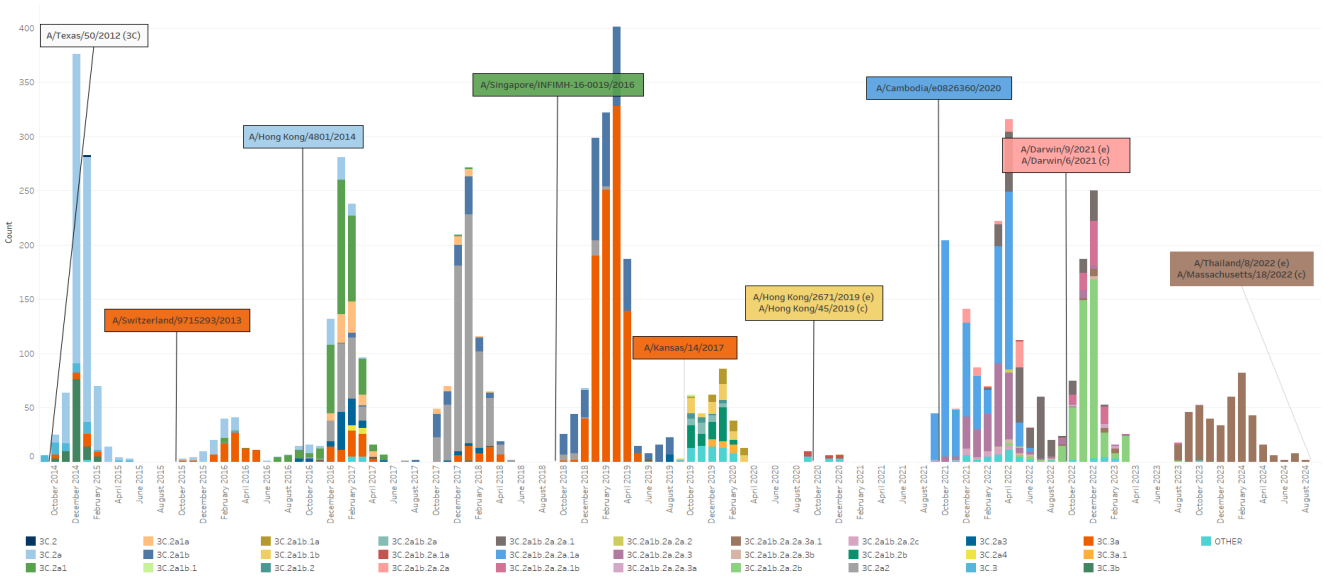
FIGURES 1a–1d. Influenza Clades for Influenza Subtype A(H1N1)pdm09, Influenza Subtype A(H3N2), Influenza Subtype B/Victoria, and Influenza Subtype B/Yamagata, October 2014–August 2024

FIGURE 1a. Influenza Subtype A(H1N1)pdm09



Note: Text boxes indicate changes to the vaccine strain composition, with the color of each text box corresponding to the associated genetic clade.

FIGURE 1b. Influenza Subtype A(H3N2)



Note: Text boxes indicate changes to the vaccine strain composition, with the color of each text box corresponding to the associated genetic clade.

site participants may prefer this option to paper questionnaires.

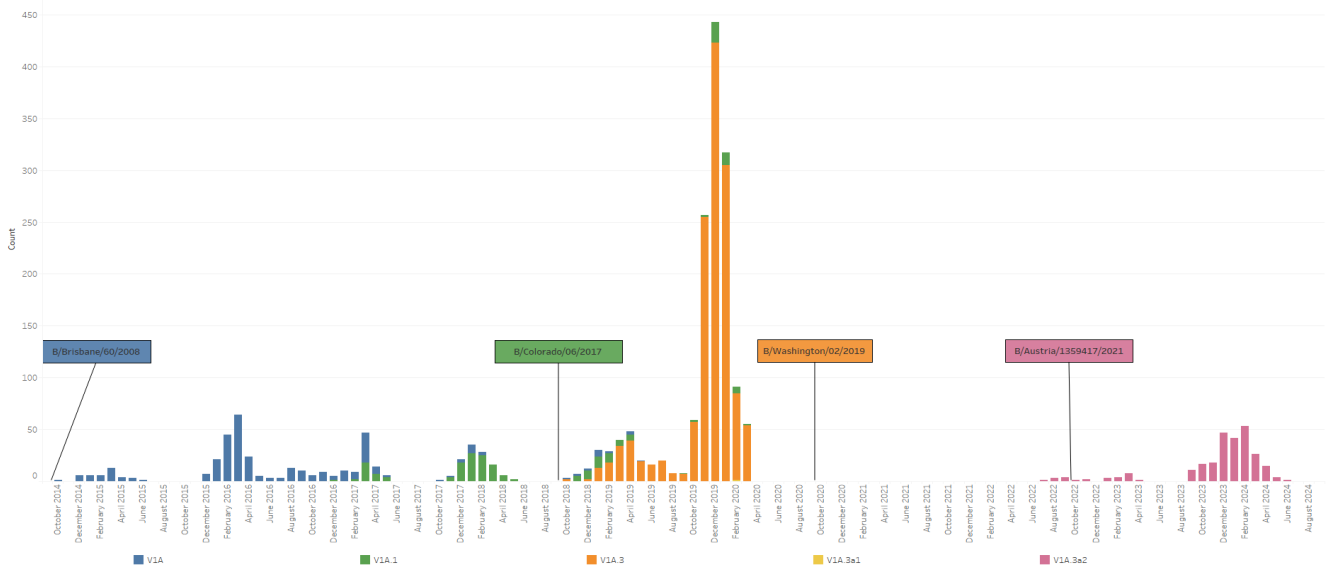
Resources such as program information, training videos, contact information, and links to the electronic or printable PDF questionnaire are available on the dashboard. Additional dashboard and report changes will not only make communicating surveillance data more efficient and timelier, but make data more easily digestible with a 'bottom line up front' (BLUF) approach and modernized tables and figures.

Data collected by the program are also shared with broader scientific and public health communities, such as with the CDC, through the Public Health Laboratory Interoperability Project (PHLIP).[15] Twice a year VE and sequencing data are contributed to the WHO Global Influenza Vaccine Effectiveness (WHO-GIVE) report, prior to the annual VRBPAC meeting for the U.S. influenza vaccine (Northern Hemisphere) strain selection, and at the end of the season for the Southern Hemisphere strain selection.

A cumulative report of the surveillance data is published in *MSMR*[16-19] and on DTIC. The program publishes specific studies, most recently a SARS-CoV-2

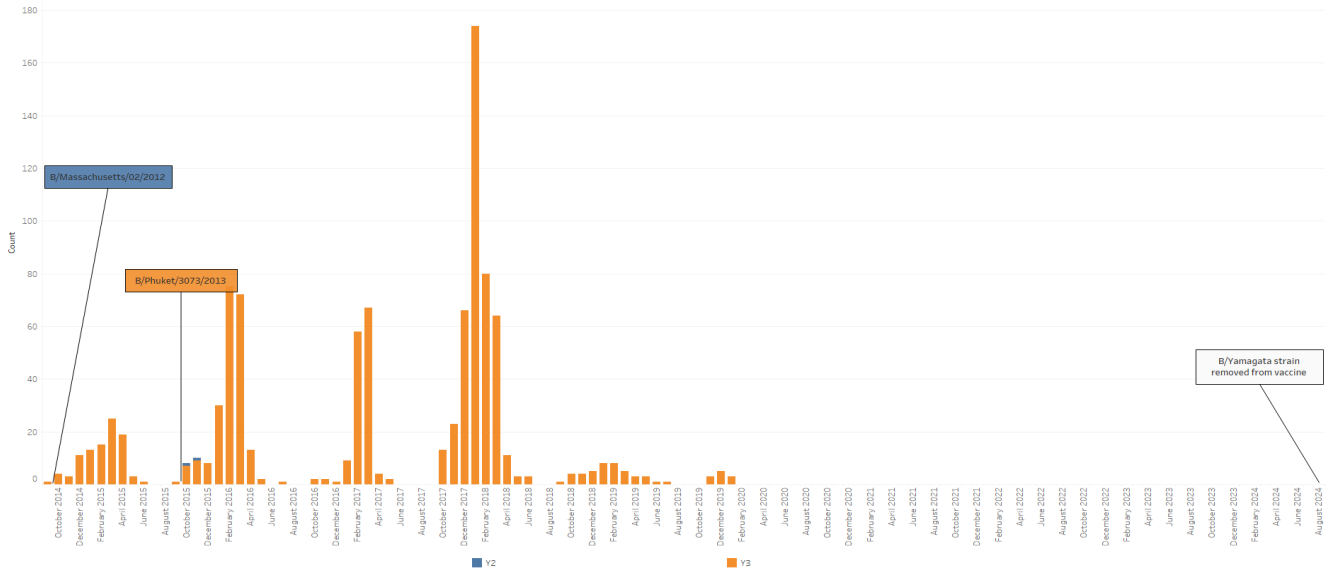
FIGURES 1a–1d. Influenza Clades for Influenza Subtype A(H1N1)pdm09, Influenza Subtype A(H3N2), Influenza Subtype B/Victoria, and Influenza Subtype B/Yamagata, October 2014–August 2024

FIGURE 1c. Influenza Subtype B/Victoria



Note: Text boxes indicate changes to the vaccine strain composition, with the color of each text box corresponding to the associated genetic clade.

FIGURE 1d. Influenza Subtype B/Yamagata



Note: Text boxes indicate changes to the vaccine strain composition, with the color of each text box corresponding to the associated genetic clade.

re-infection study in the November 2024 supplement of *Emerging Infectious Diseases*,[20] and presents posters at conferences including the Association of Public Health Laboratories, the American Society for Microbiology, the American Society of Virology, the American Society of Tropical Medicine and Hygiene, the International Conference on Emerging Infectious Diseases, and the Military Health System Research Symposium. Sequence data are de-identified and uploaded to the Global Initiative on Sharing All Influenza Data (GISAID)[21] repository and NCBI GenBank,[22] and Sequence Read Archive (SRA) repositories under USAFSAM/DCPH-D Bioprojects.[23]

DoDGRPSP recognizes the wealth of its data and potential for retrospective analyses, to inform studies and publications that can further contribute to the scientific community and advance pathogen mitigation efforts. Laboratory results, sequencing data, and syndromic and vaccination records from questionnaires in DoDGRPSP databases hold untold potential for valuable future analyses and conclusions.

DoDGRPSP is continuously evaluating improved testing platforms, procedures, analyses, and use of its surveillance data.

FIGURES 2a–2c. Vaccine Effectiveness, Influenza Subtype A(H1N1)pdm09, Influenza Subtype A(H3N2), and Influenza B, 2017–2024

FIGURE 2a. Influenza Subtype A(H1N1)pdm09

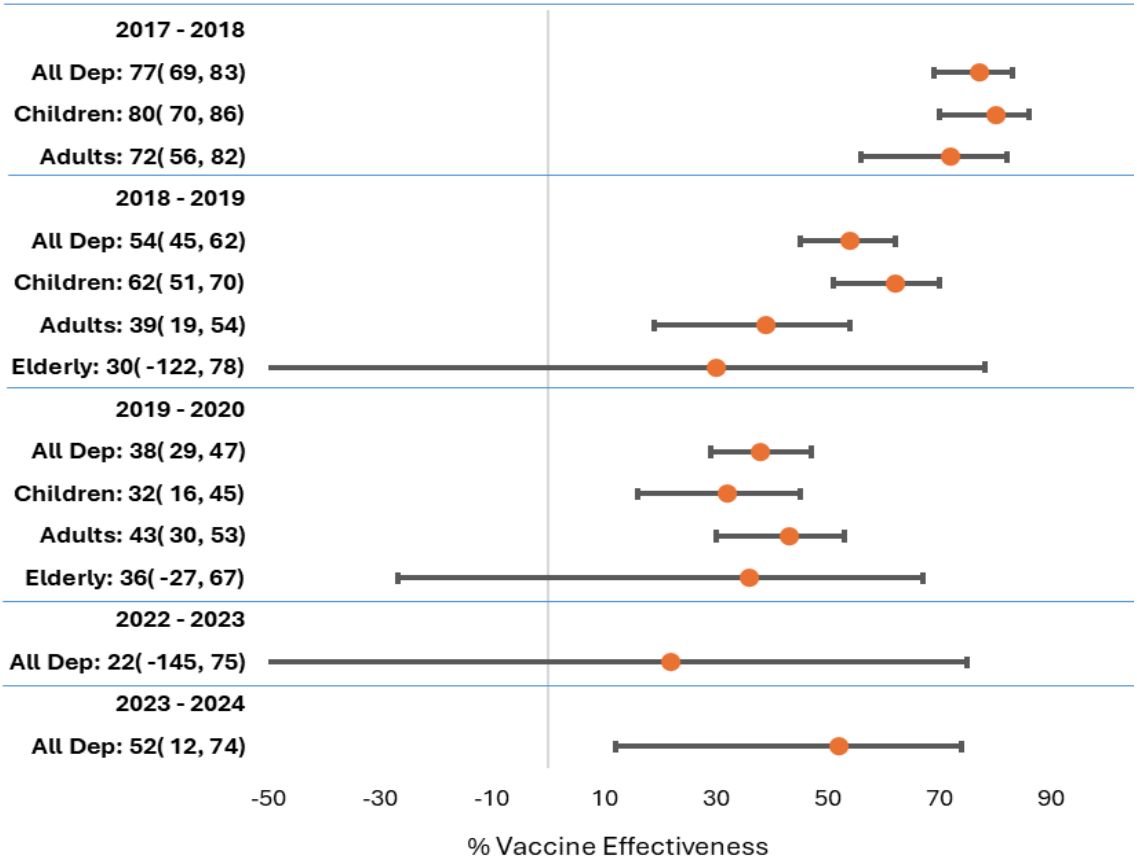
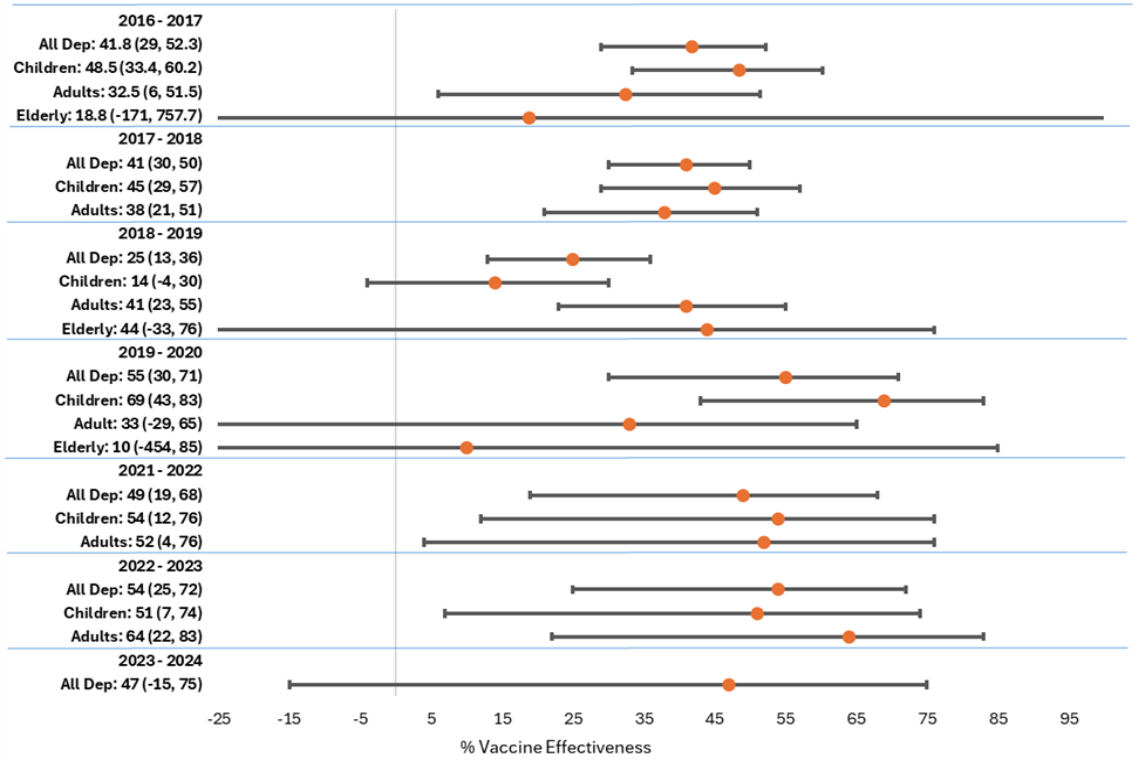
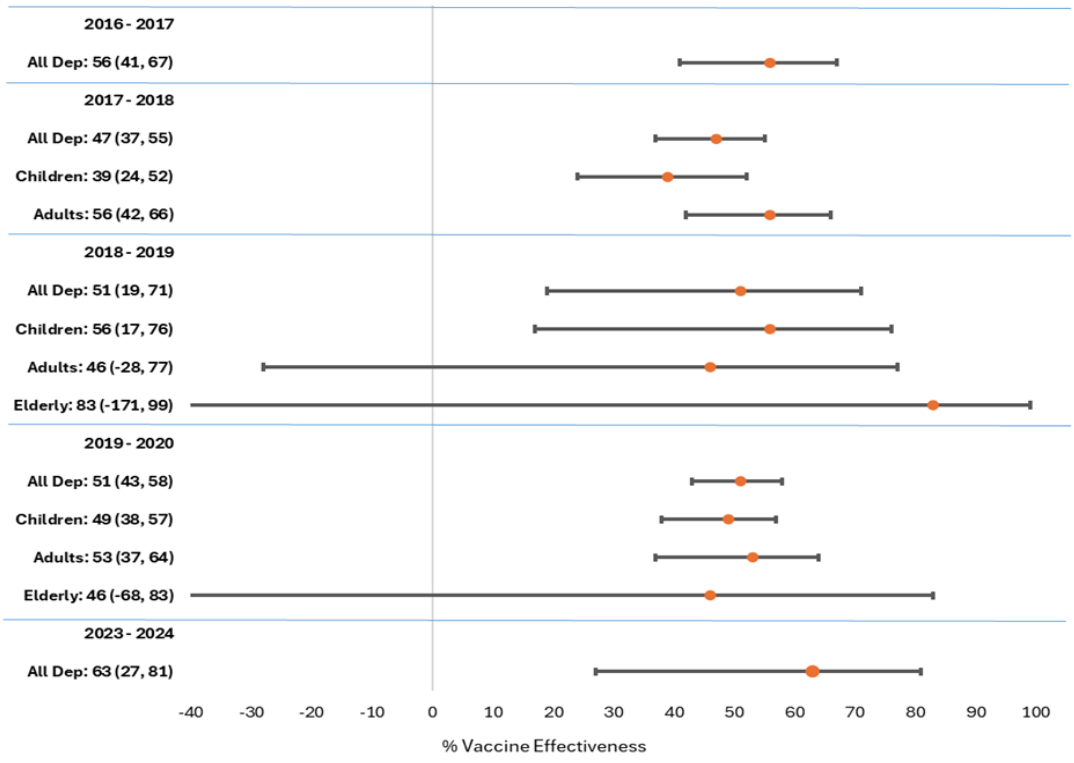


FIGURE 2b. Influenza Subtype A(H3N2)



FIGURES 2a–2c. Vaccine Effectiveness, Influenza Subtype A(H1N1)pdm09, Influenza Subtype A(H3N2), and Influenza B, 2017–2024

FIGURE 2c. Influenza B



The program assesses new instruments and assays to optimize throughput, budget, and data relevance, in addition to enhanced data reporting for optimal impacts. With the ever-changing universe of respiratory pathogens, DoDGRPSP seeks improved capacities for adaptation and response to emerging pathogens as quickly as possible, for timely and meaningful data and analysis reporting.

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Guest Editorial

Beyond the Clinic: The Importance of Department of Defense Respiratory Viral Panel Testing for Public Health Surveillance and Force Health Protection

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Historically, military populations have been at high risk for acute respiratory infections, primarily among recruits and deployed personnel due to frequent exposures to crowded conditions, deployments, and stressful work environments.[1,2] Respiratory pathogen surveillance is critical for force health protection and clinical decision-making.

The Global Emerging Infections Surveillance Branch (GEIS) of the Armed Forces Health Surveillance Division respiratory infections focus area supports routine molecular and genomic public health surveillance of respiratory pathogens in military and non-military settings where U.S. service members may come into contact with host nation civilians. Rapid detection of specific etiologic agents within a subset of clinical samples, residual samples, or in support of an outbreak[3,4] can directly enable action to reduce transmission and maintain readiness of military members, including decisions about preventive measures, medical countermeasures, and resource allocation to safeguard the health and readiness of U.S. service members, their families, and allied forces.

Early disease diagnosis can reduce likelihood of increased disease severity and prolonged recovery. Illnesses caused by respiratory viruses can affect anyone, but illness severity may be greater for older adults, young children, individuals with compromised immune systems, people with disabilities, and those who are pregnant.[5] Seasonal respiratory viral infections, such as influenza and respiratory syncytial virus (RSV) exhibit distinct patterns that can be anticipated.[6] In regions with temperate climates, seasonal epidemics occur mainly during winter, while tropical regions tend to experience more sporadic epidemics throughout the year.[7]

This editorial evaluates the clinical utility of increasingly common respiratory viral panel (RVP) diagnostic assays and discusses how these RVPs can improve support for force health protection and Military Health System (MHS) beneficiary public health surveillance.

Clinical Utility of Respiratory Viral Panels

Clinical RVPs typically use a single patient sample to run tests for common viral and bacterial infections. A RVP may refer to commercial multiplex systems or laboratory tests developed in-house. Commercial RVP multiplex systems typically include a testing platform and associated consumables, making them attractive options for high volume diagnostic laboratories.[8]

RVP molecular assays yield rapid results with high sensitivity and specificity for the most common circulating respiratory pathogens, rendering them invaluable in conjunction with clinical evaluation. Results can be obtained within a few hours depending on the specific panel and pathogens tested. While there are instances (e.g., a known outbreak or period of elevated incidence) where a rapid diagnostic test or singleplex assay may be preferred, using a RVP (i.e., multiplex test) can potentially reduce delays in result reporting compared to sequential singleplex approaches. Use of an RVP may not always be the most cost-effective diagnostic within every clinical setting.

Infections caused by non-influenza respiratory viruses (e.g., SARS-CoV-2, rhinovirus) can mimic influenza illness symptomology, particularly during periods of high influenza activity, making clinical differentiation challenging.[9] A health care provider may infer the cause of a respiratory infection based on the season, presentation and medical history, and in some cases, recent travel, but typically cannot conclusively differentiate between most respiratory viruses without further diagnostic testing.[10] Further, co-circulation and co-infection of multiple respiratory viral pathogens can contribute to uncertainty regarding the etiology of respiratory infections.

Using RVP multiplex testing in a clinical setting helps ameliorate diagnosis and treatment challenges and may enhance patient care. Identifying the specific respiratory viral pathogen enables early antiviral treatment in influenza and SARS-CoV-2 cases. Early use of influenza antivirals, such as oseltamivir or baloxavir, may reduce symptom severity and risk of complications in addition to limiting transmission.[11] Antivirals such as remdesivir and nirmatrelvir/ritonavir have been shown to reduce clinical severity in certain subsets of COVID-19 patients if administered early in the disease course.[12] RVP testing can also inform management decisions for limiting infection transmission, including antiviral chemoprophylaxis to reduce secondary attack rates in influenza cases, especially among unvaccinated individuals in congregate settings.

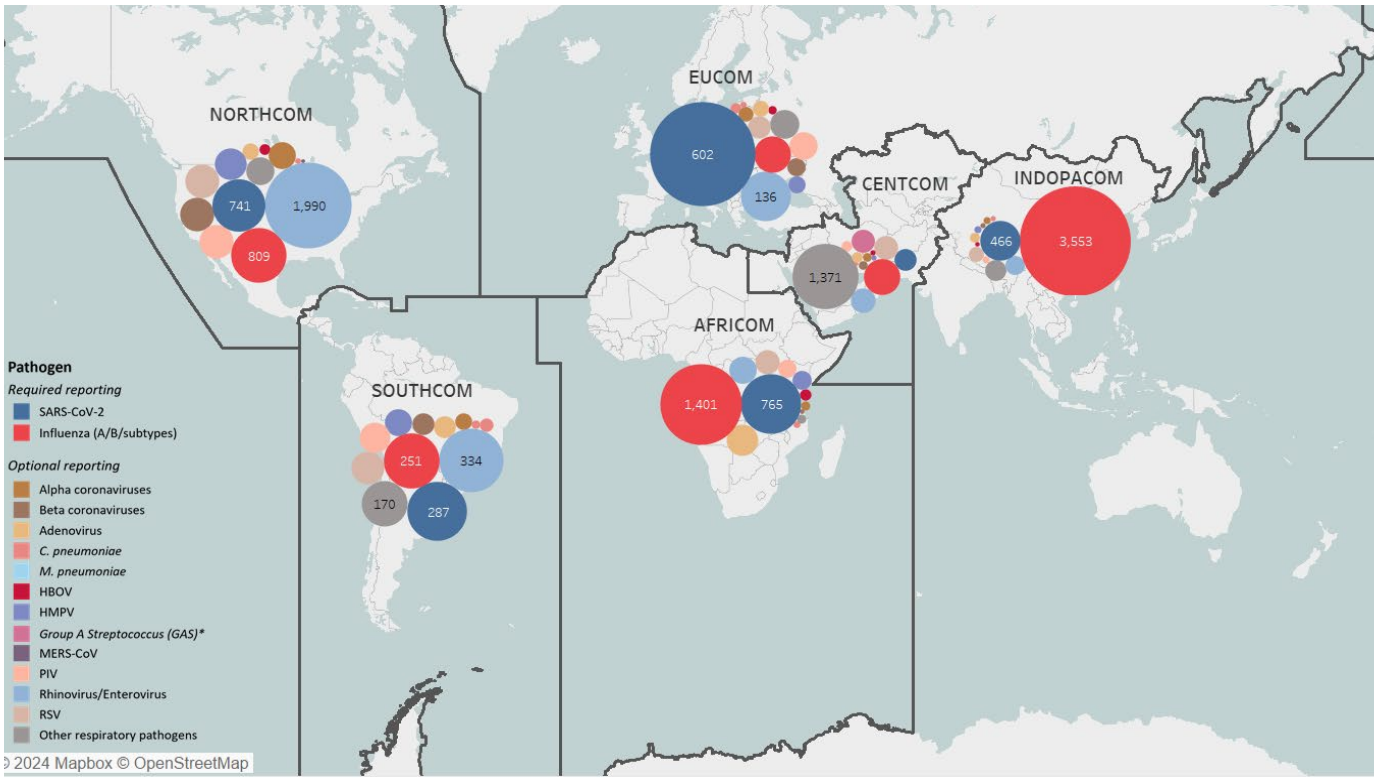
Respiratory Viral Panels for Public Health Surveillance and Force Health Protection

GEIS supports a global network of highly qualified DOD service laboratories in key locations, both domestically and internationally, to provide direct infectious disease surveillance and outbreak response. The majority of GEIS partner laboratories (GEIS-PLs) perform respiratory pathogen diagnostic testing using a RVP (or RVP in combination with singleplex testing) among U.S. service member, civilian, and foreign military and foreign national populations meeting a specific case definition for severe acute respiratory infection (SARI) or influenza-like illness (ILI).[13] To ensure ongoing surveillance results can be incorporated and used in a timely fashion, the GEIS respiratory infections focus area requires GEIS-PLs to report recent molecular testing detection data monthly for all pathogens included on the RVP (e.g., influenza, SARS-CoV-2, novel coronaviruses, RSV, adenoviruses, rhinoviruses, etc.). Monthly results are reported by 10 GEIS-PLs within all global combatant commands (GCCs) **(Figure 1)**.

Surveillance case definitions for ILI and SARI vary slightly among GEIS-PL protocols but are generally characterized by the presence of a fever and a cough or sore throat in the absence of a known cause other than influenza; the SARI case definition typically also requires hospitalization. Case definitions for ILI and SARI surveillance are not necessarily intended to capture all cases but describe trends over time. A variety of pathogens can cause SARI and ILI, and these are monitored closely to identify seasonal trends and describe the temporal and geographic circulation patterns (including trend deviations and outbreaks). This close monitoring is important because SARIs and ILIs are particularly problematic in some military environments (e.g., recruit training, shipboard populations, deployment settings).

GEIS-PLs routinely test samples from symptomatic persons meeting syndromic case definitions for ILI or SARI to identify circulating viruses and facilitate detection of new strains through laboratory testing and characterization as well as sharing samples with GEIS laboratories. Aggregation of standard RVP reporting (i.e., GEIS-PL monthly reports) and routine distribution of most current genomic sequencing results (from the Department of Defense Global Respiratory Pathogen Surveillance Program and Naval Health Research Center) helps continuously inform senior leaders, force health protection officers,

FIGURE 1. Total Number of Respiratory Pathogens Detected by GEIS-funded Laboratories Using RT-PCR, Specimen Collection Dates June 1, 2023–May 31, 2024



Note: Group A *Streptococcus* (GAS) detections were not separately reported until Oct. 2023.
Abbreviations: GEIS, Global Emerging Infections Surveillance; RT-PCR, Reverse transcription polymerase chain reaction; AFRICOM, Africa Command; CENTCOM, Central Command; EUCOM, European Command; INDOPACOM, Indo-Pacific Command; NORTHCOM, Northern Command; SOUTHCOM, Southern Command; SARS-Cov-2, severe acute respiratory syndrome coronavirus 2; *C.,* chlamydia; *M.,* mycoplasma; HBOV, human bocavirus; HMPV, human metapneumovirus; MERS-CoV, Middle East respiratory syndrome coronavirus; PIV, Parainfluenza virus; RSV, respiratory syncytial virus.

and medical personnel of the most relevant respiratory infections circulating and their decisions for treatment and quarantine. Surveillance findings indicating serious or immediate threats necessitating a change to force health protection posture or indicating that a unit is non-mission capable due to acute health issues are reported to GEIS immediately and disseminated to relevant GCC points of contact within 24 hours. Related, surveillance findings from outbreak events may result in local policy changes related to medical countermeasures[4] or preventive measures.[3]

Between June 1, 2023 and May 31, 2024, GEIS-PLs reported results from RVP (and singleplex) sample testing that detected 42,430 SARS-CoV-2 (10% positivity), 43,606 influenza (16% positivity), and 23,704 other (31% positivity) respiratory pathogens **(Table)**. The most common other respiratory pathogen detected was rhinovirus/enterovirus (17% positivity). During that period, the highest number of samples tested were submitted by U.S. Africa Command (AFRICOM), and highest percent positivity for influenza was reported by U.S. Indo-Pacific Command (INDOPACOM), for SARS-CoV-2 by Europe Command (EUCOM), and Southern Command (SOUTHCOM) for other respiratory pathogens.

Molecular Influenza Surveillance to Inform Wider Public Health Surveillance Efforts

Influenza viruses detected through public health surveillance using a RVP (or singleplex) are further analyzed by GEIS-PLs to inform selection of the specific strains for the Northern Hemisphere influenza vaccine (mandatory for service members) for the following season. A combination of epidemiologic analyses, genetic sequencing, and advanced characterization is used to generate a detailed summary of the annual influenza global landscape observed through DOD respiratory surveillance. Geographic distribution of the influenza sequences characterized, and influenza subtype ratios, are examined for the U.S. and each country surveilled.

For the 2023-2024 respiratory season, GEIS comprehensive analyses included positive samples and molecular sequencing data submitted to the Defense Global Respiratory Pathogen Surveillance Program (DoDGRPSP) from 10 GEIS-PLs and more than 100 DoDGRPSP sentinel sites. These findings were presented during the influenza Vaccines and Related Biological Products Advisory Committee (VRBPAC) meeting.[14] **Figure 2** shows the influenza subtype geographic distribution and temporal trends from June 2023 through April 2024.

Influenza subtype ratios for the U.S. **(Figure 2)** showed a higher proportion of influenza A(H1N1)pdm09 in the northern, western, and eastern regions of the country, higher influenza A(H3N2) in the central U.S., and a higher amount of influenza B/Victoria in the southern U.S. compared to northern regions. A notably higher proportion of influenza A(H3N2) was observed in AFRICOM and INDOPACOM, while influenza A(H1N1)pdm09 was higher in EUCOM. A smaller proportion of influenza B/Victoria was observed in most regions outside the U.S. Regional trends should be interpreted with consideration of potential limitations associated with sampling or ascertainment bias (i.e., collected samples may not fully represent all persons in these populations and must be considered in context with other surveillance data collected by interagency partners).[15,16]

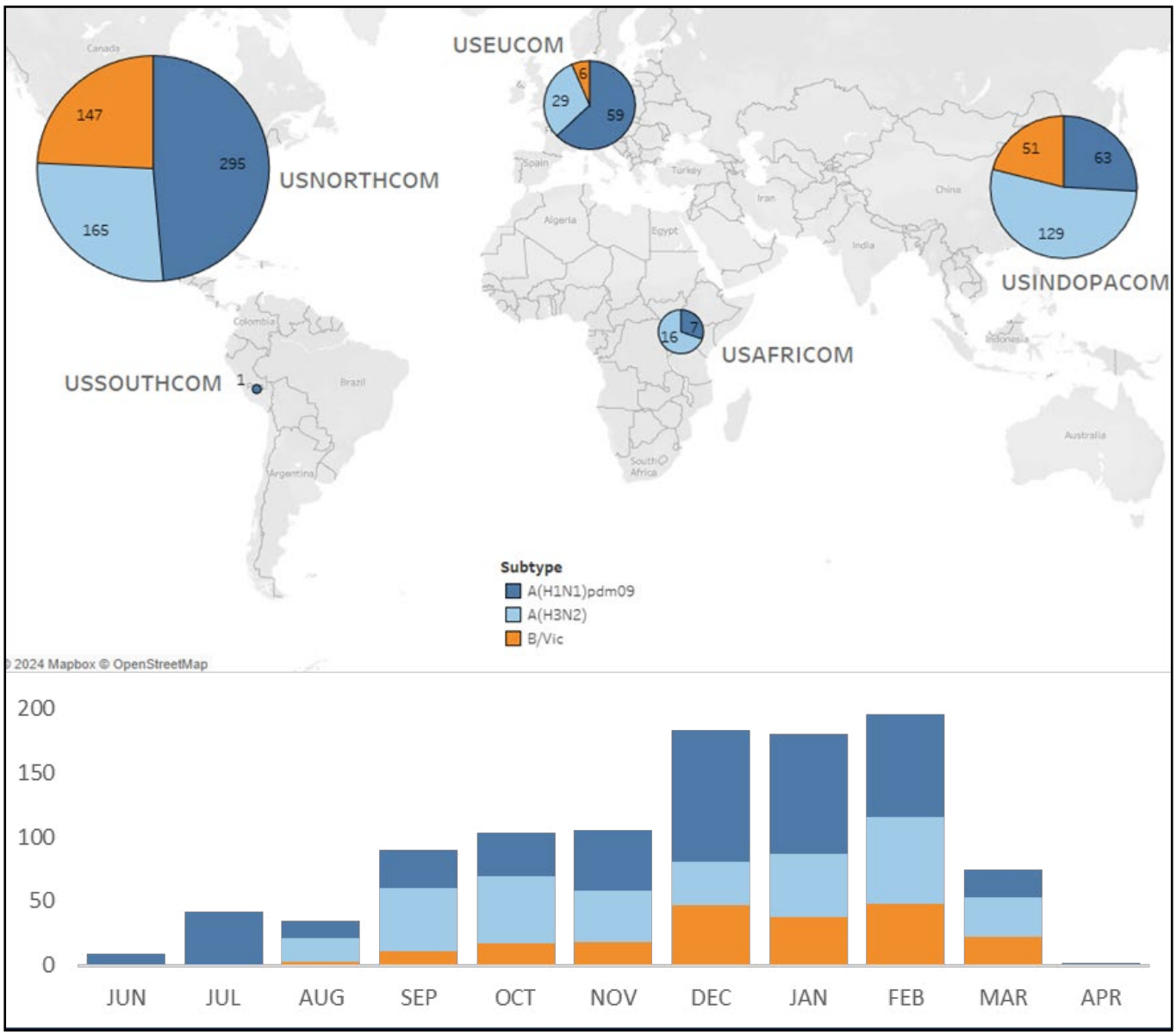
Closely monitoring influenza infections can inform vaccine decision-making with broad global implications. During the 2023-2024 respiratory season, a combination of 3 influenza subtypes (A[H1N1]pdm09, A[H3N2], B/Victoria) were observed, with no confirmed detections of circulating influenza B/Yamagata since March 2020. Based on those (and similar) data, there was agreement during the March 2024 VRBPAC meeting to transition from a quadrivalent vaccine (which included the Yamagata strain)

TABLE. RT-PCR Results from GEIS-funded Laboratories by Global Combatant Command, Specimen Collection Dates June 1, 2023–May 31, 2024

U.S. Combatant Command	Influenza			SARS-CoV-2			Other Respiratory Pathogens		
	Samples Tested (n)	% Positive	Positivity per 100,000	Samples Tested (n)	% Positive	Positivity per 100,000	Samples Tested (n)	% Positive	Positivity per 100,000
AFRICOM	14,639	9.6	9,570	19,019	4	4,022	3,305	21.9	21,876
CENTCOM	5,667	7.4	7,358	5,653	2.7	2,707	5,415	38.1	38,098
EUCOM	2,378	3.1	3,112	2,919	20.6	20,624	2,373	13.7	13,696
INDOPACOM	9,245	38.4	38,432	6,426	7.3	7,252	1,534	26.3	26,336
NORTHCOM	9,341	8.7	8,661	6,086	12.2	12,175	9,339	39.6	39,640
SOUTHCOM	2,336	10.7	10,745	2,327	12.3	12,333	1,738	48.9	48,849

Abbreviations: RT-PCR, Reverse transcription polymerase chain reaction; GEIS, Global Emerging Infections Surveillance; AFRICOM, Africa Command; CENTCOM, Central Command; EUCOM, European Command; INDOPACOM, Indo-Pacific Command; NORTHCOM, Northern Command; SOUTHCOM, Southern Command.

FIGURE 2. Influenza Subtype Temporal Trends[a] and Distribution Among Global Combatant Commands, Specimen Collection Dates June 1, 2023–April 31, 2024



Abbreviations: USNORTHCOM, U.S. Northern Command; USEUCOM, U.S. European Command; USINDOPACOM, U.S. Indo-Pacific Command; USAFRICOM, U.S. Africa Command; USCENTCOM, U.S. Central Command; USSOUTHCOM, U.S. Southern Command; A(H1N1)pdm09, influenza A virus subtype H1N1 pandemic 2009; A(H3N2), Influenza A virus subtype H3N2; B/Vic, influenza virus B Victoria lineage.
[a] Results as of Jun. 3, 2024.

to a trivalent vaccine only for U.S. use, starting in the 2024-2025 respiratory virus season.[17] Quadrivalent influenza vaccines for distribution outside the U.S. still included the B/Yamagata as the second influenza B strain for the 2024-2025 season.[18]

Limitations and Future Directions

While the GEIS network is critical for continuously monitoring respiratory infections that affect service members globally, this global network of laboratories contends with several limitations. Each GEIS-funded laboratory has different priorities and surveillance populations that determine their surveillance activities, which may result in differential applications of molecular testing for respiratory pathogen detection. While the majority of GEIS-PLs currently use a RVP (or a RVP in combination with singleplex testing), they are not formally required to test for all respiratory pathogens besides influenza and SARS-CoV-2. Likewise, there are no requirements specifying which RVP (when in use) must be used for surveillance purposes among GEIS-PLs. GEIS-PLs may acquire and implement a new RVP during the lifecycle of a project, which can affect the numbers and types of pathogens that may be detected and reported to the GEIS program office, since not all RVPs are standardized.

Because these results reflect surveillance data reported directly to the GEIS program office by funded GEIS-PLs,

it is possible these data under-represent the true incidence for the respiratory pathogens reported. Similarly, influenza sequencing analyses are based on samples and data submitted by sentinel sites or shared by GEIS-PLs with the DoDGRPSP. Only a small proportion of all respiratory infection samples were submitted by sentinel sites, and not all GEIS-PLs were able to contribute influenza samples or sequencing data. While GEIS RVP (and singleplex) data provide a unique global surveillance perspective of laboratory partners actively conducting respiratory surveillance, they might not accurately reflect a complete representation for all DOD active component personnel globally or within MHS.

Several low- and middle-income countries lack the resources or capabilities for widespread RVP testing, limiting respiratory surveillance that would otherwise inform diagnostics and treatment selection and preventive measures for MHS beneficiaries deployed to these areas. The GEIS network helps fulfill this need with respiratory surveillance through its network of partner laboratories in countries such as Tanzania and Djibouti, where RVP testing may otherwise be scarcely used or reported.[19] Deployment of RVP testing may be challenging in limited resource or forward operating areas, although possible in some early role care levels. In many austere settings, there remains a need for focused local or regional RVP surveillance to improve pre-test probability estimations.

Studies both within and outside the MHS suggest that RVPs may not always identify pathogen etiology.[20-22] Consequently, some GEIS-PLs identify a subset of SARI cases that have tested negative on a RVP for all pathogens and characterize those samples further using clinical metagenomics sequencing for public health surveillance. Metagenomic sequencing is the process of sequencing all genetic material in a sample (often using agnostic or semi-agnostic sequencing) to determine the possible infecting organism without *a priori* knowledge of a specific pathogen.[23] Clinical metagenomics has diagnostic applications for lower respiratory tract infections and has shown promise, although it is not yet widely available, cost-efficient, nor suitable to inform routine clinical care for ILI/SARI cases. Metagenomics has substantial resource requirements including wet laboratory and bioinformatic resources.[24] In addition, one challenge of metagenomics in clinical practice is differentiation between clinically relevant pathogens and incidental respiratory tract colonizers, including the transient virome.[25] GEIS-funded respiratory surveillance activities continue to delineate which residual, pathogen-negative clinical specimens may benefit from secondary agnostic or semi-agnostic metagenomic sequencing, assessing semi-agnostic platforms that may extend diagnostic yield beyond RVP results while minimizing metagenomic 'noise'.

Key GEIS-PLs share in-depth findings dynamically displayed on their respective dashboards, accessible to DOD partners via Carepoint, including the DoD Global Respiratory Pathogen Surveillance Program (>100 DOD sentinel sites) and the Naval Health Research Center Febrile Respiratory Illness (US-Mexico border, recruit sites). Notably, the Defense Center for Public Health-Portsmouth (DCPH-D) recently created the DHA Influenza Dashboard that includes influenza surveillance findings across the MHS.

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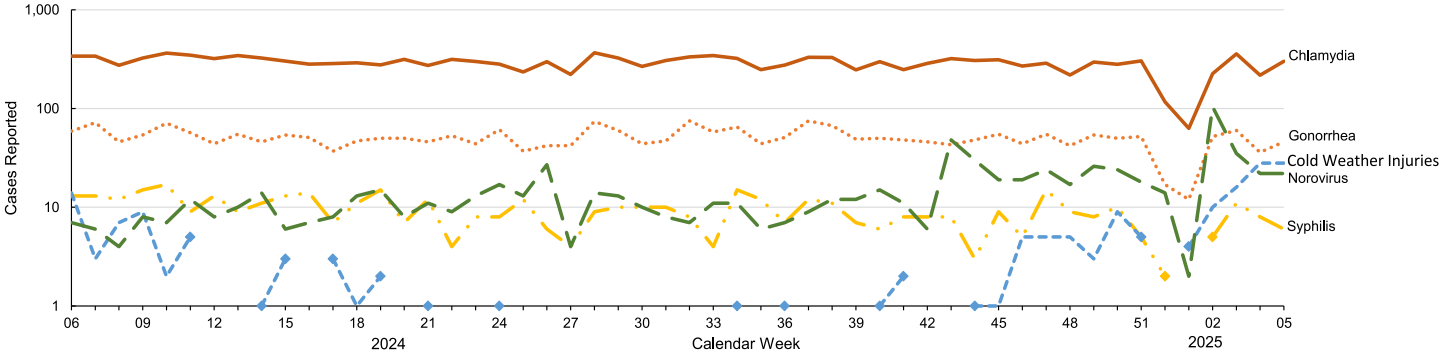
Reportable Medical Events at Military Health System Facilities Through Week 5, Ending February 1, 2025

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

TOP 5 REPORTABLE MEDICAL EVENTS[a] BY CALENDAR WEEK, ACTIVE COMPONENT (FEBRUARY 10, 2024–FEBRUARY 26, 2025)



Abbreviation: RMEs, reportable medical events.

[a]Cases are shown on a logarithmic scale.

Note: There were 0 reported cold weather injuriy cases during weeks 12-13, 16, 20, 22-23, 25-33, 35, 37-39, 42-43, 52. There were no syphilis cases reported during week 1 of 2025.

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 (January 2025) 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

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TABLE. Reportable Medical Events, Military Health System Facilities, Week Ending February 5, 2025 (Week 1)[a]

Reportable Medical Event[b]	Active Component[c]					MHS Beneficiaries[d]
	YTD 2025	January 2025	December 2024	YTD 2024	Total 2024	January 2025
	No.	No.	No.	No.	No.	No.
Amebiasis	4	4	1	0	15	0
Arboviral diseases, neuroinvasive and non-neuroinvasive	0	0	0	0	3	0
Brucellosis	0	0	0	0	1	0
COVID-19-associated hospitalization and death	3	3	2	8	41	31
Campylobacteriosis	22	22	25	17	326	13
Chikungunya virus disease	0	0	1	0	1	0
Chlamydia trachomatis	1,150	1,150	1,074	1,485	15,596	168
Cholera	1	1	0	0	3	0
Coccidioidomycosis	0	0	7	7	53	5
Cold weather injury[e]	83	83	17	72	172	N/A
Cryptosporidiosis	8	8	3	4	82	0
Cyclosporiasis	0	0	0	0	11	0
Dengue virus infection	1	1	0	1	12	0
E. coli, Shiga toxin-producing	4	4	14	3	93	3
Ehrlichiosis / anaplasmosis	0	0	0	0	1	0
Giardiasis	9	9	3	12	98	2
Gonorrhea	204	204	191	293	2,763	29
Haemophilus influenzae, invasive	0	0	0	1	3	1
Heat illness[e]	6	6	4	10	1,276	N/A
Hepatitis A	0	0	0	1	7	0
Hepatitis B, acute and chronic	6	6	7	11	106	7
Hepatitis C, acute and chronic	0	0	1	3	29	6
Influenza-associated hospitalization[f]	18	18	9	18	54	61
Lead poisoning, pediatric[g]	N/A	N/A	N/A	N/A	N/A	7
Legionellosis	0	0	0	0	5	1
Leprosy	0	0	0	0	1	0
Listeriosis	1	1	0	0	0	1
Lyme disease	0	0	1	7	101	1
Malaria	0	0	3	2	21	1
Meningococcal disease	0	0	0	0	2	0
Mpox	1	1	0	2	14	1
Mumps	0	0	0	0	0	2
Norovirus	184	184	91	23	653	90
Pertussis	4	4	3	2	39	13
Post-exposure prophylaxis against Rabies	31	31	41	58	618	23
Q fever	0	0	1	0	3	0
Salmonellosis	3	3	11	8	160	15
Schistosomiasis	0	0	0	0	1	0
Shigellosis	2	2	4	3	53	2
Spotted fever rickettsiosis	1	1	0	0	22	0
Syphilis (all)	30	30	25	63	516	9
Toxic shock syndrome	0	0	0	1	2	1
Trypanosomiasis	1	1	0	1	5	0
Tuberculosis	0	0	0	1	7	0
Tularemia	0	0	0	0	1	1
Typhoid fever	0	0	0	0	1	0
Typhus fever	1	1	0	1	2	1
Varicella	0	0	4	4	18	4
Zika virus infection	0	0	0	1	1	0
Total case counts	1,778	1,778	1,543	2,123	22,992	499

Abbreviations: MHS, Military Health System; YTD, year-to-date; No., number; *E, Escherichia*; N/A, not applicable.

[a] RMEs submitted to DRSi as of Feb. 26, 2025. RMEs were classified by date of diagnosis or, where unavailable, date of onset. Monthly comparisons are displayed for the period of Dec. 1, 2024–Dec. 31, 2024 and Jan. 1, 2025–Jan. 31, 2025. YTD comparison is displayed for the period of Jan. 1, 2025–Jan. 31, 2025 for MHS facilities. Previous year counts are provided as the following: previous YTD, Jan. 1, 2024-Jan. 31, 2024; total 2024, Jan. 1, 2024–Dec. 31, 2024.

[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 the Army, Navy, Air Force, Marine Corps, Coast Guard, and Space Force, including personnel classified as Active Duty, Cadet, Midshipman, or Recruit in DRSi.

[d] Beneficiaries included the following: individuals classified as Retired and Family Members (including Spouse, Child, Other, Unknown). National Guard, Reservists, civilians, contractors, and foreign nationals were excluded from these counts.

[e] Only reportable for service members.

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

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

Images in Health Surveillance

Ammunition Ship Explosions in Papua New Guinea and Solomon Islands, 1944 and 1945

G. Dennis Shanks, MD, MPH

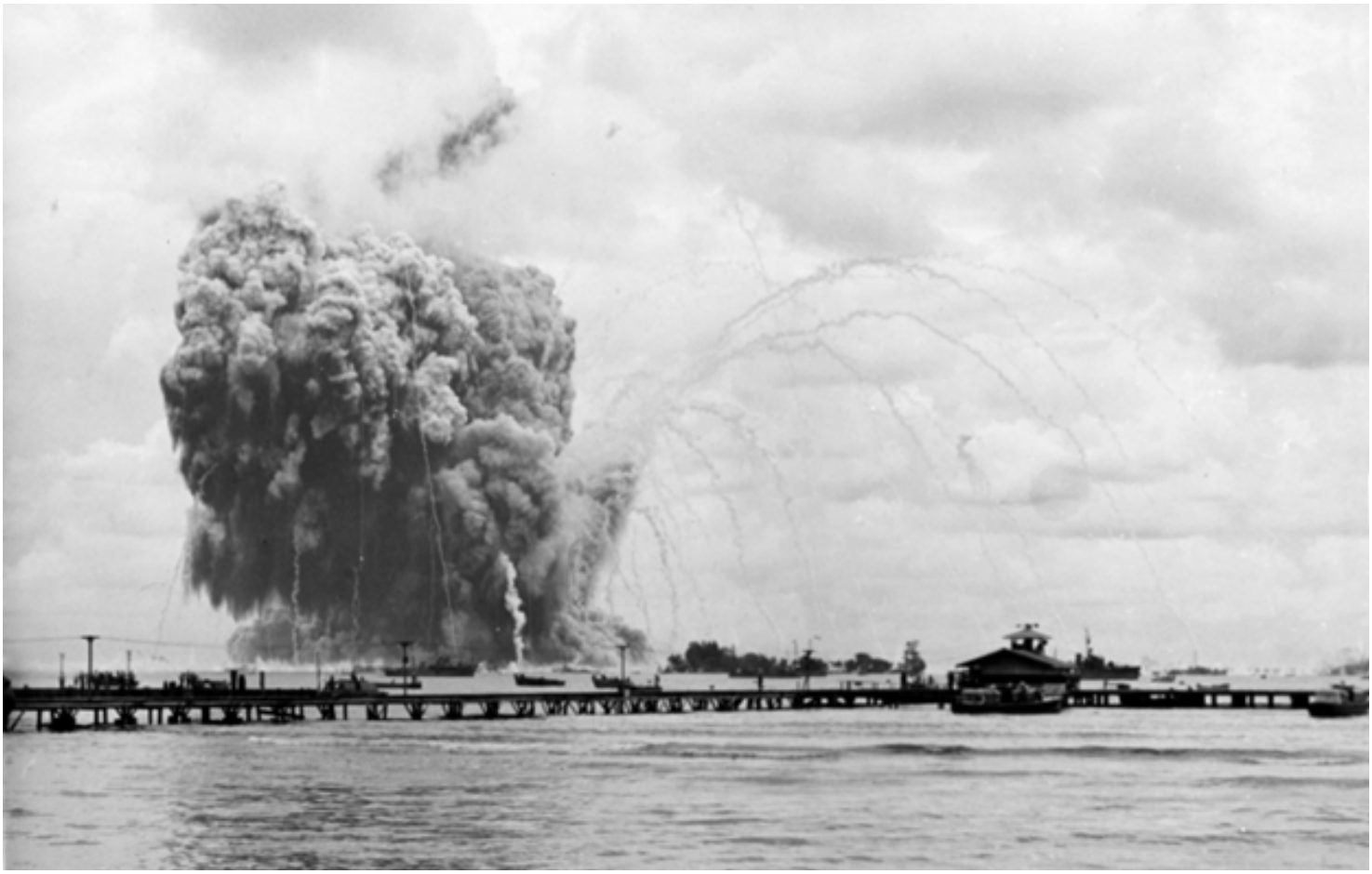

FIGURE. Explosion of *USS Mount Hood* (AE-11) in Seeadler Harbor off Manus Island in Papua New Guinea, November 10, 1944

Seeadler (Sea Eagle) Harbor on the island of Manus in Papua New Guinea was a vital logistics hub for the invasion of the Philippines during the Second World War. The USS *Mount Hood* (AE-11) was unloading munitions from all 5 holds into landing crafts medium (LCMs) while at anchor in the harbor center in November 1944. The ship suddenly exploded on November 10, 1944.[1] The blast involved more than 3,800 tons of munitions and killed all 350 on board ship and surrounding LCMs, in addition to 82 crew members on the *USS Mindanao* (ARG-3)—over 300 meters away. No identifiable human remains were recovered from the *Mount Hood*. An additional 371 men were wounded.

The largest piece of the *Mount Hood*'s wreckage located was 30 meters long, submerged in a 26 meter-deep crater in the reef. Twenty-two other ships or landing craft were either sunk or severely damaged by the blast. Subsequent investigation concluded "the most likely cause of the explosion was careless handling of ammunition."

Mishandling military explosives and ammunition has a long history of causing mass casualties. Ammunition ships were particularly high-risk environments for their crews, especially during the laborious process of transferring inherently hazardous explosives. The destruction of ammunition ships in the Indo-Pacific region during the Second World War are only marginally part of our military history as their losses were actively suppressed due to wartime concerns about security and morale.

Just over 2 months after the explosion of the *Mount Hood*, the ammunition ship USS *Serpens* (AK-97) exploded, on January 29, 1945, while loading depth charges

off Lunga Point, near Honiara, Solomon Islands. The casualties of that explosion included 250 U.S. Coast Guard crew, Army stevedores, and a medical officer. Two crew on the ship survived the blast in a bow section that continued to float temporarily after the blast.

Although the cause of the *Serpens* explosion remained unclear, the U.S. Navy noted that the loss was not due to enemy action but an "accident intrinsic to the loading process." The explosion of the USS *Serpens* remains the greatest single mortality event in the history of the U.S. Coast Guard and is marked by a mass grave and monument in the Arlington National Cemetery.[2]

These accidental ship explosions during the Second World War caused mass casualties without any enemy intervention. Lessons were uncertain and indefinite, as any forensic evidence was destroyed by the blast wave. Wartime secrecy as well as bureaucratic disinclination for admitting failure has made these accidents much less well-known then when the same munitions were used by troops to defeat Imperial Japan.[3]

Caution with ammunition is always indicated, but recent events, particularly with explosions at ammunition depots in the developing world—Lagos in 2002, Maputo in 2007, and Brazzaville in 2012—should serve as an important reminder that weapons have the potential to kill friend and foe alike if mishandled. Ammunition is both a disarmament as well as a public health danger that requires unremitting vigilance.

The author, of both *Images in Health Surveillance* featured in this issue, acknowledges the service and sacrifice of all those who served in the military during the Second World War and thanks the many unnamed military officers, scientists, historians, and medical librarians who have unselfishly provided data and ideas for these manuscripts, especially the librarians at the Australian Defence Force Library at Gallipoli Barracks, Queensland.

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The opinions expressed are those of the author and do not necessarily reflect those of the Australian Defence Force nor the Department of Foreign Affairs and Trade.

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