

# AFHSD

Armed Forces Health Surveillance Division

## ANNUAL REPORT 2021





## FRIENDS AND COLLEAGUES

It is with great pride that I present the Armed Forces Health Surveillance Division's (AFHSD) accomplishments during 2021. We are a division within the Public Health Directorate under the Assistant Director for Support (AD-S). AFHSD operates four main branches: Epidemiology & Analysis (E&A), Global Emerging Infections Surveillance (GEIS), Integrated Biosurveillance (IB), and Data Management & Technical Support (DMTS).

AFHSD continues to be the officially designated central hub for Department of Defense (DOD) Biosurveillance in accordance with the DOD Directive (DODD) 6420.02, "DOD Biosurveillance" of 17 September 2020. We are moving swiftly and boldly to meet the demands demonstrated by the "pandemic era" embracing technology and a whole of government approach. This tactic will ensure that the Defense Health Agency (DHA) actively works with other government agencies to jointly solve challenges facing our DOD population. Our offices consist of a total of 120 persons, 20 of which are assigned at the three Service public health hubs (12-Army, 3-Air Force, 5-Navy) which we call "Service Satellite Cells." This health surveillance team continues to solidify DHA's position to provide Combat Support to Combatant Commands.

AFHSD continues to provide timely surveillance and analysis to provide senior leaders and front line healthcare workers critical information to shape the battlespace and unified military strategy. Through our efforts and reporting, it has been established that our capabilities provide value to the Military Health System (MHS). We support the military public health transition to the DHA and work tirelessly to refine our role as a CSA.

As you read AFHSD's annual report, we hope it will remind you of our recent successes and the future path that we will take to ensure our mission in 2022. We look forward to continuing this effort with agility, relevancy, and timeliness in support of the Joint Force. Their ultimate goal is to help the Combatant Commands (CCMDs) and the military services make the best decisions in protecting the health and readiness of DOD's military and beneficiaries.

**PATRICK W. KENNEDY, Colonel, USAF, BSC**  
Chief, Armed Forces Health Surveillance Division

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# THE ORIGINS OF HEALTH SURVEILLANCE

AFHSD is the central epidemiologic health resource for the U.S. military. The division is one of several key sections that operate within DHA's Public Health Directorate.

AFHSD was created in February 2008 as the Armed Forces Health Surveillance Center following the merger of the Army Medical Surveillance Activity's Defense Medical Surveillance System (DMSS) with DOD Serum Repository (DODSR), the DOD Global Emerging Infections Surveillance and Response System (DOD-GEIS), and the Global Health Surveillance Activity from the Office of the Deputy Assistant Secretary of Defense for Force Health Protection and Readiness.

As the central repository of medical surveillance data for the U.S. Armed Forces, AFHSD manages the DMSS and the DODSR. The DMSS contains current and historical data on diseases and medical events such as hospitalizations, ambulatory visits, reportable medical events (RMEs), laboratory tests, immunizations, periodic health assessments (PHA), and casualty data affecting service members throughout their military careers. The DMSS contains billions of data records on service members and other MHS beneficiaries.

The DODSR was established in 1989 to store blood sera collected during the

## DEFENSE HEALTH AGENCY

The DHA is a joint, integrated CSA that enables the Army, Navy, and Air Force medical services to provide a medically ready force and ready medical force to CCMDs in both peacetime and wartime. The DHA supports the delivery of integrated, affordable, and high-quality health services to MHS beneficiaries and is responsible for driving greater integration of clinical and business processes across the MHS.

Defense Department testing program for human immunodeficiency virus (HIV) infections. Later, the DODSR was designated to receive serum specimens collected before and after operational deployments. With more than 72 million serial serum specimens from 11.6 million individuals, the DODSR is the world's largest storage facility of its kind.

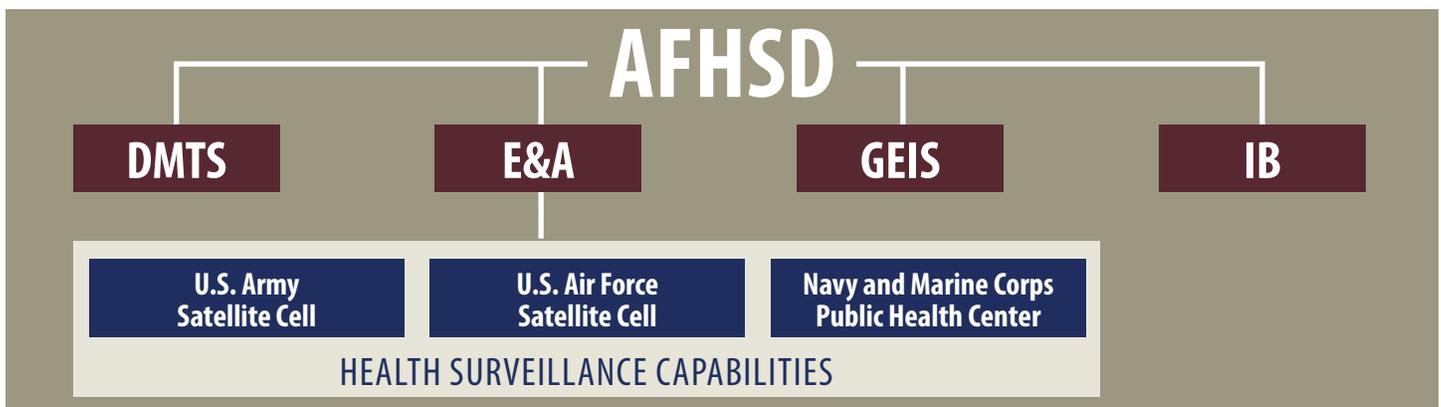
In 1997, the Defense Department established DOD-GEIS in response to a Presidential Decision Directive to expand its mission to include support of global surveillance, training, and response to emerging infectious disease (EID) threats. GEIS coordinates AFHSD's global EID surveillance activities among a network of partner organizations and executes a militarily relevant surveillance program involving

respiratory infections (RI), enteric infections (EI), febrile and vector-borne infections (FVBI), and antimicrobial resistant and sexually transmitted infections (AMR/STI). The AFHSD also plays a key role in integrating biosurveillance by collecting data in near real-time on the threats from endemic diseases and EIDs relevant to the military worldwide.

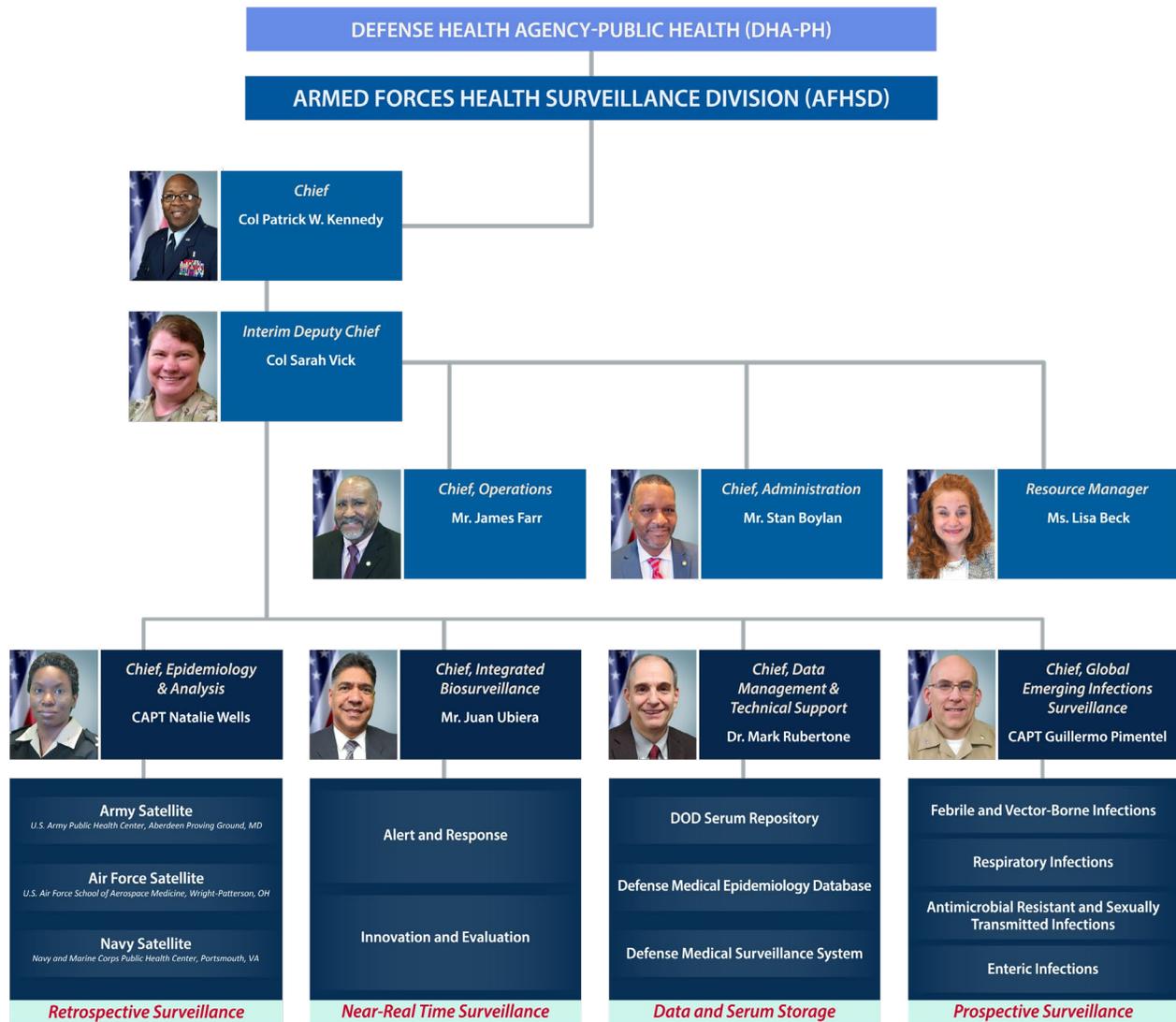
AFHSD publishes summaries of notifiable diseases, trends of illnesses of special interest, and field reports describing outbreaks and case occurrences in its peer-reviewed journal, *Medical Surveillance Monthly Report (MSMR)*. AFHSD also provides up-to-date information on diseases that could affect force health readiness and protection.

AFHSD also assumed responsibility of the health surveillance capabilities of the Service Public Health Hubs, which include personnel from the U.S. Army Public Health Center (APHC), U.S. Air Force School of Aerospace Medicine (USAFSAM), and the Navy and Marine Corps Public Health Center (NMCPHC). The Service Public Health Hubs' select surveillance personnel and assets are satellites of AFHSD.

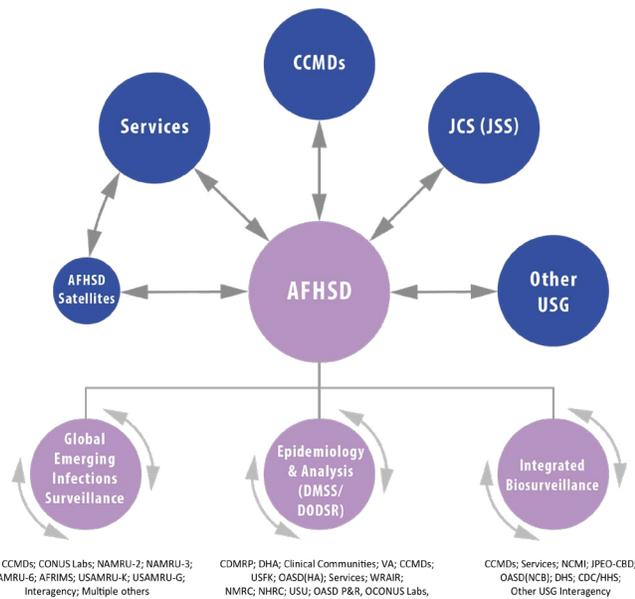
AFHSD is currently organized into four branches: Data Management and Technical Support (DMTS), E&A, GEIS, and IB.



# ORGANIZATION CHART



## CUSTOMERS AND STAKEHOLDERS



# AFHSD FINANCES

AFHSD distributed 77.2% of its funds directly to laboratory partners through the GEIS program following an extensive internal and external proposal review process. The GEIS Branch's total funding for biosurveillance was \$55.146M in Fiscal Year 2021 (FY21). This included core funding of \$51.696M and supplemental funding of \$3.45M for coronavirus disease of 2019 (COVID-19) and genomic surveillance efforts.

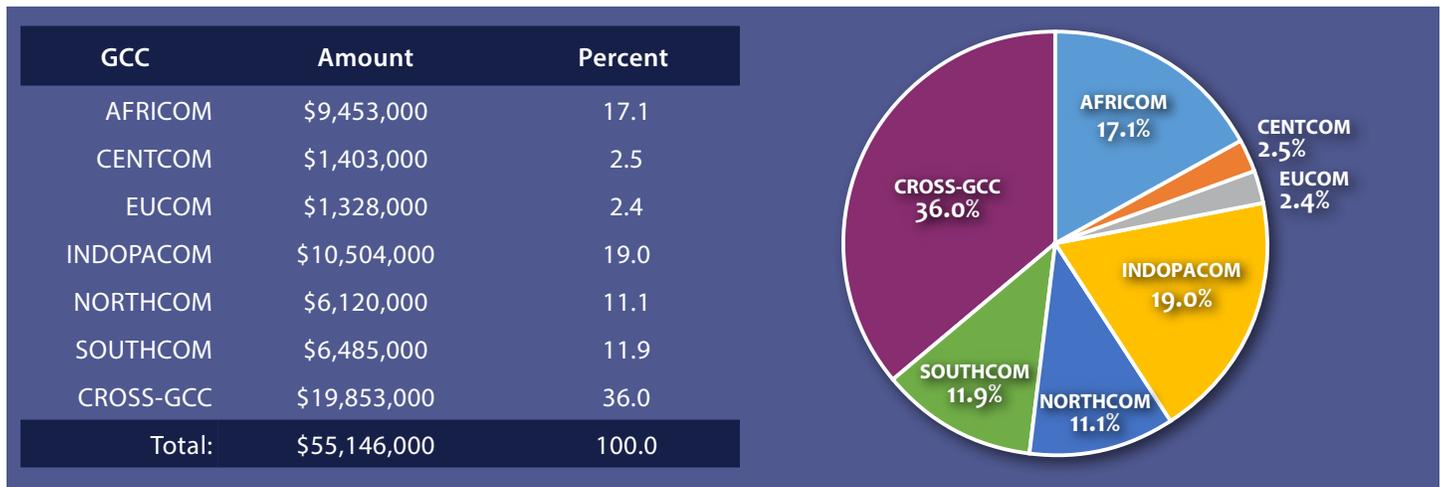
Primary recipients of GEIS core biosurveillance funding included Army and Navy Service laboratories located outside the continental United States (OCONUS): Armed Forces Research Institute of Medical Sciences (AFRIMS); U.S. Army Medical Research Directorate-Africa (USAMRD-A); U.S. Army Medical Research Directorate-Georgia (USAMRD-G); and Naval Medical Research Units No. 2, 3, and 6 (NAMRU-2, NAMRU-3, and NAMRU-6, respectively).

Multiple military and university partners based in the continental United States (CONUS) also received funding, including: the Navy and Marine Corps Public Health Center-EpiData Center (NMCPHC-EDC); Navy Entomology Center of Excellence (NECE); Naval Medical Research Center (NMRC), Naval Health Research Center (NHRC); Pharmacovigilance Center (PVC); U.S. Air Force School of Aerospace Medicine (USAFSAM); U.S. Army Medical Research Institute of Infectious Diseases

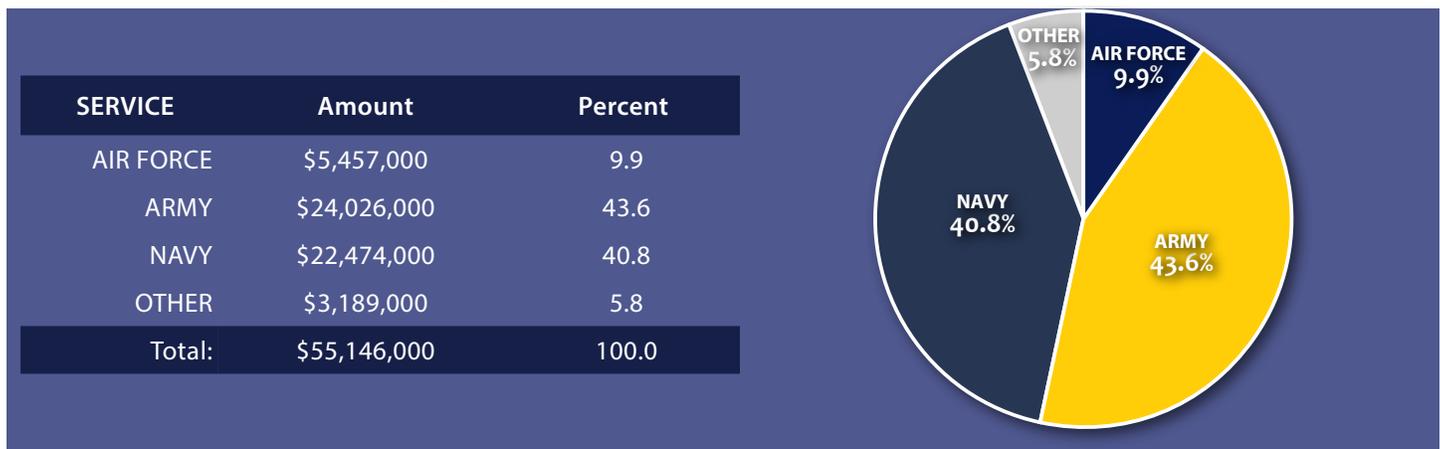
(USAMRIID); Walter Reed Army Institute of Research (WRAIR); and Uniformed Services University of the Health Sciences (USUHS), among others.

The remaining funds supported various AFHSD branches and headquarters as well as biosurveillance initiatives, comprehensive health surveillance service, support contract staff, additional contract personnel working with the *Medical Surveillance Monthly Report (MSMR)* and the DODSR, and other infrastructure costs.

**Table 1. FY21 GEIS Branch Funding Distribution by Geographic Combatant Command**



**Table 2. FY21 GEIS Branch Funding Distribution by Service**



# DATA MANAGEMENT AND TECHNICAL SUPPORT

This branch provides the technical infrastructure and database management expertise to support AFHSD's mission to conduct comprehensive surveillance and analysis of health-related information for DOD service members and military-associated populations.

## TOOLS OF SURVEILLANCE

The Defense Medical Surveillance System (DMSS) and Department of Defense Serum Repository (DODSR) are longstanding and vital assets to medical surveillance within the U.S. Armed Forces. The DMSS and DODSR have their historic roots in routine HIV screening and surveillance. However, their functions were expanded in the early 1990s to encompass all diseases and injuries relevant to the protection of U.S. forces and deployment health.

The DMSS receives data from multiple sources and integrates it in a continuously expanding longitudinal surveillance database for all individuals who have served in the military since 1990. DMSS records are maintained on person, place, and time of reference. Through traditional epidemiologic practices, users can mine the data for efficient and powerful analyses of morbidity among service members. With more than 4.5 billion data records, including more than 1 billion records on U.S. Service members alone, the DMSS remains the DOD's premier epidemiologic health surveillance resource. The Defense Medical

Epidemiology Database (DMED) is derived from the DMSS, provides select data that are de-identified and remotely accessible to online users. The purpose of DMED is to provide standard epidemiologic methodology used to analyze active duty personnel and medical event data. DMED is available to authorized users—including U.S. military medical providers, epidemiologists, medical researchers, safety officers, and medical operations and clinical support staff—who



More than  
**4.5 BILLION** data  
records are contained in the  
DMSS and include more than  
**1 BILLION** records on U.S.  
Service members.

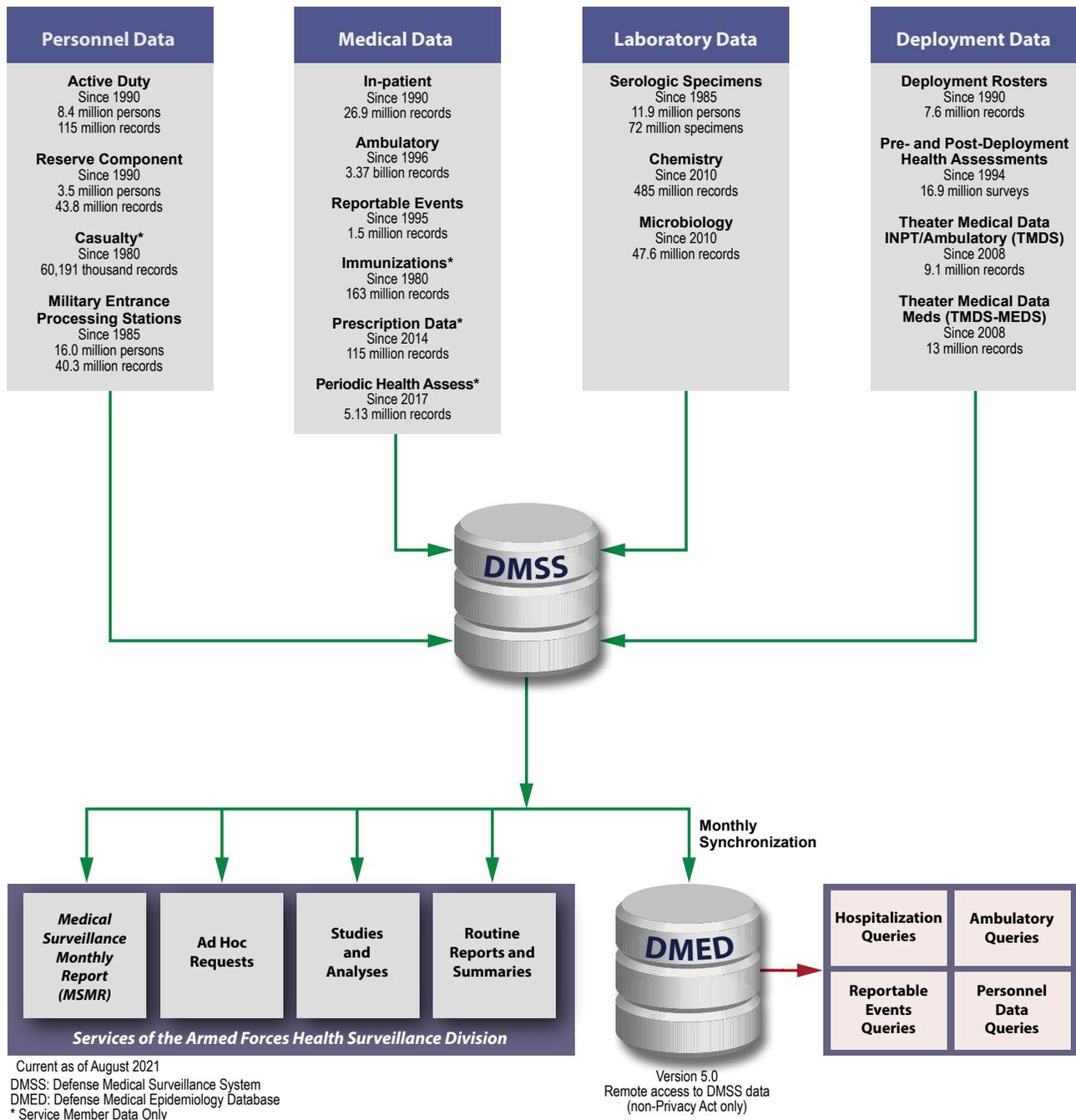
are responsible for surveying health conditions in the U.S. military and conveying this information to commanders for monitoring and enhancing the health of the active duty component. With appropriate documentation, civilian collaborators in military medical research and operations may also access DMED.

The DODSR was established in 1989 to store sera collected during the

DOD's testing program for HIV infections. Later, the DODSR was designated to receive serum specimens collected before and after operational deployments. With more than 72 million serial serum specimens from over 11.6 million individuals, the DODSR is the world's largest serum repository of its kind. The DODSR specimens are housed in modern freezers with advanced cooling equipment and technology. The DMSS database stores demographic, occupational, and medical information in longitudinal surveillance and records linked to the DODSR specimens. It is a unique and powerful resource to support the conduct of military medical surveillance, clinical care, and seroepidemiologic investigations. During 2021, AFHSD processed and dispensed serum specimens in support of 39 seroepidemiologic studies and analyses.

These studies included requests for clinical needs, operational studies (including characterizing the seroprevalence of COVID-19, *Coxiella burnetii*, melioidosis, and arboviral infections among U.S. military personnel) and in support of research studies including a study examining osteoarthritis and systemic inflammatory signals in total joint arthroplasty, spectrometric serum analysis of oropharyngeal carcinoma, analysis of the impact of repeated vaccinations on effectiveness of seasonal influenza vaccines, and proteomic serum analysis of biomarkers in pancreatic ductal adenocarcinoma.

# DMSS STRUCTURE AND FUNCTIONAL RELATIONSHIP



# EPIDEMIOLOGY AND ANALYSIS

The Epidemiology and Analysis (E&A) Branch integrates the expertise of epidemiologists, preventive medicine physicians, and data analysts to provide timely analyses and reports of actionable health information. The branch uses AFHSD health surveillance tools—the DMSS and DODSR—and provides surveillance products to DOD policymakers, military commanders, healthcare providers, public health officers, and researchers.

In addition, E&A staff analyze and interpret large data sets, publish the *MSMR*, develop and disseminate standards for case definitions, and train preventive medicine residents. The branch receives and responds to hundreds of health-related inquiries and investigations on the U.S. military with the intent of preserving the health of the U.S. Armed Forces. Many inquiries are initiated by key leaders throughout the DOD and relate to military operations. Each analysis and report distributed by the branch entails numerous hours of epidemiologic expertise and programming by analysts to extract relevant data from the billions of health records stored in the DMSS and blood sera in the DODSR.

## AFHSD E&A SATELLITES

AFHSD E&A maintains satellite staff at APHC, NMCPHC, and USAFSAM. Satellite staff primarily support Service-specific surveillance at their respective public health centers but also contribute valuable expertise to the enterprise and regularly participate in joint meetings including the bi-weekly Request Appraisal Process (RAP), quarterly E&A staff meetings, and the quarterly Health Surveillance Steering Group (HSSG).

In 2021, E&A staff members supported several ad hoc requests for data analyses and distributed hundreds of periodic reports throughout the DOD. These ad hoc requests and periodic reports look for trends over time of diseases and injuries such as communicable diseases, training-related injuries, mental health illnesses, traumatic brain injury (TBI), and deployment health. Ad hoc requests and periodic reports have helped Defense Department policymakers shape their Force Health Protection (FHP) programs and healthcare professionals develop preventive measures against diseases or injuries affecting U.S. Service members and their beneficiaries.

In 2021, E&A began three analyses in response to congressional inquiries related to military exposures including cancer incidence, and mortality for fixed wing aviators and support personnel, and all-cause mortality in personnel who spent any time at an Uzbekistan base from 2001–2005. E&A also continued to support important DOD research studies including former Vice President Joe Biden’s Cancer Moonshot initiative, which aims to accelerate cancer research

and make additional therapies available to patients while also improving the ability to prevent cancer and detect it at an early stage.

Examples of Select AFHSD Periodic Reports in 2021:

- ▶ Deployment Health Compliance Report
- ▶ DOD Consolidated Influenza Surveillance Report
- ▶ Malaria Case-Finding Report
- ▶ DOD Health of the Force Report
- ▶ Army Heat and Cold Weather Injury Report
- ▶ DOD Eye Injury Report
- ▶ U. S. Army Training and Doctrine Command (TRADOC) Training-related Injuries
- ▶ U.S. Army Special Operations Command (USASOC) Reportable Events
- ▶ Health Affairs (HA) Mental Health Report
- ▶ HA TBI Report
- ▶ HA PTSD Report
- ▶ PHA Tobacco Use Report

**THE NAVY SATELLITE** staff work within the EpiData Center (EDC) which, along with Health Analysis, and Health Promotion and Wellness, is part of the NMCPHC Population Health Directorate. Navy satellite staff serve as subject matter experts in behavioral and operational health, reportable and emerging infections, and data systems and application development.

**THE ARMY SATELLITE** staff support several division within APHC

including the Behavioral and Social Health Outcomes Practice (BSHOP), Injury Prevention, Disease Epidemiology, Army Hearing, and Vision Conservation and Readiness.

**THE AIR FORCE SATELLITE** staff work closely with the DOD Global Respiratory Pathogen Surveillance (DODGRPS) program, which performs global sentinel site based respiratory surveillance analyzing more than 22,000 specimens annually from sentinel sites around the world.

## SURVEILLANCE METHODS AND STANDARDS

AFHSD's Surveillance Methods and Standards (SMS) working group develops, documents, and publishes standard surveillance case definitions and methodologies for studies that utilize DMSS data. The case definitions primarily use ICD-9 and ICD-10 codes to identify conditions of interest diagnosed in the MHS and serve as guidelines for other DOD health surveillance and research organizations.

The working group includes representatives from all services and consults, when needed, with experts from the Defense Department during the case definition development process. These case definitions allow Defense Department public health practitioners to measure disease trends and related biological phenomena in different environments and situations over time.

In 2019, the SMS working group developed and documented 10 new case definitions and updated, among

others, all of the published case definitions in the Mental Health and Oncology categories, and continued its efforts to develop ICD-10 code sets for its existing case definitions. Newly documented case definitions include the AFHSD Burden of Illness and Injury (Burden Dictionary) case definition and code set which is now available on the AFHSD website ([www.health.mil/AFHSB](http://www.health.mil/AFHSB)). To date, there are more than 125 condition-specific case definitions in 18 categories available on AFHSD's website.

## MEDICAL SURVEILLANCE MONTHLY REPORT (MSMR)



**PAGE 2** Cross-sectional analysis of the association between perceived barriers to behavioral health care and intentions to leave the U.S. Army  
*Gabrielle E. Kaplansky, MPH; Lucinda Ackah-Toffey, MPH; Matthew R. Beymer, PhD, MPH; Katherine C. L. Schaughency, PhD, MHS*

**PAGE 8** Is suicide a social phenomenon during the COVID-19 pandemic? Differences by birth cohort on suicide among active component Army soldiers, 1 January 2000–4 June 2021  
*Katherine C. L. Schaughency, PhD, MHS; Eren Youmans Watkins, PhD, MPH; Samuel L. Preston III, DO*

**PAGE 13** Brief report: Relationships between self-reported psychological conditions and aggressive behaviors among crew members of a U.S. Navy aircraft carrier, January 2021  
*Lisa H. Glassman, PhD; Emily A. Schmied, PhD; Robyn M. Englert, MPH; Elizabeth M. Harrison, PhD; Cynthia J. Thomsen, PhD*

**PAGE 17** Surveillance snapshot: A simple model estimating the impact of COVID-19 on lost duty days among U.S. service members  
*Luke E. Mease, MD, MPH; Arron M. Smith, MD*

**PAGE 18** Update: Routine screening for antibodies to human immunodeficiency virus, civilian applicants for U.S. Military Service and U.S. Armed Forces, active and reserve components, January 2016–June 2021

*A publication of the Armed Forces Health Surveillance Division*

Launched in 1995, the *MSMR* is the flagship publication for AFHSD. The monthly journal's articles provide evidence-based estimates of the incidence, distribution, impact, and trends of illness and injuries among U.S. military service members and associated populations.

The *MSMR's* readership includes professionals throughout the MHS, such as public health officials, clinicians, researchers, academicians, healthcare planners, policy-makers, and analysts. The *MSMR* is indexed on MEDLINE and has more than 1,300 online subscribers. During 2021, the *MSMR* received 3,851 total LinkOut hits from within PubMed, a 30% increase compared to 2020. The average number of page hits per month was 166. Articles published in the *MSMR* have generated media coverage in diverse publications, including Reuters, Stars and Stripes, and Military Times.

In 2021, the *MSMR* published a total of 50 articles, including 26 original full reports, 11 updates of previously published data analyses, 5 brief reports, 2 historical perspectives, and 6 surveillance snapshots.

Twenty-six of the articles were submitted by authors not affiliated with the *MSMR* editorial staff. The most frequent topics of original articles and updates in 2021 were COVID-19, mental health, healthcare burden of

disease and injury, influenza, vector-borne diseases, heat injuries, and sexually transmitted infections (STIs). The *MSMR* continues to welcome manuscript submissions for relevant articles on topics in military public health, epidemiology, surveillance, and disease and injury prevention.

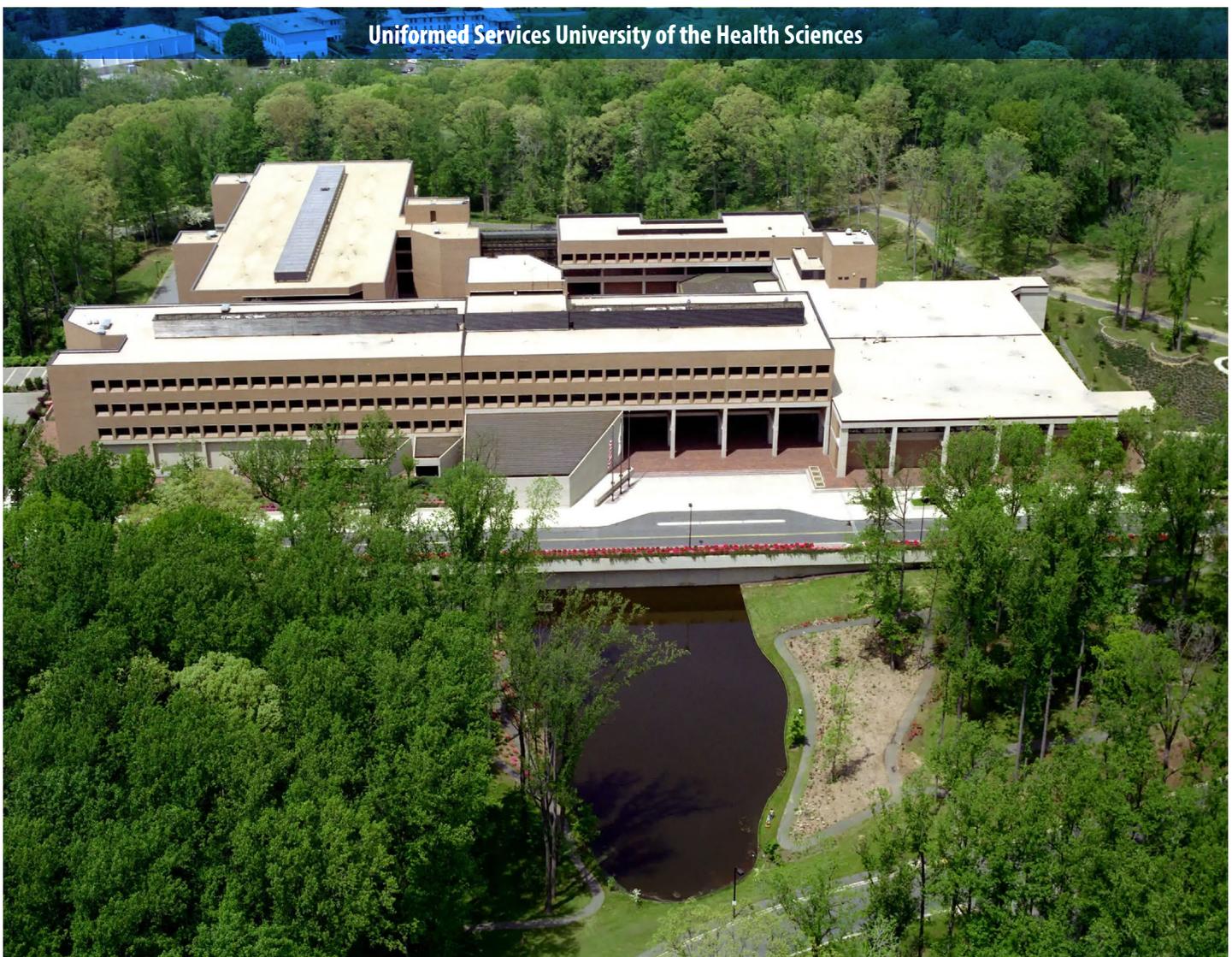
## RESIDENCY TRAINING

As a key DOD source for health surveillance and epidemiologic training, AFHSD hosts preventive medicine residents from USU for a five-week practicum rotation under the supervision of senior staff. Residents enhance their understanding of the complexities of health surveillance systems, knowledge and application of epidemiology, and critical analytical skills. They also are exposed to AFHSD daily operations and initiatives. Central to their rotation, residents design and execute a data analysis project using the DMSS. Residents begin with a hypothesis and design an epidemiologic

study in which they analyze and interpret data and generate a publishable manuscript and an oral presentation.

Since 2008 AFHSD has trained 75 residents with diverse academic backgrounds from the three military services as well as two Doctor of Public Health students. In 2021, there were two Air Force residents, two Navy residents, and one Army resident. Resident and student projects have resulted in published articles such as “Disparities in COVID-19 vaccine initiation and completion among active component service members and healthcare personnel, 11 December 2020–12 March 2021,”

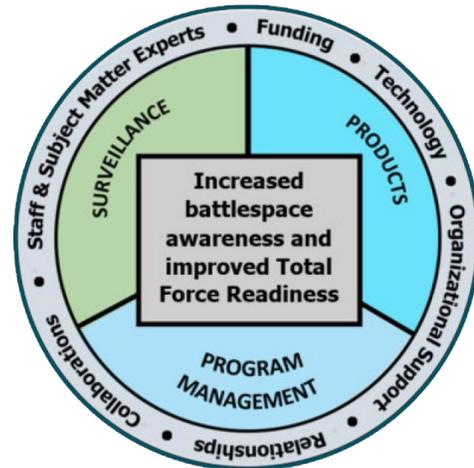
“Long-acting reversible contraceptive use, active component service women, U.S. Armed Forces, 2016–2020,” and “Sepsis hospitalizations among active component service members, U.S. Armed Forces, 2011–2020.” All of the residents trained in 2021 and their completed resident projects are published in the *MSMR* or other peer-reviewed journals or presented at the 2022 American College of Preventive Medicine meeting. Additionally, the E&A branch offers rotation and practicum opportunities for occupational and environmental medicine residents and Master of Public Health and Master of Science in Public Health degrees at USU.



# GLOBAL EMERGING INFECTIONS SURVEILLANCE

The GEIS Branch oversees and manages a portfolio of infectious disease surveillance projects that are executed through a strategically positioned global network of U.S. Army, Navy, and Air Force laboratory partners. The GEIS Branch's Vision and Mission are accomplished through three strategic pillars (i.e., Strategic Ends): Surveillance, Products, and Program Management. The GEIS Branch implements these pillars by:

- ▶ Funding GEIS Partner Laboratories (GEIS-PLs) to conduct **SURVEILLANCE** for emerging infections that threaten the health of the Force and/or military operations;
- ▶ Developing and disseminating surveillance information **PRODUCTS** to stakeholders that provide early warning of emerging threats and battlespace awareness of infectious diseases across geographical locations;
- ▶ Providing **PROGRAM MANAGEMENT** for the GEIS network of laboratory partners through a robust annual business cycle that incorporates strategic guidance, program evaluation, and sound fiscal stewardship.



The GEIS Branch conducts surveillance designed to provide near-real time data on infectious disease threats to inform DOD decision-makers. Timely communication about operational public health threats is critical to enabling GCC Force Health Protection (FHP) decision-making and mission success. As such, the GEIS Branch coordinates directly with the GCC Command Surgeons and GCC and Service component FHP Officers to capture operational infectious disease priorities. These priorities are communicated to the GEIS Branch through strategic guidance documents in the annual Request for Proposals. The GEIS-PLs utilize these guidance documents to develop and execute surveillance activities within four Focus Areas: Antimicrobial Resistant and Sexually-Transmitted Infections (AMR/STI), Enteric Infections (EI), Febrile and Vector-Borne Infections (FVBI), and Respiratory Infections (RI).

Each GEIS Focus Area defines their strategy and direction through portfolio Roadmaps, review of annual proposals, collection of data from funded projects, and translation of findings into products which are packaged and disseminated to GEIS audience members. The GEIS-PLs review the GEIS Strategy, Focus Area Roadmaps, and GEIS-GCC Alignment Documents for guidance on how to design and conduct surveillance activities that align with priorities and gaps via annual proposals.

In FY21, the GEIS Branch distributed \$51.696 million in funding to 23 DOD laboratories and military hospitals to conduct infectious disease surveillance to inform FHP. The GEIS Branch also distributed \$3.45 million in funding to support the DOD's SARS-CoV-2 genetic sequencing expansion efforts. The GEIS-PLs work with host nations and regional partners to conduct disease surveillance.

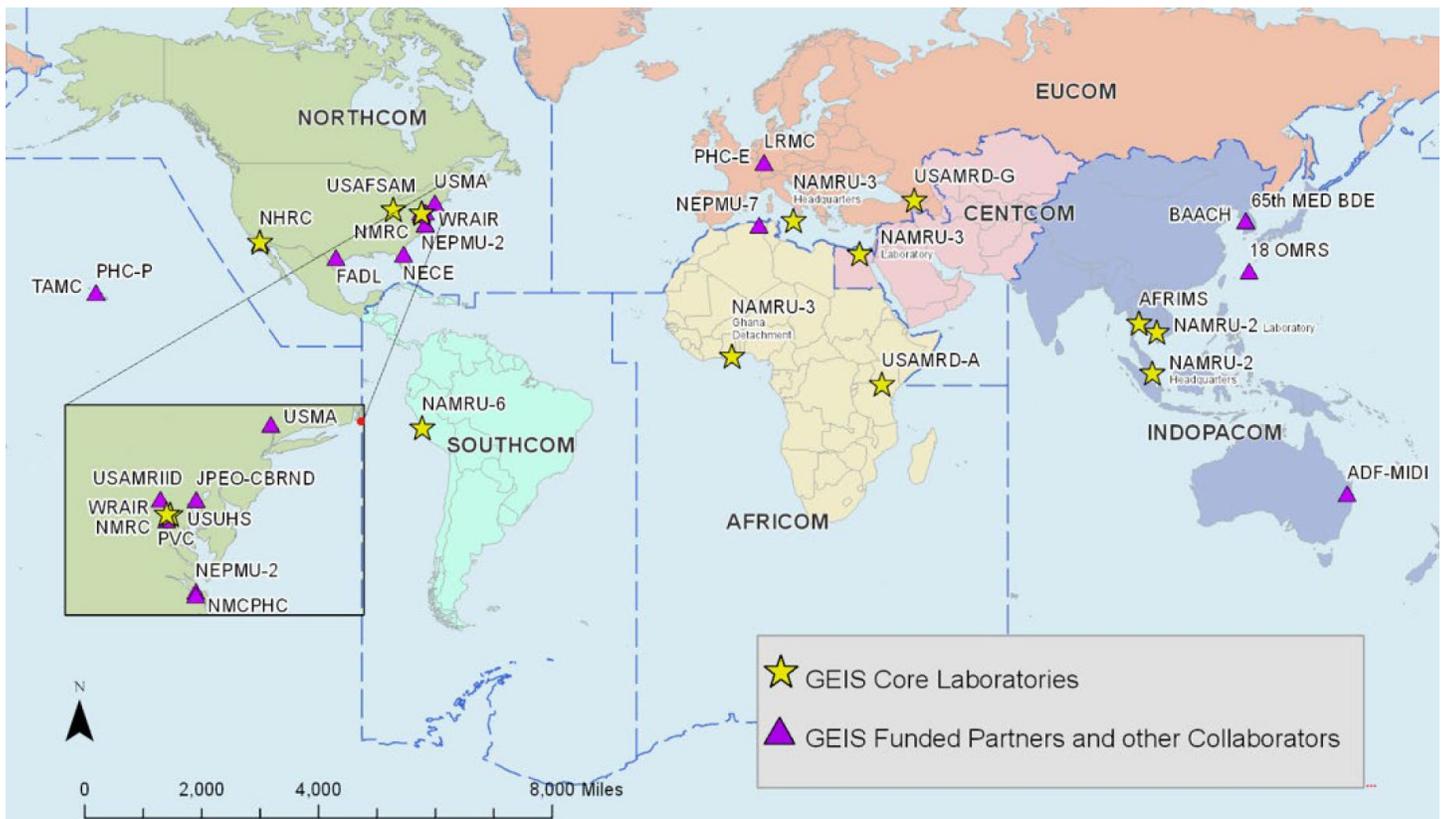
## Vision

To ensure operational success through mitigating infectious diseases threats, enabling the health and readiness of U.S. service members.

## Mission

To increase battlespace awareness and improve Total Force Readiness in support of the unified Combatant Commands via a global laboratory network focused on mitigating the threat of emerging infectious diseases to U.S. service members.

# GEIS PARTNERS



## GEIS PARTNER LABORATORIES:

Naval Medical Research Center (NMRC), including Naval Medical Research Unit (NAMRU)-2, NAMRU-3, NAMRU-6, and Naval Health Research Center (NHRC); Walter Reed Army Institute of Research (WRAIR), including U.S. Army Medical Directorate-Armed Forces Research Institute of Medical Sciences (USAMD-AFRIMS), U.S. Army Medical Research Directorate (USAMRD)-Georgia, and USAMRD-Africa; U.S. Air Force School of Aerospace Medicine (USAFSAM); Uniformed Services University of the Health Sciences (USUHS)

## ADDITIONAL DOD PARTNERS:

18th Operational Medical Readiness Squadron (18 OMRS), 65th Medical Brigade (65th MED BDE), Navy Entomology Center of Excellence (NECE), Pharmacovigilance Center (PVC), U.S. Army Medical Research Institute of Infectious Diseases (USAMRIID), and U.S. Military Academy West Point (USMA)

## MILITARY HOSPITAL PARTNERS:

Brian Allgood Army Community Hospital (BAACH), Landstuhl Regional Medical Center (LRMC), and Tripler Army Medical Center (TAMC)

## PUBLIC HEALTH COMMAND/CENTER PARTNERS:

Navy and Marine Corps Public Health Center-EpiData Center (NMCPHC-EDC), Navy Environmental Preventive Medicine Unit (NEPMU)-2, NEPMU-5, NEPMU-7, Public Health Command (PHC) Europe, and PHC Pacific

# GEIS BRANCH INITIATIVES

## GEIS CUSTOMER ENGAGEMENT

In 2020–2021, GEIS held Coordination Meetings with five GCCs to accomplish two primary objectives: (1) define how the GEIS Branch supports the operational and strategic priorities of each GCC and Service components and (2) improve the GEIS Branch’s understanding of how to optimally support FHP decision-making through the effective sharing of infectious disease surveillance information generated in each Area of Responsibility (AOR). Attendees included GCC Command Surgeons; FHP, Preventive Medicine, Environmental Science and Engineering, and Public Health Officers; DHA Veterinary Corps Officers; liaison officers from the CDC; representatives from the Biological Threat Reduction Program; GEIS partners, and Branch staff. Outcomes of the meetings included discussions of priorities and threats in each AOR; an enhanced understanding of how the GEIS Branch provides critical information on infectious disease surveillance for FHP decision-making, and recommendations for enhancing GEIS products such as reports, visualizations, and dashboards that communicate surveillance findings. The outcomes of these meetings ultimately informed the solicitation, submission, and selection of proposals for GEIS funding in FY21 and FY22 and will shape how the GEIS Branch provides value to the GCCs and the broader GEIS audience<sup>1</sup> by communicating surveillance findings in an effective manner.

## GEIS DATA, REPORTING, AND PRODUCT INITIATIVES

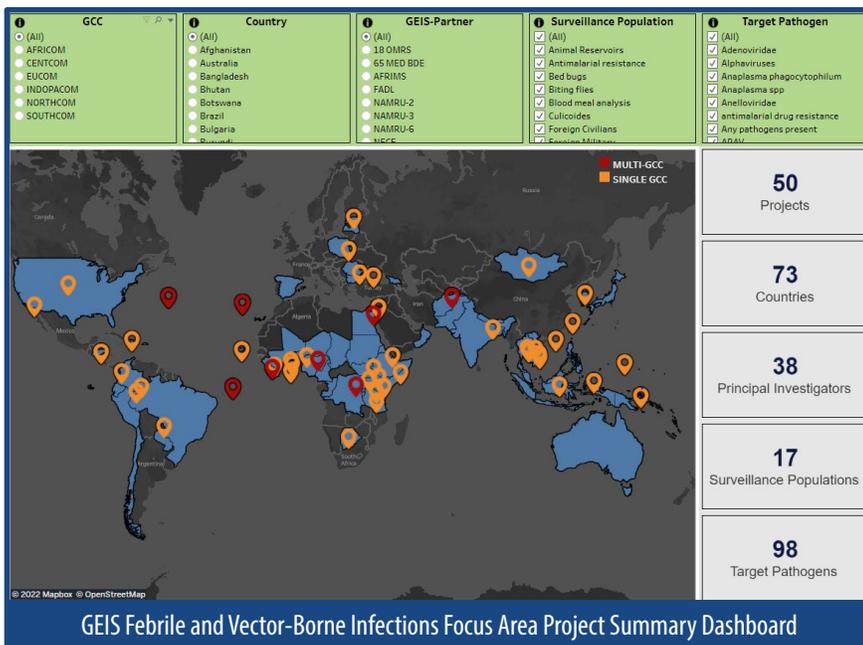
The GEIS Branch continued to implement, evaluate, and refine the Data-to-Decision Initiative that was launched in late 2017. The goal of this initiative is to rapidly communicate infectious disease surveillance findings from GEIS-funded projects to the GEIS audience to inform FHP decision-making. Over the course of 2021, GEIS-PLs continued to provide surveillance findings to the GEIS Branch on a monthly basis. The GEIS Branch developed and disseminated **11** Monthly Surveillance Reports that communicated notable surveillance findings to GEIS audience members. Additionally, the GEIS Branch disseminated over **100** SPOT reports that urgently communicated High and Moderate threat surveillance findings to GEIS audience members, the majority of which shared surveillance findings resulting from SARS-CoV-2 whole genome sequencing efforts.

1. The GEIS audience includes DOD decision-makers, such as GCC and Service component FHP Officers, preventive medicine and infectious disease clinicians, public health professionals, and global health engagement specialists.

Over the past year, the Data-to-Decision Initiative has accomplished several goals. First, the GEIS Branch collaborated with the Joint Program Executive Office, Defense Healthcare Management Systems to work towards implementing a cloud-based data lake environment for the GEIS Branch. The data lake environment, to be completed by 2023, will enable seamless data sharing between GEIS-PLs and the GEIS Branch. Adopting a highly flexible data architecture will allow the GEIS Branch to keep pace with the changing disease and technology landscapes in a scalable manner. With the implementation of automation processes in the data lake, the GEIS Branch will be able to focus on more high-value activities, such as providing relevant analyses and products to the GCCs and other GEIS audience members, rather than time-consuming data collection and management processes.

Second, in response to requests from GEIS partners and audience members for improved accessibility to GEIS surveillance products and project information, the GEIS Branch established a CAC-enabled CarePoint site (<https://carepoint.health.mil/sites/AFHSB/geis/>). This site allows GEIS partners and audience members to access surveillance reports, programmatic documents, and newly-developed dynamic dashboards. As part of the development of the GEIS CarePoint Site, the GEIS Branch developed Focus Area-specific Project Summary Dashboards that have enabled GEIS-funded partners and potential future partners and collaborators to explore projects receiving funding across the GEIS Branch. This tool will continue to foster cross-talk between partners with overlapping interests and to identify potential gaps in surveillance.

Finally, GEIS has implemented a more refined product development plan for creating surveillance products that meet GEIS audience members’ needs, incorporating feedback from attendees of the 2020–2021 GEIS-GCC Coordination meetings. The new plan outlines specific products that will be produced in partnership with the GEIS-PLs to rapidly communicate surveillance findings. In line with this plan, the GEIS Branch has developed several interactive dashboards hosted on the GEIS CarePoint site that display surveillance data and serve as a tool for FHP decision-making. For example, the Camp Lemmonier and Chabelley Airfield Vector Surveillance and Control Dashboard has been used by leadership and personnel at Camp Lemmonier, Djibouti to inform proactive assessments of the potential for malaria outbreaks and to drive decisions around logistics of pest management and control.



of the WGS expansion effort, standardized SARS-CoV-2 metadata was routinely collected and reported to the GEIS Branch, resulting in a rich dataset that was curated and maintained throughout the pandemic. This information was subsequently analyzed and shared in multiple important surveillance products and DHA leadership communications throughout 2020 and 2021. The GEIS Branch developed four new weekly reports and three new data collection forms to provide timely information to external audiences. The GEIS Branch also pivoted to respond to more specific requests for updates on variant distribution and GCC-specific surveillance highlights, including a new variant-specific map on the Health Surveillance Explorer (HSE). In addition, staff from the GEIS Branch participated in several interagency working groups to exchange findings among government and public health institutions.

## GEIS NEXT GENERATION SEQUENCING AND BIOINFORMATICS CONSORTIUM

The increasing availability and affordability of next-generation sequencing (NGS) technologies has dramatically increased the capability of DOD medical and public health laboratories to detect, characterize, and respond to infectious disease threats. As a result, NGS has become a critical component of comprehensive biosurveillance programs within DOD. In 2017, the GEIS Branch established the Next-Generation Sequencing and Bioinformatics (BI) Consortium (NGS-BC) to promote collaboration, training and development, and harmonization of NGS and BI capabilities among the GEIS-PLs, with the end goal of increasing the availability and quality of genomic data and information products to advise FHP decision-making. As a result, in early 2020, the NGSBC, including several partners with existing sequencing capabilities were able to rapidly pivot to SARS-CoV-2 genomic surveillance in response to the COVID-19 pandemic. Early Consortium actions included the evaluation, development, and dissemination of standardized sequencing protocols, bioinformatics practices, and sample metadata reporting for SARS-CoV-2 genomic surveillance. The NGSBC also began performing viral culture of SARS-CoV-2 isolates to aid in investigation of emerging variants and development and monitoring of medical countermeasures.

In 2021, the GEIS Branch formalized its coordinating role for DOD genomic surveillance activities with the implementation and execution of the *SARS-CoV-2 Whole Genome Sequencing (WGS) Action Plan for the Department of Defense Military Health System (MHS)*. As the pandemic progressed and new variants of SARS-CoV-2 emerged, this resulted in a dramatic scale up of SARS-CoV-2 sample collection and sequencing domestically and expansion to new sites overseas. As part

The GEIS Branch was able to support expansion of SARS-CoV-2 sequencing efforts at two OCONUS military hospitals: LPMC in Germany and TAMC in Hawaii. Five core laboratories of the NGSBC (e.g., NHRC, NMRC, USAFSAM, USAMRIID, and WRAIR), TAMC, and four OCONUS partners continue to actively sequence SARS-CoV-2 samples, monitor for emerging variants, and report their findings to the GEIS Branch on a weekly or monthly basis. These partners produced **67** SPOT reports between Oct. 01, 2020–Sept. 30, 2021 related to SARS-CoV-2 sequencing, which included descriptions of key emerging mutations among SARS-CoV-2 viruses, emergence and detection of novel variants in MHS beneficiaries, severe clinical outcomes related to infection, and outbreak investigations on Naval vessels, recruit training centers, military academies and overseas installations.

Given the unique challenges around genomic data sharing and collection during the pandemic, the GEIS Branch is pursuing a more coordinated approach for future data sharing and reporting that will allow for even more rapid and efficient response to emerging threats through use of DOD-approved platforms like the Digital Biobank. The GEIS Branch is optimistic that this will be a future solution to aid in genomic data sharing and analysis between GEIS partners, and to bring more sustainable solutions for analysis to the DOD OCONUS sequencing laboratories.

## STAYING ON THE LEADING EDGE

The GEIS Branch is responsible for several cross-cutting initiatives that are beneficial to both the Branch and the GEIS-PLs and enrich the support provided for their surveillance activities. For example, as genetic sequencing capabilities have evolved and grown, so has the desire to have mobile platforms that could shorten the time from sample collection to reporting of results. To support the deployment and

utilization of this technology, the GEIS Branch established a user group for partners leveraging the MinION, one type of mobile genetic sequencing platform. Since 2019, the MinION User Group has served as a forum for government-funded users of the Oxford Nanopore MinION to share information and best practices, discuss troubleshooting and challenges, and encourage collaboration. Currently, the group has 130 participants from 30 DOD organizations. Over the last year, there were **11** presentations given by GEIS partners. The GEIS Branch will continue to offer the opportunity for partners to present their findings and learn from others through this forum.

In an effort to promote harmonization and synchronization among GEIS-PLs, the GEIS Branch established the GEIS Laboratory Capability Database in 2019 with collated, detailed information on the various capabilities of each of the GEIS-PLs. This database is a resource for laboratories looking to collaborate across the network, particularly if there is a need to identify a partner with specific instrumentation or ca-

pability. The database also contains an assay matrix, which allows partners to view, compare, or select assays that are currently in use at GEIS-PLs, which may result in more consistent and comparable testing amongst the network. The GEIS Branch plans to move the database to its GEIS CarePoint Site to make it more accessible and user friendly for the network.

The GEIS Branch has also established a GEIS Partner Publication Database to maintain records of GEIS-funded publications and to track publications as a component of evaluating project progress and outcomes. From 2017 to 2020, the GEIS Branch logged **276** publications in 94 unique journals. Of those, 220 publications were collectively cited 1915 times, demonstrating the expansive impact and scientific contributions of the network.

These GEIS initiatives have provided tremendous value to the GEIS Branch. The GEIS Branch will continue to seek further opportunities for innovation to stay on the Leading Edge.

## GEIS FOCUS AREA OVERVIEWS

### ANTIMICROBIAL RESISTANT & SEXUALLY-TRANSMITTED INFECTIONS FOCUS AREA:

The Antimicrobial Resistant and Sexually-Transmitted Infections (AMR/STI) Focus Area portfolio addresses the surveillance of antibiotic resistant organisms, especially multidrug-resistant organisms (MDROs), in Service members and other relevant populations around the world. The AMR/STI Focus Area predominantly targets pathogens responsible for the most concerning MDROs, including multidrug-resistant gonococcal (GC) infections and those resistant to critical last line antibiotics (e.g. carbapenems and colistin). Projects in the AMR/STI portfolio are selected to surveil the scope of the MDRO burden, elucidate AMR patterns in wound and traumatic injuries, and support the DOD's contributions to the U.S. Government's 2020–2025 National Action Plan (NAP) for Combating Antibiotic-Resistant Bacteria (CARB)

### CURRENT PORTFOLIO:

In 2021, the AMR/STI Focus Area supported 21 sustainment projects at 10 DOD partner laboratories, totaling approximately \$8.1 million. This amount included \$4.1 million in CARB activity funding, which supported CARB surveillance activities in the MHS, a limited subset of GEIS OCONUS surveillance activities, and maintenance of two critical MDRO pathogen repositories – the WRAIR Multidrug-Resistant Organism Repository and Surveillance Network (MRSN) and the DOD GC Reference Laboratory & Repository. Overall, the AMR/STI portfolio maintained prospective surveillance

in 17 operationally important countries around the world. While the COVID-19 pandemic created obstacles for AMR/STI surveillance, the majority of surveillance efforts remained active, reporting new monthly findings for most of the year.

### WHERE WE ARE GOING:

The AMR/STI Focus Area will concentrate on additional FHP relevant targets, including community-acquired infections and MDRO infections in traumatic injuries. In support of the GEIS Branch's designated activities in the 2020–2025 NAP for CARB, the AMR/STI Focus Area will introduce a One Health surveillance category that will increase surveillance efforts of non-human isolate sources to further our understanding of MDRO transmission in community settings. The AMR/STI Focus Area will also continue to improve data harmonization, optimizing data sharing from GEIS-PLs and ensuring bacterial genomic sequencing and NGS is complementary to the efforts of the NGSBC. The AMR/STI Focus Area is committed to advancing surveillance techniques, pathogen targets, and data quality to provide FHP relevant information.

### RECENT ACCOMPLISHMENTS:

- ▶ WRAIR MRSN generated seven SPOT reports responding to detection of high-risk extensively-drug resistant (XDR) and pan-drug resistant (PDR) organisms that were introduced in the MHS. WRAIR MRSN coordinated with a deployed tertiary care facility and infection

prevention experts to monitor and target interventions for on-going nosocomial outbreaks of XDR and PDR carbapenemase-producing organisms, which are rare occurrences in the MHS. The MRSN connected isolates from this facility with known isolates collected from multiple CONUS and OCONUS MHS locations.

- ▶ NMCPHC-EDC developed methods to refine and synthesize the Theater Medical Data Store (TMDS) data stream with other MHS data sets to provide snapshots of AMR in forward austere secondary and tertiary care facilities in the MHS. Successful implementation of this effort may improve visibility of AMR in those locations for MHS and DOD decision-makers.
- ▶ USAMRD-A identified the first *Klebsiella pneumoniae* in a human clinical isolate from Kenya with mobilized colistin resistance (*mcr*) genes. Similarly, AFRIMS reported the first occurrence of the *mcr* genes in two clinical *Escherichia coli* isolates in the Philippines. The *mcr* gene is a highly mobile plasmid mediated resistance factor that confers resistance to a critical last-line antibiotics. This gene is viewed as an indicator for the potential emergence of PDR bacteria. Novel detection of the *mcr* gene in new locations is of critical operational importance due to the risk of introduction into the MHS and CONUS healthcare systems.
- ▶ USAMRD-G noted the emergence of the first documented cases of presumptive PDR *A. baumannii* in the Republic of Georgia. Three isolates were identified from different hospital facilities and were notably resistant to all tested drug classes, including colistin and carbapenems. Two isolates were highly related, suggesting a common infectious source and carried a rare plasmid mediated resistance factor for carbapenem resistance. Conversely, there was no plasmid-mediated transmission of colistin resistance in these isolates, but rather a number of mutations observed in the core genome. This highlights the multiple ways in which AMR can emerge. Continuing work to improve the understanding of the different pathways and drivers in AMR may help future decision makers in assigning risk for service members living and working in diverse geographic locations.

### ENTERIC INFECTIONS FOCUS AREA:

The Enteric Infections (EI) Focus Area portfolio addresses militarily-relevant enteric pathogens, that degrade readiness, through 1) surveillance for acute gastroenteritis



GEIS Antimicrobial Resistant and Enteric Infections Focus Areas staff, Maj Amy Bogue, Mr. Michael Cziner, and MAJ Ashley Hydrick (left to right), discuss current surveillance sites where GEIS-funded activities are taking place.

in the U.S. military (including recruit, shipboard, and forward-deployed populations) and in foreign military and civilian populations; 2) characterization of enteric disease with a focus on the category of travelers' diarrhea in immune-naïve travelers; 3) advanced characterization of enteric pathogens that includes antimicrobial susceptibility testing (AST) and molecular testing of antimicrobial resistance genes; and 4) detecting emerging pathogens in previously tested "pathogen negative" stool samples.

### CURRENT PORTFOLIO:

In FY21, the EI Focus Area supported one competed project and 11 sustainment projects at nine DOD partner laboratories totaling approximately \$4.2 million. The multisite Global Travelers' Diarrhea (GTD) Study continued prospective surveillance efforts in Djibouti, Egypt, Honduras, Kenya, Nepal, Peru, and the Republic of Georgia. The GEIS Branch supported AFRIMS and USAMRD-G's enteric surveillance activities during military exercises in the IN-DOPACOM and EUCOM AORs, respectively. Additionally, advanced characterization of enteric pathogens was expanded to include a focus on antibiotics used for empiric treatment for diarrheal illness and a testing priority list for molecular markers that will enhance the understanding of resistance genes, antibiotic resistance patterns, and dispersion of enteric pathogens geographically.

### WHERE WE ARE GOING:

The EI Focus Area will further expand AST and sequencing of enteric pathogens to better understand resistance trends

and support treatment recommendations. Furthermore, the EI Focus Area will continue optimizing the GTD Study's protocol by standardizing reporting of infection rates, case severity, performance limitations, and treatment outcomes across sites in five continents. Surveillance activities across One Health domains (e.g., human-animal-environmental) will also become a focus of the EI Focus Area, incorporating surveillance that uses animal and environmental sentinels to improve data collected for FHP decision-making. This will produce opportunities to fund different types of projects, such as those that surveil wastewater and animal or environmental food-borne pathogens. These efforts will lead to improved actionable information for FHP in the most cost-effective manner across militarily relevant geographic locations within each GCC.

### RECENT ACCOMPLISHMENTS:

- ▶ NHRC and NMRC Biological Defense Research Directorate (BDRD) conducted a study on SARS-CoV-2 fecal shedding by analyzing recruit and advanced trainee surveillance specimens to detect SARS-CoV-2 in stool. NMRC BDRD successfully extracted RNA from 12 specimens. All 12 specimens were sequenced and identified as SARS-CoV-2 lineage A or Nextstrain clade G2, which were consistent with strains circulating during the collection period of May–June 2020. The findings were consistent with current literature. Almost 50% of SARS-CoV-2 positive patients shed SARS-CoV-2 virus in the stool for up to two weeks.
- ▶ AFRIMS and USAMRD-A continued conducting targeted AST as part of ongoing enteric surveillance efforts. Surveillance findings suggest emerging resistance to azithromycin in Thailand and Kenya. Azithromycin is a first line agent for the treatment of travelers' diarrhea and is commonly used to treat severe diarrhea cases. This new trend in resistance to azithromycin in enteric isolates is concerning and requires continued surveillance.
- ▶ LRMC collected and tested 838 samples from 21 clinics in the EUCOM and CENTCOM AORs, with enteropathogenic *E. coli* (103, 12%) and *Campylobacter* spp. (63, 8%) being the most commonly identified. This project also detected mixed pathogen infections, as well as a case of *Vibrio cholerae*, among Afghan evacuees transiting through EUCOM as part of Operation Allies Refuge.
- ▶ NHRC, in collaboration with the GEIS Branch, has continued to refine and strengthen protocols for the Global Travelers' Diarrhea Study. Protocols are actively being updated to include multiplex testing (e.g., using the BioFire® FilmArray platform) and more AST guidance. The GTD Study uses standard protocols and study enrollments to compare data on travelers' diarrhea at five OCONUS DOD laboratories (sites located in: Nepal,

Kenya, Honduras, Peru, and Egypt). The GEIS Branch has also drafted a prioritized list for selecting enteric isolates for whole genome sequencing (WGS) at NHRC. This list, included in the FY23 Enteric Infections Focus Area Roadmap, will assist in future characterization and analysis of AMR genes in enteric isolates.

### FEBRILE AND VECTOR-BORNE INFECTIONS FOCUS AREA:

The Febrile and Vector-Borne Infections (FVBI) Focus Area portfolio focuses on actionable surveillance of vector-borne and zoonotic infections that threaten the health of U.S. service members. The FVBI Focus Area seeks to better characterize the composite risk of vector-borne and zoonotic diseases to U.S. personnel, inform FHP decision-makers and commanders, and contribute to countermeasure development. To accomplish these objectives, the FVBI Focus Area surveillance projects fall into three general areas: characterizing acute febrile illnesses (AFI) by linking syndromes to causative pathogens; documenting the geographic and temporal distributions of vectors, reservoirs, and associated pathogens; and assessing the effectiveness of FHP countermeasures to vector-borne infections.

### CURRENT PORTFOLIO:

In FY21, the FVBI Focus Area supported 18 competed projects and 33 sustainment projects at 17 partner laboratories, funded at approximately \$17.1 million. The FVBI Focus Area maintained interest in acute febrile illness surveillance across OCONUS partner labs, expanding pathogen discovery efforts to countries such as Brazil and Uganda. FVBI projects brought a renewed emphasis on vector surveillance. In particular, an enhanced focus on insecticide resistance testing sought to address the rise of permethrin resistance in vector populations globally. Data showed high insecticide resistance levels in *Aedes* mosquitoes in Thailand (AFRIMS) was a possible cause for increased dengue cases in those same regions. WRAIR also re-launched VectorMap, which helped establish ecological niche models and determine knowledge gaps used to guide future surveillance site selection in collaboration with other partner labs.

### WHERE WE ARE GOING:

The FVBI Focus Area will increase value for DOD customers by further refining its surveillance niche and harnessing efficiencies made possible by new tools or techniques. First, the FVBI Focus Area will continue mobilizing efforts and resources toward unique DOD FHP needs, constraints, and gaps, which may not be addressed in the surveillance conducted by interagency and coalition partners. For the FVBI Focus Area, familiarity with DOD personnel, tools, and operations enables tailored and actionable surveillance. Second, the FVBI Focus Area will enter the next phases



AFHSD's Senior Vector Surveillance Specialist Stephanie Cinkovich, PhD, visited the Navy Entomology Center of Excellence (NECE) in Jacksonville, Florida in summer 2021.



Left: As the team lead for Febrile and Vector-Borne Infections Focus Area, LT Neil Milan, toured NECE's insectary. This facility contained mosquitoes used for evaluation and testing projects. Right: LT Milan viewed sequencers that analyzed raw sequence data obtained from mosquitoes caught in the wild.

in its initiative to harmonize surveillance procedures and data integration across the GEIS branch. This harmonization will enable the FVBI Focus Area to draw more valuable and actionable surveillance from already completed, ongoing, and prospective work. Third, the FVBI Focus Area will shift how it conducts AFI surveillance to increase the value and timeliness of results. AFI is a global operational FHP concern, but seeking answers to narrower, regional questions may be the most efficient means to providing actionable AFI surveillance information.

#### RECENT ACCOMPLISHMENTS:

▶ NAMRU-3 vector surveillance provided key insights into the effectiveness of DOD-approved pyrethroids on an important disease vector, *Aedes aegypti*, across eight Local Government Areas (LGAs) in Nigeria. Results

demonstrated that *Ae. aegypti* mosquitoes collected across three of the LGAs were resistant to diagnostic concentrations of permethrin. This insecticide resistance data increased understanding of control options for a key vector species and guided decision-making for strategies that help reduce risk to U.S. personnel.

▶ NAMRU-6 genetically characterized circulating *Leishmania* spp. species in endemic areas of Peru, Brazil and Honduras, and characterized regions within those countries for risk of visceral (VL) and cutaneous leishmaniasis (CL). Their findings helped strengthen evidence that leishmaniasis remains a high risk near the borders between Peru, Brazil and Bolivia. This region has renewed importance as a major migration route and nexus of drug trafficking and illegal mining activities.

- ▶ USAMRD-A analyzed serum samples collected during October 2021 from patients presenting febrile illness across multiple sites in the Lamu and Mombasa counties of Kenya. Samples were tested by quantitative RT-PCR for alphaviruses and flaviviruses; about 40% of samples from Lamu County Hospital and about 4% from the Mtongwe Naval Base were positive for dengue virus serotypes. There had been an ongoing outbreak of dengue fever along the coast since January 2021, so characterizing virus serotypes and monitoring distribution was important to assessing the threat and informing outbreak response.
- ▶ The Walter Reed Biosystematics Unit (WRBU) re-launched the VectorMap portal and developed 42 ecological niche models in collaboration with USAMRD-A, USAMRD-G, NAMRU-3, and NAMRU-6. The VectorMap team worked to conduct vector surveillance gap analyses for 14 priority countries to help drive future surveillance site selection. WRBU produced six Vector Hazard Reports, which updated critical information on the identification, biology, and distribution of important disease vectors around the world.

### RESPIRATORY INFECTIONS FOCUS AREA:

The Respiratory Infections (RI) Focus Area portfolio addresses rapid pathogen detection and response, especially for those respiratory infections with pandemic potential. This is accomplished through the surveillance of U.S. military members (including recruit, shipboard, and deployed populations), other MHS beneficiaries, and foreign military and civilian populations as well as those at the human–animal interface. Advanced characterization is also conducted to monitor concerns such as SARS-CoV-2 variants and influenza antigenic drift and shift and to evaluate vaccine effectiveness and response.

### CURRENT PORTFOLIO:

In FY21, the RI Focus Area supported two competed and 20 sustainment projects at 14 DOD partner laboratories, totaling approximately \$18.98 million. The SARS-CoV-2 pandemic continued to represent the highest portion of respiratory disease surveillance and threat to FHP, though influenza detections increased later in 2021. Other respiratory illness such as rhinovirus and enterovirus persisted throughout the pandemic, while others (such as respiratory syncytial virus (RSV) and adenovirus) continued to be detected at low levels. The RI Focus Area continued surveillance at the human-animal interface with surveillance

among swine and birds in South America, Africa, and Asia. Additionally, shipboard surveillance for rapid identification and response to respiratory and gastrointestinal outbreaks has expanded with deployment of more equipment and capability on Navy ships. Respiratory projects also leveraged the NGSBC to provide high-quality sequencing data for surveillance, vaccine formulation, and FHP efforts.

### WHERE WE ARE GOING:

The RI Focus Area continues to support the DOD Global Respiratory Pathogen Surveillance Program (DOD GRPS) to provide broad surveillance of RIs; annual sentinel site evaluation will optimize surveillance across the MHS. Surveillance at the human-animal interface will continue, with emphasis on the One Health approach. Pandemic preparedness and surge capability will be considered in future funding, as well as pathogen identification processes. Another area of emphasis will include improving awareness of partner findings and resources to enhance network collaboration, particularly in the area of next-generation sequencing and bioinformatics. We also aim to coordinate with external organizations to decrease duplication of effort and improve synchronization.

### RECENT ACCOMPLISHMENTS:

- ▶ NHRC identified a mixed cluster of illness caused by *Streptococcus pneumoniae* and *S. pyogenes* that resulted in three hospitalizations and a fatality in a training setting. This timely identification allowed for increased surveillance and prophylaxis, reducing further impacts on trainees.
- ▶ USAFSAM identified and tracked an influenza outbreak of over 250 cases of influenza A/H3N2 at the United States Naval Academy in Oct.–Dec. 2021.
- ▶ USAFSAM continued to manage the DGRPSP in FY22, finalizing results on 47,303 specimens from 98 locations and conducting further analysis on a portion of SARS-CoV-2 and influenza samples to determine geographic distribution and subtyping/presence of variants.
- ▶ AFHSD, USAFSAM, and NMRC collected data on influenza that were collated and presented by the RI Focus Area Lead at the Food and Drug Administration’s annual Vaccine and Related Biological Products Advisory Committee meeting on influenza vaccine, supporting the selection of virus strains for the 2022–2023 Northern Hemisphere influenza vaccine.

# INTEGRATED BIOSURVEILLANCE

Integrated Biosurveillance (IB) provides near real-time communication of infectious disease and health threats to military populations within DOD. This branch is part of a global network that maintains key partnerships with inter-agency counterparts that include the National Center for Medical Intelligence (NCMI), Department of Homeland Security/National Biosurveillance Integration Center, CDC, Department of State, and Defense Threat Reduction Agency (DTRA). IB provides critical biosurveillance information for CCMD development of FHP Guidance and serves as a “One-Stop Shop” that distributes analysis and information from reliable resources (NCMI, CDC, WHO, etc.).

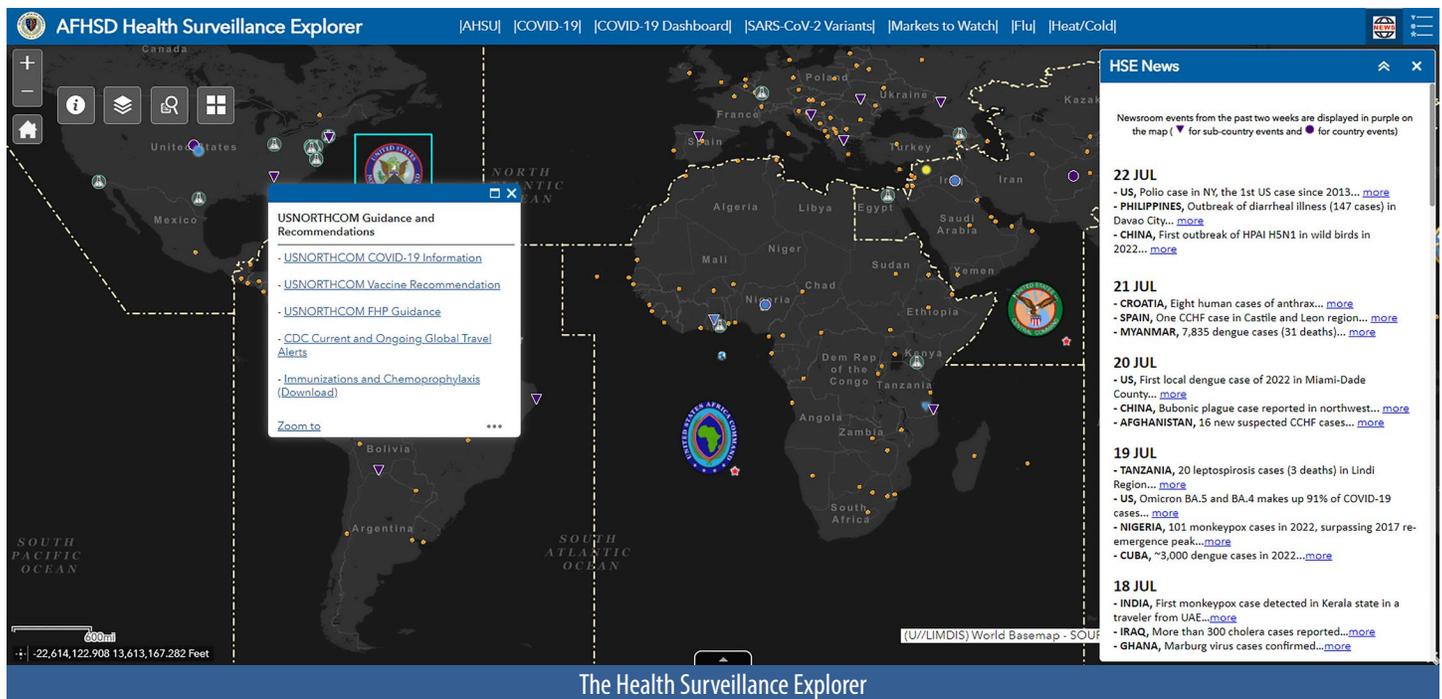
This branch is comprised of three sections, Alert and Response, Innovation and Evaluation, and Geographic Information System. IB generates EXSUM's, SPOT reports and Surveillance Summaries in addition to the weekly AFHSD Health Surveillance Update (AHSU). As the integrators of biosurveillance information, IB epidemiologists scan and analyze open source surveillance data, collaborate with partners and other DHA divisions, and distribute the health surveillance information via email. These products are also accessible in the Health Surveillance Explorer (HSE) mapping application.

The HSE is an interactive web-based application created by the AFHSD IB Branch to provide CCMD decision makers timely, relevant, actionable, and comprehensive health surveillance information to promote, maintain, and enhance

the health of military and militarily-associated populations. Such information provides a near real-time picture of military-relevant global health threats, disease outbreaks, and other events of military interest. Additional information about the HSE can be found at [www.health.mil/hse](http://www.health.mil/hse).

## ALERT AND RESPONSE OPERATIONS (ARO) FY21 ACCOMPLISHMENTS INCLUDE:

- ▶ Improved FHP and minimized risk to mission/risk to force for Joint Staff, Services and CCMDs with timely response to requests for disease surveillance.
- ▶ Routinely provided information products focused on informing commander FHP posture decisions to lower the risk of disease transmission and non-battle injury (DNBI) and illness and eliminate preventable DNBI evacuations from Geographic Combatant Command Areas of Responsibility.
- ▶ Produced and distributed 52 AHSUs (one per week) reporting on more than 156 new public health events of interest to the Global CCMDs and 620 updates for those events. The most reported events, in addition to COVID-19, were dengue, chikungunya, malaria, West Nile virus, and yellow fever.
- ▶ Produced and distributed 48 COVID-19 EXSUMs, two Ebola EXSUMs (new Ebola virus disease (EVD)

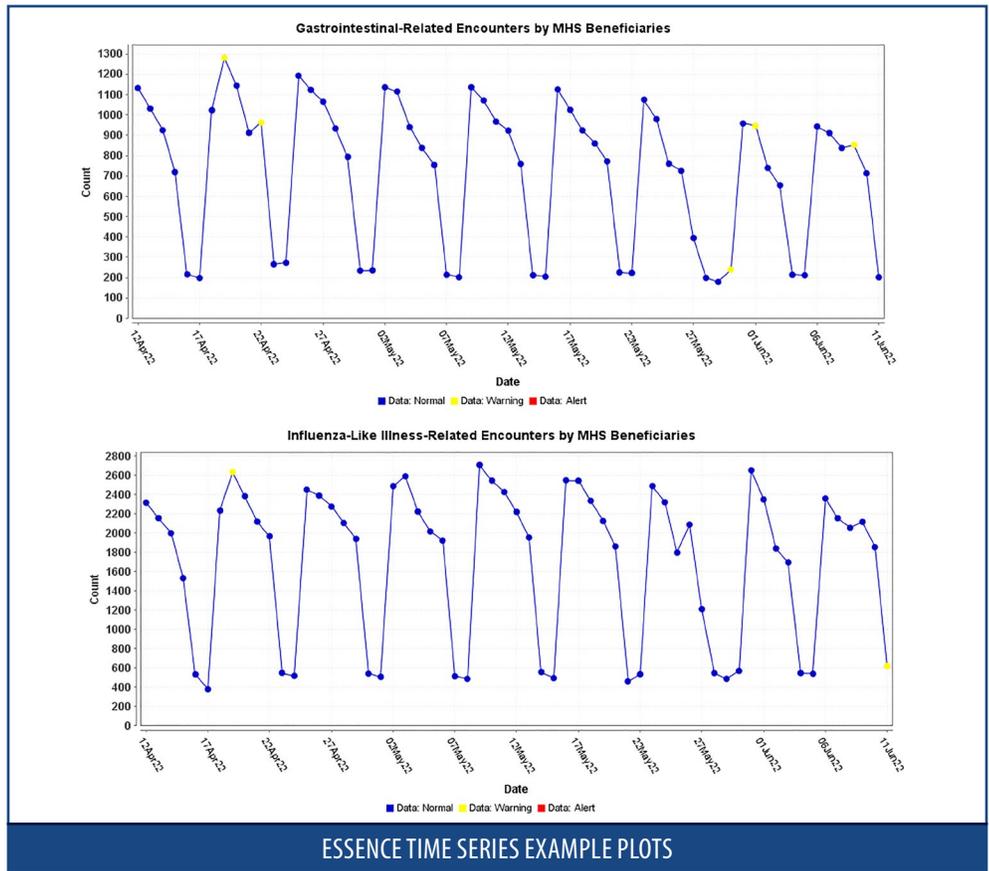


outbreak in the Democratic Republic of the Congo; first EVD case detected in Côte d'Ivoire in more than 25 years), and eight novel avian influenza EXSUMs (e.g., the first human case of infection with avian influenza A(H10N3)).

- ▶ Produced and distributed 48 COVID-19 Surveillance Summaries reporting information on this novel disease in the MHS population and worldwide, as well as providing updated information on medical countermeasures, diagnostics, and transmission.
- ▶ Produced and distributed four EVD Surveillance Summaries reporting information on the outbreaks in North Kivu Province, eastern Democratic Republic of Congo, and N'Zérékoré Prefecture, southern Guinea.
- ▶ Developed 48 fully unclassified (NATO) versions of the weekly AHSU and shared with non-governmental organizations and foreign nations (e.g., Germany, France).
- ▶ Responding to Requests for Information from the CCMDs on topics including the COVID-19 situation in civilians and MHS beneficiaries in Afghanistan from March 2020 to June 2021, and influenza situation in Kenya from 2017 to 2020.
- ▶ More than 2,500 subscribers received the AHSU and other surveillance products. Furthermore, the number of subscriptions continued to increase each year (~500 in FY21).

**INNOVATION AND EVALUATION (IE) FY21 ACCOMPLISHMENTS INCLUDE:**

- ▶ Continued to collaborate with the services to improve the functionality of ESSENCE, which brings advanced visualization capability on par with the civilian sector. Upgrading to same code as civilian ESSENCE provides an opportunity to share future system enhancements and allow for easier data sharing across agencies.
- ▶ Conducted the 2020-2021 DOD Influenza, COVID-like illness (CLI) and influenza-like illness (ILI), and COVID-19 Forecasting projects with academic and government participants, analyzing medical encounter and labo-



ESSENCE TIME SERIES EXAMPLE PLOTS

ratory data and applying internal forecasting models at military hospitals and market locations. Forecast results are displayed on three dashboards.

- ▶ Conducted a five-month long surveillance study looking for Multisystem Inflammatory Syndrome in children (MIS-C) using ESSENCE. IB identified 10 confirmed cases using the system.

**GEOSPATIAL INFORMATION SYSTEM (GIS) FY21 ACCOMPLISHMENTS INCLUDE:**

- ▶ More than 10,000 HSE views.
- ▶ In collaboration with GEIS, created a web-map to display information on the SARS-CoV-2 variants of concern and vaccine breakthrough infections detected in the MHS population.
- ▶ On the COVID-19 dashboard, created and added the risk level and areas of concerns maps at markets/installations.
- ▶ Added new countries features in the HSE including ECDC and COVID-19 (Our World data).
- ▶ Created the HSE Newsroom, which presents daily news about health threats, outbreaks, vaccines, new viruses, SARS-CoV-2 variants, and more.

# PARTNER PUBLICATIONS 2020–2021

1. Hassell JM, Newbold T, Dobson AP, et al. Towards an ecosystem model of infectious disease [published correction appears in *Nat Ecol Evol.* 2021 May 26]. *Nat Ecol Evol.* 2021;5(7):907–918. doi:10.1038/s41559-021-01454-8
2. Ngim CF, Husain SMT, Hassan SS, et al. Rapid testing requires clinical evaluation for accurate diagnosis of dengue disease: A passive surveillance study in Southern Malaysia. *PLoS Negl Trop Dis.* 2021;15(5):e0009445. Published 2021 May 20. doi:10.1371/journal.pntd.0009445
3. Kim HC, Jiang J, Hang J, et al. Detection of *Rickettsia lusitaniae* Among *Ornithodoros sawaii* Soft Ticks Collected From Japanese Murrelet Seabird Nest Material From Gugul Island, Republic of Korea. *J Med Entomol.* 2021;58(3):1376–1383. doi:10.1093/jme/tjab005
4. Truong AT, Noh J, Park Y, et al. Molecular Detection and Phylogeny of Tick-Borne Pathogens in Ticks Collected from Dogs in the Republic of Korea. *Pathogens.* 2021;10(5):613. Published 2021 May 17. doi:10.3390/pathogens10050613
5. Park K, Lee SH, Kim J, et al. Multiplex PCR-Based Nanopore Sequencing and Epidemiological Surveillance of *Hantaan orthohantavirus* in *Apodemus agrarius*, Republic of Korea. *Viruses.* 2021;13(5):847. Published 2021 May 6. doi:10.3390/v13050847
6. Cho S, Allison JC, Park K, et al. A Clinical Case of Scrub Typhus in the United States Forces Korea Patient with Eschar and Genetic Identification of *Orientia tsutsugamushi* Using Multiplex PCR-Based Next-Generation Sequencing. *Pathogens.* 2021;10(4):424. Published 2021 Apr 2. doi:10.3390/pathogens10040424
7. Lakhali-Naouar I, Mukbel R, DeFraités RF, et al. The human immune response to saliva of *Phlebotomus alexandri*, the vector of visceral leishmaniasis in Iraq, and its relationship to sand fly exposure and infection. *PLoS Negl Trop Dis.* 2021;15(6):e0009378. Published 2021 Jun 3. doi:10.1371/journal.pntd.0009378
8. Odoyo E, Matano D, Georges M, et al. Ten Thousand-Fold Higher than Acceptable Bacterial Loads Detected in Kenyan Hospital Environments: Targeted Approaches to Reduce Contamination Levels. *Int J Environ Res Public Health.* 2021;18(13):6810. Published 2021 Jun 25. doi:10.3390/ijerph18136810
9. Fung CK, Li T, Pollett S, et al. Effect of low-passage number on dengue consensus genomes and intra-host variant frequencies. *J Gen Virol.* 2021;102(3):001553. doi:10.1099/jgv.0.001553
10. Hughes JJ, Yang Y, Fries AC, et al. Complete Genome Sequences of Two Human Adenovirus Type 55 Isolates from South Korea and the United States. *Microbiol Resour Announc.* 2021;10(5):e01347-20. Published 2021 Feb 4. doi:10.1128/MRA.01347-20
11. Li T, Chung HK, Pireku PK, et al. Rapid High-Throughput Whole-Genome Sequencing of SARS-CoV-2 by Using One-Step Reverse Transcription-PCR Amplification with an Integrated Microfluidic System and Next-Generation Sequencing. *J Clin Microbiol.* 2021;59(5):e02784-20. Published 2021 Apr 20. doi:10.1128/JCM.02784-20
12. Berry IM, Melendrez MC, Pollett S, et al. Precision Tracing of Household Dengue Spread Using Inter- and Intra-Host Viral Variation Data, Kamphaeng Phet, Thailand. *Emerg Infect Dis.* 2021;27(6):1637–1644. doi:10.3201/eid2706.204323
13. Pollett S, Gathii K, Figueroa K, et al. The evolution of dengue-2 viruses in Malindi, Kenya and greater East Africa: Epidemiological and immunological implications. *Infect Genet Evol.* 2021;90:104617. doi:10.1016/j.meegid.2020.104617
14. Salje H, Wesolowski A, Brown TS, et al. Reconstructing unseen transmission events to infer dengue dynamics from viral sequences. *Nat Commun.* 2021;12(1):1810. Published 2021 Mar 22. doi:10.1038/s41467-021-21888-9
15. Sapoval N, Mahmoud M, Jochum MD, et al. SARS-CoV-2 genomic diversity and the implications for qRT-PCR diagnostics and transmission. *Genome Res.* 2021;31(4):635–644. doi:10.1101/gr.268961.120
16. Valdivia HO, Thota P, Braga G, et al. Field validation of a magneto-optical detection device (Gazelle) for portable point-of-care *Plasmodium vivax* diagnosis. *PLoS One.* 2021;16(6):e0253232. Published 2021 Jun 22. doi:10.1371/journal.pone.0253232
17. Flores-Mendoza C, Loyola S, Jiang J, et al. Molecular Characterization of *Bartonella* Species Discovered in Ectoparasites Collected from Domestic Animals, Cuzco, Peru. *Vector Borne Zoonotic Dis.* 2021;21(5):330–341. doi:10.1089/vbz.2020.2697
18. Velasco JM, Chinnawirotpisan P, Valderama MT, et al. Coding-Complete Genome Sequences of 11 SARS-CoV-2 B.1.1.7 and B.1.351 Variants from Metro Manila, Philippines. *Microbiol Resour Announc.* 2021;10(28):e0049821. doi:10.1128/MRA.00498-21
19. Ashbaugh HR, Early JM, Johnson ME, et al. A prospective observational study describing severity of acquired diarrhea among U.S. military and Western travelers participating in the Global Travelers' Diarrhea Study. *Travel Med Infect Dis.* 2021;43:102139. doi:10.1016/j.tmaid.2021.102139
20. de Almeida JV, de Souza CF, Fuzari AA, et al. Diagnosis and identification of *Leishmania* species in patients with cutaneous leishmaniasis in the state of Roraima, Brazil's Amazon Region. *Parasit Vectors.* 2021;14(1):32. Published 2021 Jan 7. doi:10.1186/s13071-020-04539-8
21. Cardenas JC, Giraldo-Parra SY, Gonzalez MU, et al. Laboratory Findings in Patients with Probable Dengue Diagnosis from an Endemic Area in Colombia in 2018. *Viruses.* 2021;13(7):1401. Published 2021 Jul 19. doi:10.3390/v13071401

22. Valdivia HO, Zorrilla VO, Espada LJ, et al. Diversity, distribution and natural Leishmania infection of sand flies from communities along the Intercoceanic Highway in the Southeastern Peruvian Amazon. *PLoS Negl Trop Dis*. 2021;15(2):e0009000. Published 2021 Feb 10. doi:10.1371/journal.pntd.0009000
23. Bang WJ, Kim HC, Ryu J, et al. Multiplex PCR assay for the identification of eight Anopheles species belonging to the Hyrcanus, Barbirostris and Lindesayi groups. *Malar J*. 2021;20(1):287. Published 2021 Jun 28. doi:10.1186/s12936-021-03808-w
24. Kim MS, Kim HC, Bellis GA, Chong ST, Kim HS, Klein TA. Seasonal Abundance of Culicoides at Yongsan US Army Garrison (USAG) and Camp Humphreys USAG, Republic of Korea, 2010–2013 and 2014–2017 [published correction appears in Korean J Parasitol. 2021 Aug;59(4):433]. *Korean J Parasitol*. 2021;59(3):273–280. doi:10.3347/kjp.2021.59.3.273
25. Lee SH, No JS, Kim K, et al. Novel Paju Apodemus paramyxovirus 1 and 2, harbored by Apodemus agrarius in the Republic of Korea. *Virology*. 2021;562:40–49. doi:10.1016/j.virol.2021.06.011
26. Lee DE, Kim HC, Chong ST, Klein TA, Kim JH, Lee SH. Prediction of species composition ratios in pooled specimens of the Anopheles Hyrcanus group using quantitative sequencing. *Malar J*. 2021;20(1):338. Published 2021 Aug 6. doi:10.1186/s12936-021-03868-y
27. Zorrilla VO, Lozano ME, Espada LJ, et al. Comparison of sand fly trapping approaches for vector surveillance of Leishmania and Bartonella species in ecologically distinct, endemic regions of Peru. *PLoS Negl Trop Dis*. 2021;15(7):e0009517. Published 2021 Jul 14. doi:10.1371/journal.pntd.0009517
28. Agaba BB, Anderson K, Gresty K, et al. Genetic diversity and genetic relatedness in Plasmodium falciparum parasite population in individuals with uncomplicated malaria based on microsatellite typing in Eastern and Western regions of Uganda, 2019–2020. *Malar J*. 2021;20(1):242. Published 2021 May 31. doi:10.1186/s12936-021-03763-6
29. Barhoumi W, Chelbi I, Fares W, et al. Risk Assessment of the Role of the Ecotones in the Transmission of Zoonotic Cutaneous Leishmaniasis in Central Tunisia. *Int J Environ Res Public Health*. 2021;18(17):9274. Published 2021 Sep 2. doi:10.3390/ijerph18179274
30. Morrison AC, Schwarz J, Mckenney JL, et al. Potential for community based surveillance of febrile diseases: Feasibility of self-administered rapid diagnostic tests in Iquitos, Peru and Phnom Penh, Cambodia. *PLoS Negl Trop Dis*. 2021;15(4):e0009307. Published 2021 Apr 26. doi:10.1371/journal.pntd.0009307
31. Muriuki CW, Ogonda LA, Kyanya C, et al. Phenotypic and Genotypic Characteristics of Uropathogenic Escherichia coli Isolates from Kenya. *Microb Drug Resist*. 2022;28(1):31–38. doi:10.1089/mdr.2020.0432
32. Liyai R, Kimita G, Masakhwe C, et al. The spleen bacteriome of wild rodents and shrews from Marigat, Baringo County, Kenya. *PeerJ*. 2021;9:e12067. Published 2021 Sep 2. doi:10.7717/peerj.12067
33. Seo HJ, Noh J, Kim HC, et al. Molecular Detection and Phylogenetic Analysis of Anaplasma and Borrelia Species in Ticks Collected from Migratory Birds at Heuksan, Hong, and Nan Islands, Republic of Korea. *Vector Borne Zoonotic Dis*. 2021;21(1):20–31. doi:10.1089/vbz.2020.2629
34. Chapeau RR, Christian M, Connors B, et al. Early Identification of SARS-CoV-2 Emergence in the Department of Defense via Retrospective Analysis of 2019–2020 Upper Respiratory Illness Samples. *MSMR*. 2021;28(6):2–5. Published 2021 Jun 1.
35. Oransathid W, Sukhchat P, Margulieux K, et al. First Report: Colistin Resistance Gene mcr-3.1 in Salmonella enterica Serotype Choleraesuis Isolated from Human Blood Sample from Thailand. *Microb Drug Resist*. 2022;28(1):102–105. doi:10.1089/mdr.2020.0553
36. Chaorattanakawee S, Korkusol A, Tippayachai B, Promsathaporn S, Poole-Smith BK, Takhampunya R. Amplicon-Based Next Generation Sequencing for Rapid Identification of Rickettsia and Ectoparasite Species from Entomological Surveillance in Thailand. *Pathogens*. 2021;10(2):215. Published 2021 Feb 16. doi:10.3390/pathogens10020215
37. Musila L, Kyanya C, Maybank R, Stam J, Oundo V, Sang W. Detection of diverse carbapenem and multidrug resistance genes and high-risk strain types among carbapenem non-susceptible clinical isolates of target gram-negative bacteria in Kenya. *PLoS One*. 2021;16(2):e0246937. Published 2021 Feb 22. doi:10.1371/journal.pone.0246937
38. Velasco JM, Navarro FC, Diones PC, et al. SARS-CoV-2 Among Military and Civilian Patients, Metro Manila, Philippines. *Mil Med*. 2021;186(7-8):e760–e766. doi:10.1093/milmed/usaa525
39. Velasco JM, Valderama MT, Diones PC, et al. Performance of a Rapid Diagnostic Test for Influenza in a Tertiary Military Hospital, Philippines. *Mil Med*. 2022;187(1–2):e197–e200. doi:10.1093/milmed/usab006
40. Cattel J, Haberkorn C, Laporte F, et al. A genomic amplification affecting a carboxylesterase gene cluster confers organophosphate resistance in the mosquito Aedes aegypti: From genomic characterization to high-throughput field detection. *Evol Appl*. 2021;14(4):1009–1022. Published 2021 Feb 16. doi:10.1111/eva.13177
41. Egyir B, Bentum J, Attram N, et al. Whole Genome Sequencing and Antimicrobial Resistance of Staphylococcus aureus from Surgical Site Infections in Ghana. *Pathogens*. 2021;10(2):196. Published 2021 Feb 12. doi:10.3390/pathogens10020196
42. Agbodzi B, Yousseu FBS, Simo FBN, et al. Chikungunya viruses containing the A226V mutation detected retrospectively in Cameroon form a new geographical subclade. *Int J Infect Dis*. 2021;113:65–73. doi:10.1016/j.ijid.2021.09.058
43. Kietsiri P, Muangnapoh C, Lurchachaiwong W, et al. Characterization of Arcobacter spp. Isolated from human diarrheal, non-diarrheal and food samples in Thailand. *PLoS One*. 2021;16(2):e0246598. Published 2021 Feb 5. doi:10.1371/journal.pone.0246598

44. Omar K, Thabet HS, TagEldin RA, et al. Ecological niche modeling for predicting the potential geographical distribution of *Aedes* species (Diptera: Culicidae): A case study of Enugu State, Nigeria. *Parasite Epidemiol Control*. 2021;15:e00225. Published 2021 Sep 15. doi:10.1016/j.parepi.2021.e00225
45. Owens LA, Colitti B, Hirji I, et al. A *Sarcina* bacterium linked to lethal disease in sanctuary chimpanzees in Sierra Leone [published correction appears in *Nat Commun*. 2021 Mar 26;12(1):2035]. *Nat Commun*. 2021;12(1):763. Published 2021 Feb 3. doi:10.1038/s41467-021-21012-x
46. Wan XF, Tang CY, Ritter D, et al. SARS-CoV-2 show no infectivity at later stages in a prolonged COVID-19 patient despite positivity in RNA testing. *J Med Virol*. 2021;93(7):4570–4575. doi:10.1002/jmv.27001
47. Pollett S, Conte MA, Sanborn M, et al. A comparative recombination analysis of human coronaviruses and implications for the SARS-CoV-2 pandemic. *Sci Rep*. 2021;11(1):17365. Published 2021 Aug 30. doi:10.1038/s41598-021-96626-8
48. Villena FE, Lizewski SE, Joya CA, Valdivia HO. Population genomics and evidence of clonal replacement of *Plasmodium falciparum* in the Peruvian Amazon. *Sci Rep*. 2021;11(1):21212. Published 2021 Oct 27. doi:10.1038/s41598-021-00806-5
49. Stevens L, Lima-Cordón RA, Helms Cahan S, et al. Catch me if you can: Under-detection of *Trypanosoma cruzi* (Kinetoplastea: Trypanosomatida) infections in *Triatoma dimidiata* s.l. (Hemiptera: Reduviidae) from Central America. *Acta Trop*. 2021;224:106130. doi:10.1016/j.actatropica.2021.106130
50. Pagac BB, Spring AR, Stawicki JR, et al. Incursion and establishment of the Old World arbovirus vector *Aedes* (*Fredwardsius*) *vittatus* (Bigot, 1861) in the Americas. *Acta Trop*. 2021;213:105739. doi:10.1016/j.actatropica.2020.105739
51. Prosser C, Gresty K, Ellis J, et al. *Plasmodium falciparum* Histidine-Rich Protein 2 and 3 Gene Deletions in Strains from Nigeria, Sudan, and South Sudan. *Emerg Infect Dis*. 2021;27(2):471–479. doi:10.3201/eid2702.191410
52. Barazorda KA, Salas CJ, Braga G, et al. Validation study of Boil & Spin Malachite Green Loop Mediated Isothermal Amplification (B&S MG-LAMP) versus microscopy for malaria detection in the Peruvian Amazon. *PLoS One*. 2021;16(10):e0258722. Published 2021 Oct 25. doi:10.1371/journal.pone.0258722
53. Lee SH, Kim K, Kim J, et al. Discovery and Genetic Characterization of Novel Paramyxoviruses Related to the Genus *Henipavirus* in *Crocidura* Species in the Republic of Korea. *Viruses*. 2021;13(10):2020. Published 2021 Oct 7. doi:10.3390/v13102020
54. Seo HJ, Truong AT, Kim KH, et al. Molecular Detection and Phylogenetic Analysis of Tick-Borne Pathogens in Ticks Collected from Horses in the Republic of Korea. *Pathogens*. 2021;10(9):1069. Published 2021 Aug 24. doi:10.3390/pathogens10091069
55. Pérez-Sautu U, Wiley MR, Prieto K, et al. Novel viruses in hard ticks collected in the Republic of Korea unveiled by metagenomic high-throughput sequencing analysis. *Ticks Tick Borne Dis*. 2021;12(6):101820. doi:10.1016/j.ttbdis.2021.101820
56. Tang CY, Wang Y, McElroy JA, et al. Reinfection with two genetically distinct SARS-CoV-2 viruses within 19 days. *J Med Virol*. 2021;93(10):5700–5703. doi:10.1002/jmv.27154
57. Sanborn MA, Wuertz KM, Kim HC, et al. Metagenomic analysis reveals *Culex* mosquito virome diversity and Japanese encephalitis genotype V in the Republic of Korea. *Mol Ecol*. 2021;30(21):5470–5487. doi:10.1111/mec.16133
58. Tang CY, Segovia K, McElroy JA, et al. Cell-Adapted Mutations and Antigenic Diversity of Influenza B Viruses in Missouri, 2019–2020 Season. *Viruses*. 2021;13(10):1896. Published 2021 Sep 22. doi:10.3390/v13101896
59. Hu W, Gruner WE, DeMarcus LS, et al. Influenza Surveillance Trends and Influenza Vaccine Effectiveness Among Department of Defense Beneficiaries During the 2019–2020 Influenza Season. *MSMR*. 2021;28(3):2–8.
60. Hu W, DeMarcus LS, Sjoberg PA, Robbins AS. Inactivated influenza vaccine effectiveness among department of defense beneficiaries aged 6 months–17 years, 2016–2017 through 2019–2020 influenza seasons. *PLoS One*. 2021;16(8):e0256165. Published 2021 Aug 27. doi:10.1371/journal.pone.0256165
61. Thervil JW, DeMarcus LS, Eick-Cost A, et al. Department of Defense mid-season vaccine effectiveness estimates for the 2019–2020 influenza season. *MSMR*. 2021;28(6):16–19. Published 2021 Jun 1.
62. Bourke BP, Justi SA, Caicedo-Quiroga L, Pecor DB, Wilkerson RC, Linton YM. Phylogenetic analysis of the Neotropical *Albitarsis* Complex based on mitogenome data. *Parasit Vectors*. 2021;14(1):589. Published 2021 Nov 27. doi:10.1186/s13071-021-05090-w
63. Justi SA, Dale C. Designation of the neotype of *Triatomadimidiata* (Latreille, 1811) (Hemiptera, Reduviidae, Triatominae), with full integrated redescription including mitogenome and nuclear ITS-2 sequences. *Zookeys*. 2021;1076:9–24. Published 2021 Dec 8. doi:10.3897/zookeys.1076.72835
64. Mihreteab S, Anderson K, Pasay C, et al. Epidemiology of mutant *Plasmodium falciparum* parasites lacking histidine-rich protein 2/3 genes in Eritrea 2 years after switching from HRP2-based RDTs. *Sci Rep*. 2021;11(1):21082. Published 2021 Oct 26. doi:10.1038/s41598-021-00714-8
65. St John HK, Masuoka P, Jiang J, et al. Geographic distribution and modeling of ticks in the Republic of Korea and the application of tick models towards understanding the distribution of associated pathogenic agents. *Ticks Tick Borne Dis*. 2021;12(4):101686. doi:10.1016/j.ttbdis.2021.101686

66. Pinto A, Archaga O, Mejía Á, et al. Evidence of a Recent Bottleneck in *Plasmodium falciparum* Populations on the Honduran-Nicaraguan Border. *Pathogens*. 2021;10(11):1432. Published 2021 Nov 4. doi:10.3390/pathogens10111432
67. Fontecha G, Pinto A, Archaga O, et al. Assessment of Plasmodium falciparum anti-malarial drug resistance markers in pfcrt and pfmdr1 genes in isolates from Honduras and Nicaragua, 2018–2021. *Malar J*. 2021;20(1):465. Published 2021 Dec 14. doi:10.1186/s12936-021-03977-8
68. Gómez-Camargo DE, Egurrola-Pedraza JA, Cruz CD, et al. Evidence of Oropouche Orthobunyavirus Infection, Colombia, 2017. *Emerg Infect Dis*. 2021;27(6):1756–1758. doi:10.3201/eid2706.204405
69. Nahid MA, Griffin JM, Lustik MB, et al. A Longitudinal Evaluation of the Bacterial Pathogens Colonizing Chronic Non-Healing Wound Sites at a United States Military Treatment Facility in the Pacific Region. *Infect Drug Resist*. 2021;14:1–10. Published 2021 Jan 6. doi:10.2147/IDR.S260708
70. Larson D, Brodniak SL, Voegtly LJ, et al. A Case of Early Reinfection With Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2). *Clin Infect Dis*. 2021;73(9):e2827–e2828. doi:10.1093/cid/ciaa1436
71. Agaba BB, Anderson K, Gresty K, et al. Molecular surveillance reveals the presence of pfhrp2 and pfhrp3 gene deletions in Plasmodium falciparum parasite populations in Uganda, 2017–2019. *Malar J*. 2020;19(1):300. Published 2020 Aug 26. doi:10.1186/s12936-020-03362-x
72. Podenas S, Podeniene V, Seo HY, et al. New Atypophthalmus (Diptera: Limoniidae) from South Korea. *Zootaxa*. 2020;4732(2):zootaxa.4732.2.3. Published 2020 Feb 12. doi:10.11646/zootaxa.4732.2.3
73. Kim WK, No JS, Lee D, et al. Active Targeted Surveillance to Identify Sites of Emergence of Hantavirus. *Clin Infect Dis*. 2020;70(3):464–473. doi:10.1093/cid/ciz234
74. Pollett S, Fauver JR, Maljkovic Berry I, et al. Genomic Epidemiology as a Public Health Tool to Combat Mosquito-Borne Virus Outbreaks. *J Infect Dis*. 2020;221(Suppl 3):S308–S318. doi:10.1093/infdis/jiz302
75. Pollett S, Johansson M, Biggerstaff M, et al. Identification and evaluation of epidemic prediction and forecasting reporting guidelines: A systematic review and a call for action. *Epidemics*. 2020;33:100400. doi:10.1016/j.epidem.2020.100400
76. Maljkovic Berry I, Melendrez MC, Bishop-Lilly KA, et al. Next Generation Sequencing and Bioinformatics Methodologies for Infectious Disease Research and Public Health: Approaches, Applications, and Considerations for Development of Laboratory Capacity. *J Infect Dis*. 2020;221(Suppl 3):S292–S307. doi:10.1093/infdis/jiz286
77. Maljkovic Berry I, Rutvisuttinunt W, Voegtly LJ, et al. A Department of Defense Laboratory Consortium Approach to Next Generation Sequencing and Bioinformatics Training for Infectious Disease Surveillance in Kenya. *Front Genet*. 2020;11:577563. Published 2020 Sep 25. doi:10.3389/fgene.2020.577563
78. Maljkovic Berry I, Rutvisuttinunt W, Sippy R, et al. The origins of dengue and chikungunya viruses in Ecuador following increased migration from Venezuela and Colombia. *BMC Evol Biol*. 2020;20(1):31. Published 2020 Feb 19. doi:10.1186/s12862-020-1596-8
79. Langat SK, Eyase FL, Berry IM, et al. Origin and evolution of dengue virus type 2 causing outbreaks in Kenya: Evidence of circulation of two cosmopolitan genotype lineages. *Virus Evol*. 2020;6(1):veaa026. Published 2020 Jun 2. doi:10.1093/ve/veaa026
80. Hang J, Kajon AE, Graf PCF, et al. Human Adenovirus Type 55 Distribution, Regional Persistence, and Genetic Variability. *Emerg Infect Dis*. 2020;26(7):1497–1505. doi:10.3201/eid2607.191707
81. Eyase F, Langat S, Berry IM, et al. Emergence of a novel chikungunya virus strain bearing the E1:V80A substitution, out of the Mombasa, Kenya 2017–2018 outbreak. *PLoS One*. 2020;15(11):e0241754. Published 2020 Nov 6. doi:10.1371/journal.pone.0241754
82. Valdivia HO, Villena FE, Lizewski SE, Garcia J, Alger J, Bishop DK. Genomic surveillance of Plasmodium falciparum and Plasmodium vivax cases at the University Hospital in Tegucigalpa, Honduras. *Sci Rep*. 2020;10(1):20975. Published 2020 Dec 1. doi:10.1038/s41598-020-78103-w
83. Villena FE, Maguiña JL, Santolalla ML, et al. Molecular surveillance of the Plasmodium vivax multidrug resistance 1 gene in Peru between 2006 and 2015. *Malar J*. 2020;19(1):450. Published 2020 Dec 4. doi:10.1186/s12936-020-03519-8
84. Barazorda KA, Salas CJ, Bishop DK, Lucchi N, Valdivia HO. Comparison of real time and malachite-green based loop-mediated isothermal amplification assays for the detection of Plasmodium vivax and P. falciparum. *PLoS One*. 2020;15(6):e0234263. Published 2020 Jun 11. doi:10.1371/journal.pone.0234263
85. Cho S, Kim HC, Chong ST, et al. Monitoring of Pyrethroid Resistance Allele Frequency in the Common Bed Bug (Cimex lectularius) in the Republic of Korea. *Korean J Parasitol*. 2020;58(1):99–102. doi:10.3347/kjp.2020.58.1.99
86. Chong,ST, Kim HC, Suh SJ, Klein TA, Robbins RG. 2020. Morphological abnormalities in ticks (Acari: Ixodidae) from the Republic of Korea. *Systematic & Applied Acarology* 25(11): 1994–2002.
87. Egizi A, Bulaga-Seraphin L, Alt E, et al. First glimpse into the origin and spread of the Asian longhorned tick, Haemaphysalis longicornis, in the United States. *Zoonoses Public Health*. 2020;67(6):637–650. doi:10.1111/zph.12743
88. Hwang MJ, Kim HC, Klein TA, et al. Comparison of climatic factors on mosquito abundance at US Army Garrison Humphreys, Republic of Korea. *PLoS One*. 2020;15(10):e0240363. Published 2020 Oct 21. doi:10.1371/journal.pone.0240363
89. Hwang MJ, Kim JH, Kim HC, et al. Temporal Trend of Aedes albopictus in Local Urban Parks of the Republic of Korea. *J Med Entomol*. 2020;57(4):1082–1089. doi:10.1093/jme/tjaa039

90. Choi KS, Kim HC, Chong ST, et al. Seasonal surveillance of deer and horse flies (Diptera: Tabanidae), Gyeonggi province, Republic of Korea. *Journal of Asia-Pacific Entomology*. 2020;23:315–319.
91. Lee DE, Kim HC, Chong ST, et al. Regional and seasonal detection of resistance mutation frequencies in field populations of Anopheles Hyrcanus Group and Culex pipiens complex in Korea. *Pestic Biochem Physiol*. 2020;164:33–39. doi:10.1016/j.pestbp.2019.12.005
92. Lee SH, Kim WK, Park K, et al. Genetic diversity and phylogeography of Jeju Orthohantavirus (Hantaviridae) in the Republic of Korea. *Virology*. 2020;543:13–19. doi:10.1016/j.virol.2020.01.012
93. Perez-Sautu U, Gu SH, Caviness K, et al. A Model for the Production of Regulatory Grade Viral Hemorrhagic Fever Exposure Stocks: From Field Surveillance to Advanced Characterization of SFTSV. *Viruses*. 2020;12(9):958. Published 2020 Aug 29. doi:10.3390/v12090958
94. Park HJ, Kim J, Choi YJ, et al. Tick-borne rickettsiae in Midwestern region of Republic of Korea. *Acta Trop*. 2021;215:105794. doi:10.1016/j.actatropica.2020.105794
95. Ashbaugh HR, Early JM, Johnson ME, et al. A Multisite Network Assessment of the Epidemiology and Etiology of Acquired Diarrhea among U.S. Military and Western Travelers (Global Travelers' Diarrhea Study): A Principal Role of *Norovirus* among Travelers with Gastrointestinal Illness. *Am J Trop Med Hyg*. 2020;103(5):1855–1863. doi:10.4269/ajtmh.20-0053
96. Wolff GG. Influenza vaccination and respiratory virus interference among Department of Defense personnel during the 2017–2018 influenza season. *Vaccine*. 2020;38(2):350–354. doi:10.1016/j.vaccine.2019.10.005
97. Hang J, Kajon AE, Graf PCF, et al. Human Adenovirus Type 55 Distribution, Regional Persistence, and Genetic Variability. *Emerg Infect Dis*. 2020;26(7):1497–1505. doi:10.3201/eid2607.191707
98. Kosoltanapiwat N, Tongshoob J, Singkhaimuk P, Nitatsukprasert C, Davidson SA, Ponlawat A. Entomological Surveillance for Zika and Dengue Virus in *Aedes* Mosquitoes: Implications for Vector Control in Thailand. *Pathogens*. 2020;9(6):442. Published 2020 Jun 4. doi:10.3390/pathogens9060442
99. Krairojananan P, Thaipadungpanit J, Leepitakrat S, et al. Low Prevalence of *Leptospira* Carriage in Rodents in Leptospirosis-Endemic Northeastern Thailand. *Trop Med Infect Dis*. 2020;5(4):154. Published 2020 Sep 30. doi:10.3390/tropicalmed5040154
100. Velasco JM, Gaurano N, Valderama MT, et al. Multidrug Resistant Mycobacterium tuberculosis Among Military and Civilian Personnel seen at a Tertiary Military Hospital, Manila, Philippines (2015–2018). *Mil Med*. 2020;185(7–8):e1106–e1111. doi:10.1093/milmed/usz456
101. Velasco JMS, Valderama MTG, Margulieux KR, et al. First report of the mcr-1 colistin resistance gene identified in two *Escherichia coli* isolates from clinical samples, Philippines, 2018. *J Glob Antimicrob Resist*. 2020;21:291–293. doi:10.1016/j.jgar.2019.12.018
102. Velasco JM, Chinnawirotpisan P, Joonlasak K, et al. Coding-Complete Genome Sequences of 23 SARS-CoV-2 Samples from the Philippines. *Microbiol Resour Announc*. 2020;9(43):e01031-20. Published 2020 Oct 22. doi:10.1128/MRA.01031-20
103. Velasco JM, Valderama MT, Margulieux K, et al. Comparison of Carbapenem-Resistant Microbial Pathogens in Combat and Non-combat Wounds of Military and Civilian Patients Seen at a Tertiary Military Hospital, Philippines (2013–2017). *Mil Med*. 2020;185(1–2):e197–e202. doi:10.1093/milmed/usz148
104. Walters WA, Reyes F, Soto GM, et al. Epidemiology and associated microbiota changes in deployed military personnel at high risk of traveler's diarrhea. *PLoS One*. 2020;15(8):e0236703. Published 2020 Aug 12. doi:10.1371/journal.pone.0236703
105. Espinoza N, Rojas J, Pollett S, et al. Validation of the T86I mutation in the gyrA gene as a highly reliable real time PCR target to detect Fluoroquinolone-resistant *Campylobacter jejuni*. *BMC Infect Dis*. 2020;20(1):518. Published 2020 Jul 16. doi:10.1186/s12879-020-05202-4
106. Kyanya C, Musila L. Colistin Resistance Gene *mcr-8* in a High-Risk Sequence Type 15 *Klebsiella pneumoniae* Isolate from Kenya. *Microbiol Resour Announc*. 2020;9(39):e00783-20. Published 2020 Sep 24. doi:10.1128/MRA.00783-20
107. Odoyo E, Kyanya C, Mutai W, Musila L. High levels of toxigenic *Clostridioides difficile* contamination of hospital environments: a hidden threat in hospital-acquired infections in Kenya. *Access Microbiol*. 2020;2(12):acmi000171. Published 2020 Sep 18. doi:10.1099/acmi.0.000171
108. Velasco JM, Shrestha S, Valderama MT, et al. A multi-country field validation of the FluChip-8G Insight Assay. *J Virol Methods*. 2021;289:114029. doi:10.1016/j.jviromet.2020.114029
109. Chinnawirotpisan P, Chusri S, Manasatienkij W, et al. Complete Coding Sequences of 22 East/Central/South African Genotype Chikungunya Virus Isolates from Thailand (2018 to 2019). *Microbiol Resour Announc*. 2020;9(42):e00438-20. Published 2020 Oct 15. doi:10.1128/MRA.00438-20
110. Bosco AB, Nankabirwa JI, Yeka A, et al. Limitations of rapid diagnostic tests in malaria surveys in areas with varied transmission intensity in Uganda 2017–2019: Implications for selection and use of HRP2 RDTs. *PLoS One*. 2020;15(12):e0244457. Published 2020 Dec 31. doi:10.1371/journal.pone.0244457
111. Elson WH, Reiner RC, Siles C, et al. Heterogeneity of Dengue Illness in Community-Based Prospective Study, Iquitos, Peru. *Emerg Infect Dis*. 2020;26(9):2077–2086. doi:10.3201/eid2609.191472

112. Siles C, Elson WH, Vilcarromero S, et al. Guaroa Virus and Plasmodium vivax Co-Infections, Peruvian Amazon. *Emerg Infect Dis.* 2020;26(4):731–737. doi:10.3201/eid2604.191104
113. Opanda S, Bulimo W, Gachara G, Ekuttan C, Amukoye E. Assessing antigenic drift and phylogeny of influenza A (H1N1) pdm09 virus in Kenya using HA1 sub-unit of the hemagglutinin gene. *PLoS One.* 2020;15(2):e0228029. Published 2020 Feb 11. doi:10.1371/journal.pone.0228029
114. Nyataya J, Maraka M, Lemtudo A, et al. Serological Evidence of Yersiniosis, Tick-Borne Encephalitis, West Nile, Hepatitis E, Crimean-Congo Hemorrhagic Fever, Lyme Borreliosis, and Brucellosis in Febrile Patients Presenting at Diverse Hospitals in Kenya. *Vector Borne Zoonotic Dis.* 2020;20(5):348–357. doi:10.1089/vbz.2019.2484
115. Tucker CJ, Melocik KA, Anyamba A, Linthicum KJ, Fagbo SF, Small JL. Reanalysis of the 2000 Rift Valley fever outbreak in Southwestern Arabia [published correction appears in PLoS One. 2021 Mar 8;16(3):e0248462]. *PLoS One.* 2020;15(12):e0233279. Published 2020 Dec 14. doi:10.1371/journal.pone.0233279
116. Oheneba-Dorny, Theresa & Soebiyanto, Radina & Hutchinson, Sarah & Anyamba, Assaf & Steen, Tomoko & Garrison, Destini. (2020). Cholera, Conflict, Climate Variability and Implications on the Yemen Public Health System. 10.13140/RG.2.2.15627.11049.
117. Weiss CD, Wang W, Lu Y, et al. Neutralizing and Neuraminidase Antibodies Correlate With Protection Against Influenza During a Late Season A/H3N2 Outbreak Among Unvaccinated Military Recruits. *Clin Infect Dis.* 2020;71(12):3096–3102. doi:10.1093/cid/ciz1198
118. Abarca K, Martínez-Valdebenito C, Angulo J, et al. Molecular Description of a Novel Orientia Species Causing Scrub Typhus in Chile. *Emerg Infect Dis.* 2020;26(9):2148–2156. doi:10.3201/eid2609.200918
119. Bennett AJ, Paskey AC, Ebinger A, et al. Relatives of rubella virus in diverse mammals [published correction appears in Nature. 2020 Dec;588(7836):E2]. *Nature.* 2020;586(7829):424–428. doi:10.1038/s41586-020-2812-9
120. Bennett AJ, Paskey AC, Kuhn JH, Bishop-Lilly KA, Goldberg TL. Diversity, Transmission, and Cophylogeny of Ledanteviruses (*Rhabdoviridae: Ledantevirus*) and Nycteribiid Bat Flies Parasitizing Angolan Soft-Furred Fruit Bats in Bundibugyo District, Uganda. *Microorganisms.* 2020;8(5):750. Published 2020 May 17. doi:10.3390/microorganisms8050750
121. Weitzel T, Acosta-Jamett G, Jiang J, et al. Human seroepidemiology of Rickettsia and Orientia species in Chile – A cross-sectional study in five regions. *Ticks Tick Borne Dis.* 2020;11(6):101503. doi:10.1016/j.ttbdis.2020.101503
122. Lippi CA, Gaff HD, White AL, St John HK, Richards AL, Ryan SJ. Exploring the Niche of Rickettsia montanensis (Rickettsiales: Rickettsiaceae) Infection of the American Dog Tick (Acari: Ixodidae), Using Multiple Species Distribution Model Approaches. *J Med Entomol.* 2021;58(3):1083–1092. doi:10.1093/jme/tjaa263
123. Fralish MS, Mangalindan KE, Farris CM, Jiang J, Green MC, Blaylock JM. African Tick-Bite Fever. *Am J Med.* 2020;133(9):1051–1053. doi:10.1016/j.amjmed.2020.03.031
124. Vitale M, Lupone CD, Kenneson-Adams A, et al. A comparison of passive surveillance and active cluster-based surveillance for dengue fever in southern coastal Ecuador. *BMC Public Health.* 2020;20(1):1065. Published 2020 Jul 6. doi:10.1186/s12889-020-09168-5
125. Takhampunya R, Thaloengsok S, Tippayachai B, et al. Retrospective Survey of Borrelia spp. From Rodents and Ticks in Thailand. *J Med Entomol.* 2021;58(3):1331–1344. doi:10.1093/jme/tjaa279
126. Kersellius GD, Gruner WE, Fries AC, DeMarcus LS, Robbins AS. Respiratory pathogen surveillance trends and influenza vaccine effectiveness estimates for the 2018–2019 season among Department of Defense beneficiaries. *MSMR.* 2020;27(1):17–23.
127. Nyataya J, Waitumbi J, Mobegi VA, Noredin A, El Zowalaty ME. *Plasmodium falciparum* Histidine-Rich Protein 2 and 3 Gene Deletions and Their Implications in Malaria Control. *Diseases.* 2020;8(2):15. Published 2020 May 20. doi:10.3390/diseases8020015
128. Nyang'au EM, Bulimo WD, Mobegi V, Opanda S, Magiri E. Genetic analysis of HA1 domain of influenza A/H3N2 viruses isolated in Kenya during the 2007–2013 seasons reveal significant divergence from WHO-recommended vaccine strains. *Int J Infect Dis.* 2020;95:413–420. doi:10.1016/j.ijid.2020.04.001
129. Rowneki M, Aronson N, Du P, et al. Detection of drug resistant Mycobacterium tuberculosis by high-throughput sequencing of DNA isolated from acid fast bacilli smears. *PLoS One.* 2020;15(5):e0232343. Published 2020 May 8. doi:10.1371/journal.pone.0232343
130. Wang W, Alvarado-Facundo E, Vassell R, et al. Comparison of A(H3N2) Neutralizing Antibody Responses Elicited by 2018–2019 Season Quadrivalent Influenza Vaccines Derived from Eggs, Cells, and Recombinant Hemagglutinin. *Clin Infect Dis.* 2021;73(11):e4312–e4320. doi:10.1093/cid/ciaa1352
131. Ergünay K, Dinçer E, Kar S, et al. Multiple orthonairoviruses including Crimean-Congo hemorrhagic fever virus, Tamdy virus and the novel Meram virus in Anatolia. *Ticks Tick Borne Dis.* 2020;11(5):101448. doi:10.1016/j.ttbdis.2020.101448
132. Sallum MAM, Obando RG, Carrejo N, Wilkerson RC. Identification key to the Anopheles mosquitoes of South America (Diptera: Culicidae). III. Male genitalia. *Parasit Vectors.* 2020;13(1):542. Published 2020 Oct 31. doi:10.1186/s13071-020-04300-1
133. Sallum MAM, Obando RG, Carrejo N, Wilkerson RC. Identification keys to the Anopheles mosquitoes of South America (Diptera: Culicidae). I. Introduction. *Parasit Vectors.* 2020;13(1):583. Published 2020 Nov 18. doi:10.1186/s13071-020-04298-6

134. Sallum MAM, Obando RG, Carrejo N, Wilkerson RC. Identification keys to the Anopheles mosquitoes of South America (Diptera: Culicidae). II. Fourth-instar larvae. *Parasit Vectors*. 2020;13(1):582. Published 2020 Nov 18. doi:10.1186/s13071-020-04299-5
135. Sallum MAM, Obando RG, Carrejo N, Wilkerson RC. Identification keys to the Anopheles mosquitoes of South America (Diptera: Culicidae). IV. Adult females. *Parasit Vectors*. 2020;13(1):584. Published 2020 Nov 18. doi:10.1186/s13071-020-04301-0
136. Foley DH, Wilkerson RC, Kim HC, et al. Wing size and parity as markers of cohort demography for potential Anopheles (Culicidae: Diptera) malaria vectors in the Republic of Korea. *J Vector Ecol*. 2020;45(2):366–379. doi:10.1111/jvec.12406
137. Spring MD, Lon C, Sok S, et al. Prevalence of CYP2D6 Genotypes and Predicted Phenotypes in a Cohort of Cambodians at High Risk for Infections with *Plasmodium vivax*. *Am J Trop Med Hyg*. 2020;103(2):756–759. doi:10.4269/ajtmh.20-0061
138. Stahlman S, Hiban K, Mahaney H, Ford S. Incident COVID-19 Infections, Active and Reserve Components, 1 January 2020–31 August 2021. *MSMR*. 2021;28(12):14–21.
139. Williams V, Ying S, Stahlman S. Update: Osteoarthritis and Spondylosis, Active Component, U.S. Armed Forces, 2016–2020. *MSMR*. 2021;28(12):2–13.
140. Snitchler CL, Patel DM, Stahlman SL, Chauhan AV, Wells NY, Mcquistan AA. Sepsis hospitalizations among active component service members, U.S. Armed Forces, 2011–2020. *MSMR*. 2021;28(11):2–8. Published 2021 Nov 1.
141. Young JM, Stahlman SL, Clausen SS, Bova ML, Mancuso JD. Racial and Ethnic Disparities in COVID-19 Infection and Hospitalization in the Active Component US Military. *Am J Public Health*. 2021;111(12):2194–2201. doi:10.2105/AJPH.2021.306527
142. Clark L, Fan M, Stahlman S. Surveillance of mental and behavioral health care utilization and use of telehealth, active component, U.S. Armed Forces, 1 January 2019–30 September 2020. *MSMR*. 2021;28(8):22–27. Published 2021 Aug 1.
143. Kieffer JW, Stahlman S. Mental health disorders, behavioral health problems, fatigue and sleep outcomes in remotely piloted aircraft/manned aircraft pilots, and remotely piloted aircraft crew, U.S. Air Force, 1 October 2003–30 June 2019. *MSMR*. 2021;28(8):14–21. Published 2021 Aug 1.
144. Lotridge JA, Stahlman SL, Patel DM, Chauhan AV, Mcquistan AA, Wells N. Long-acting reversible contraceptive use, active component service women, U.S. Armed Forces, 2016–2020. *MSMR*. 2021;28(7):2–10. Published 2021 Jul 1.
145. Hakre S, Sanborn AD, Krauss SW, et al. Serological and RT-PCR Surveillance for COVID-19 in an Asymptomatic US Army Trainee Population. *Open Forum Infect Dis*. 2021;8(9):ofab407. Published 2021 Jul 29. doi:10.1093/ofid/ofab407
146. Clark LL, Oh GT, Stahlman S. Brief report: Medical encounters for snakebite envenomation, active and reserve components, U.S. Armed Forces, 2016–2020. *MSMR*. 2021;28(6):13–15. Published 2021 Jun 1.
147. Stahlman S, Williams VF, Oh GT, Tribble DR, Millar EV. Skin and soft tissue infections, active component, U.S. Armed Forces, January 2016–September 2020. *MSMR*. 2021;28(4):27–38.
148. Thervil JW, DeMarcus LS, Eick-Cost A, et al. Department of Defense mid-season vaccine effectiveness estimates for the 2019–2020 influenza season. *MSMR*. 2021;28(6):16–19. Published 2021 Jun 1.
149. Rossi KR, Echeverria D, Carroll A, Luse T, Rennix C. Development and Evaluation of Perl-Based Algorithms to Classify Neoplasms From Pathology Records in Synoptic Report Format. *JCO Clin Cancer Inform*. 2021;5:295–303. doi:10.1200/CCI.20.00152
150. Echeverria D, Rossi KR, Carroll A, Luse T, Rennix C. Development of a Semiautomated Search Tool to Identify Grading From Pathology Reports for Tumors of the CNS and Prostate Cancers. *JCO Clin Cancer Inform*. 2021;5:1189–1196. doi:10.1200/CCI.21.00049
151. Forrest LJ, Jones BH, Barnes SR, et al. The cost of lower extremity fractures among active duty U.S. Army soldiers, 2017. *MSMR*. 2021;28(6):6–12. Published 2021 Jun 1.
152. Hauret KG, Steelman RA, McCabe AK, Chervak MC. Graduation and Injury Outcomes during 22-Week Infantry One Station Unit Training Cycles: Fiscal Years 2018–2019. *U.S. Army Public Health Center Technical Report No. S.0047239-20*. March 2021.
153. Hauschild VD, Schuh-Renner A, McCabe AK, Hauret K, Inscore MC, Jones BH, Canham-Chervak M. Fiscal Year (FY) 2022 Update: A Taxonomy of Injuries for Public Health Monitoring and Reporting. *U.S. Army Public Health Center Public Health Information Paper (PHIP) No.12-01-0717*. October 2021.
154. Kaplansky GF, Ackah-Toffey L, Beymer MR, Schaughency KC. Cross-sectional analysis of the association between perceived barriers to behavioral health care and intentions to leave the U.S. Army. *MSMR*. 2021;28(9):2–7. Published 2021 Sep 1.
155. Kebisek J, Maule A, Smith J, et al. Integration of Multiple Surveillance Systems to Track COVID-19 in the U.S. Army Population [published online ahead of print, 2021 Dec 23]. *Mil Med*. 2021;usab501. doi:10.1093/milmed/usab501
156. Schaughency KCL, Watkins EY, Barnes S, et al. Financial costs to the U.S. Army for suicides by newly enlisted Soldiers. *Suicide Life Threat Behav*. 2021;51(5):907–915. doi:10.1111/sltb.12771

# AFHSD

Armed Forces Health Surveillance Division

## SUMMARY REPORT 2020

**THIS REPORT OUTLINES THE ACTIVITIES PERFORMED BY AFHSD DURING THE YEAR THAT SARS-CoV-2 SPREAD AROUND THE GLOBE.**

# EPIDEMIOLOGY AND ANALYSIS

The Epidemiology and Analysis (E&A) Branch began working seven days a week and formulated new methods to retrieve near real-time data to address questions for leaders. Traditional methods of retrospective analysis were not ideal to answer emerging FHP questions for operational and garrison units.

## **WERE ANY NEW PROCEDURES, REPORTS OR PRODUCTS DEVELOPED DURING THAT TIME?**

In 2020, E&A engaged with AFHSD's Integrated Biosurveillance branch and Service public health centers to produce a real-time daily COVID-19 report, including a master positive list of cases. E&A established additional daily reports to evaluate trends in COVID-19 cases and encounters for COVID-like illness by DHA market. It was through existing relationships and processes that E&A began receiving daily laboratory data from the NMCPHC and the consolidated Disease Reporting System internet (DRSi) data from APHC. In addition, E&A partnered with the Armed Forces Medical Examiner System, who shared daily active duty deaths so that E&A could track deaths in active duty military members. The E&A branch compiled this data to create a comprehensive Military Health System list of COVID-19 cases. This line list was used in disease forecasting models and leveraged to address concerns about COVID-19 mitigation measures.

## **DESCRIBE E&A'S MOST SIGNIFICANT COVID-19 EFFORTS:**

- ▶ E&A analyzed data for a large DOD-wide COVID-19 seroprevalence study initiated by Office of the Assistant Secretary of Defense for Health Affairs (HA).

Approximately 2,000 DODSR specimens were pulled each month to be tested for antibodies against COVID-19 in order to provide more accurate data on the speed and degree of spread among Service members.

- ▶ E&A completed survival analysis for Office of the Secretary of Defense (OSD) task force to determine the impact of shortening Restriction of Movement from 14 days to 10 days.

## **WHAT SUCCESSES AND/OR CHALLENGES DID E&A EXPERIENCE?**

E&A created a list of COVID-19 deaths validated by medical records or unit reporting for military members. This validated list was used to analyze common characteristics of COVID-19 deaths in military members and other beneficiaries.

## **IDENTIFY WAYS THAT E&A SUPPORTED AND CONTRIBUTED TO DOD'S COVID-19 REPORTING.**

E&A's daily list of COVID-19 cases helped answer questions related to percent lab positivity, setting health protection conditions on bases, and supported the COVID-19 registry as well as the advanced analytics data system (ADVANA). These advanced analytics are used in a large data platform used by DOD and other federal agencies.

In 2020 E&A completed 329 ad-hoc requests, 955 recurring reports, published 50 Military Surveillance Monthly report articles, and trained seven General Preventive Medicine residents in the conduct of surveillance studies.



# GLOBAL EMERGING INFECTIONS SURVEILLANCE

The COVID-19 pandemic necessitated several actions by GEIS. They expanded staff and their responsibilities; increased coordination efforts with the GEIS laboratory partner network; and produced products for key audience members. In early 2020, GEIS adapted a full telework environment. The team not only increased its productivity, but met the demand for new SARS-CoV-2 surveillance information products.

GEIS leveraged its subject-matter experts in genomics and molecular epidemiology to consult with Service Component Public Health entities. They offered insight into the use of epidemiology and other novel capabilities to investigate outbreaks, and monitor countermeasure or intervention effectiveness. In March 2020, the NGSBC began conducting WGS on positive SARS-CoV-2 cases from the MHS and partner nations across all GCCs.

As the pandemic progressed, GEIS and its partners continuously worked to meet the needs of DOD decision-makers by evolving and adapting products to rapidly communicate the most important aspects of SARS-CoV-2 surveillance from across the laboratory network.

## **WERE ANY NEW PROCEDURES, REPORTS OR PRODUCTS DEVELOPED DURING THAT TIME?**

GEIS provided funding to, and coordinated with, NGSBC partners at Army (Walter Reed Army Institute of Research, U.S. Army Medical Research Institute of Infectious Diseases), Navy (Naval Medical Research Center, Naval Health Research Center), and Air Force (U.S. Air Force School of Aerospace Medicine) laboratories. Sequencing capabilities were also expanded to DOD laboratories in AFRICOM, EUCOM, INDOPACOM, and SOUTHCOM in support of the GCCs.

In early 2020, GEIS coordinated funding and logistical support to procure reagents and develop new Research Use Only (RUO) real-time reverse-transcription polymerase chain reaction (qRT-PCR) diagnostic kits. This allowed the Navy to deploy mobile laboratories across multiple large deck ships to conduct surveillance among the crews. For example, it allowed the detection of a SARS-CoV-2 outbreak on the *USS Theodore Roosevelt*.

The GEIS-N also led early efforts in viral isolation and banking of SARS-CoV-2 specimens, which supported development and assessment of medical countermeasures. GEIS and its partners conducted a rapid assessment of WGS capabilities. In collaboration with the NGSBC, GEIS and its partner laboratories developed, validated, and

implemented harmonized protocols for sequencing SARS-CoV-2 from COVID-19 positive cases.

GEIS disseminated 10 *Monthly Surveillance Updates* that communicated routine surveillance findings (including SARS-CoV-2 qRT-PCR and sequencing data) and five *SARS-CoV-2 SPOT Reports* that communicated new or rapidly evolving SARS-CoV-2 health threats identified by the GEIS-N.

When the first SARS-CoV-2 Variants of Concern (VOCs) and Variants of Interest (VOIs) emerged in late 2020, GEIS developed information papers. Since the development of the information paper on the B.1.1.7 (WHO named Alpha) variant, nine additional *SARS-CoV-2 Variant Updates* have been developed and distributed. To meet requests, GEIS coordinated with the NGSBC to collect the location of sequenced samples. They also partnered with AFHSD-IB to develop an interactive map of VOCs and VOIs that can be filtered by location in the HSE. Information on vaccine breakthrough (VBT) cases was also added to the HSE. They continue prepare a *Weekly Installation Report* of SARS-CoV-2 VOCs and VBT cases by installation.

In 2020, GEIS greatly expanded its product distribution list to include senior leadership (e.g., Office of the Joint Staff Surgeon, Director of Defense Health Agency, etc.) and a wider audience. The branch played a critical role in coordination of SARS-CoV-2 genetic sequencing efforts within the DOD and among the U.S. interagency. Throughout 2020 into 2021, GEIS coordinated with the DOD COVID-19 Task Force to establish an Action Plan for expanding genetic sequencing of SARS-CoV-2 throughout the DOD and MHS.

GEIS routinely provided near-real time information on SARS-CoV-2 genomic surveillance data to the Office of the Joint Staff Surgeon and other senior leaders. It continues to share bi-weekly reports of SARS-CoV-2 genomic surveillance data with the SARS-CoV-2 Interagency Risk Assessment Meeting attendees.

## **WHAT SUCCESSES AND/OR CHALLENGES DID YOUR BRANCH EXPERIENCE?**

Significant barriers limited the ability of GEIS partners to obtain and sequence SARS-CoV-2 samples. Similar to civilian public health settings, DOD experienced slow approval processes. Another challenge during the pandemic was managing large quantities of genomic surveillance data. Prior to the pandemic, the GEIS-PO did not collect genomic surveillance data from partners who performed WGS.

To improve data management, GEIS developed an automated process for ingesting, cleaning, analyzing, and reporting surveillance data. The pandemic highlighted a continued need for cloud-based data management and analysis solutions. At the end of 2020, a GEIS CarePoint site <https://carepoint.health.mil/sites/AFHSB/geis/> was developed to share infectious disease surveillance information products.

#### ARE THERE ADDITIONAL HIGHLIGHTS FROM 2020?

GEIS distributed **\$5.142 million** in FY20 COVID-19 supplemental funding to GEIS-N partners executing surveillance studies.

They established a new process for collecting, managing, and analyzing standardized respiratory surveillance data from the GEIS-N. Through its existing surveillance network, GEIS coordinated with laboratory partners to collect standardized qRT-PCR data on SARS-CoV-2 and other respiratory pathogens. The new reporting process used a standard questionnaire and data submission form to consolidate line level data versus the reporting of aggregate data. The new respiratory reporting process resulted in the analysis of SARS-CoV-2 qRT-PCR and sequencing data.

Additionally, GEIS was integral to the establishment and coordination of the DOD's SARS-CoV-2 genomic surveillance program with robust analysis of VOCs and

VOIs. The GEIS-PO developed and implemented the sample submission questionnaire used to pair clinical and epidemiological data with SARS-CoV-2 genetic sequence results for surveillance purposes. GEIS also worked closely with IB to ensure SARS-CoV-2 VOC and VOI findings were captured on the HSE in new map layers.

After clearance for public release, SARS-CoV-2 consensus genomes generated by GEIS partners were deposited into public databases including GISAID and GenBank. SARS-CoV-2 genomes were primarily generated from MHS beneficiaries residing in NORTHCOM; however, these efforts provided some of the only SARS-CoV-2 sequence data available from locations such as Cuba, Iraq, and Romania in 2020.

In July 2020, AFHSD was tasked by the Assistant Secretary of Defense for Health Affairs (ASD(HA)) to develop and execute a study with the objective of understanding the impact of SARS-CoV-2 infection on the Total Force using a seroprevalence analytical approach. In collaboration with AFHSD-E&A and laboratory partners at the U.S. Army Medical Research Institute of Infectious Diseases, GEIS coordinated an effort that analyzed 28,000 samples submitted to the DOD Serum Repository from May 2020 to June 2021. Periodic reports on these findings were provided to ASD(HA) leadership and helped inform modeling efforts used to guide DOD response to the pandemic.



# INTEGRATED BIOSURVEILLANCE

Integrated Biosurveillance first reported on the emergence of Coronavirus in January 2021. IB closely monitored this novel disease when it appeared in December 2020. It worked closely with Inter-agency partners in characterizing the spread of the disease. IB also worked with closely the E&A branch to gather data from both civilian and military communities.

## WHAT NEW PROCEDURES, REPORTS OR PRODUCTS WERE DEVELOPED DURING THAT TIME?

IB reported global trends in the weekly AHSU. In addition, IB created the weekly *COVID-19 Surveillance Summary* which provided Military case numbers, global numbers and summarized clinical and scientific information about the disease. In addition, IB created on a weekly basis the Executive Summary report specifically for senior leaders. IB also created the COVID-19 Dashboard in the Health Surveillance Explorer mapping application to present DOD relevant information CONUS and OCONUS information. The cases were organized and reported by Geographic Combatant Command, Countries where U.S. military forces were stationed, State and military installations. IB in collaboration with E&A also generated daily tables and presentations for the Assistant Director's Update Brief. IB utilized E&A and interagency data to create *Markets to Watch* slides. These slides showed the number of COVID cases at CONUS military installations and the surrounding civilian communities. This provided the commanders situational awareness on COVID-19 activity at their installation, and nearby civilian communities, in addition, provided early warning on which areas were projected to get better or worse.

## What successes and/or challenges did IB experience?

The established relationship with interagency partners highlights the early warning network that worked closely together at the beginning of the pandemic. Early communications with NBIC and CDC provided indication of a novel disease, and allowed IB to inform its audiences early on.

One challenge that IB experienced was the ineffective Syndromic Surveillance system. It did not work appropriately and the team was unable to track COVID-19 cases in a timely fashion. DOD established the Electronic Surveillance System for the Notification of Community based Epidemics (ESSENCE) in 2001 after the Anthrax



attacks in the U.S. ESSENCE was designed to detect syndromes such as COVID-19 from clinical, laboratory and pharmacy data collected at the Military Treatment facilities. IB was not able to receive data into ESSENCE from all DOD locations where MHS GENESIS was established. This lack of data was highlighted at the beginning of the pandemic when no data from the Pacific Northwest was received—it also and in other regions of the country.

## Please identify ways that IB supported DOD's COVID-19 Reporting:

IB created a variety of products to provide situational awareness of the COVID-19 cases within the military and civilian communities. The *Markets to Watch* report provided situational awareness and predictive analysis on the spread of COVID-19. The team also did the following:

- ▶ Produced and distributed 52 AHSUs, 75 COVID-19 EX-SUMs, 48 COVID-19 Surveillance Summaries, and 48 fully unclassified NATO versions of the AHSU.
- ▶ Created the AFHSD COVID-19 Dashboard which reports the pandemic in the MHS population by GCC, country, state/territory, and DOD installation.
- ▶ Created the 2020-2021 DOD CLI+ILI and COVID-19 Forecasting projects.

# ACRONYMS

AD-S	Assistant Director for Support
AFHSD	Armed Forces Health Surveillance Division
AFRICOM	U.S. Africa Command
AFRIMS	U.S. Armed Forces Research Institute of Medical Sciences
AGE	acute gastroenteritis
AHSU	AFHSD Health Surveillance Update
AMR	antimicrobial resistance
APHC	U.S. Army Public Health Center
AOR	Area of Responsibility
ARO	Office of Alert and Response Operations
BAACH	Brian Allgood Army Community Hospital
CAC	Common Access Card
CARB	Combating Antibiotic Resistant Bacteria
CCMD	Combatant Command
CDC	Centers for Disease Control and Prevention
CENTCOM	U.S. Central Command
CONUS	Contiguous United States
CSA	Combat Support Agency
DHA	Defense Health Agency
DMED	Defense Medical Epidemiology Database
DMSS	Defense Medical Surveillance System
DMTS	Data Management and Technical Support
DOD	Department of Defense
DODGRPS	DOD Global Respiratory Pathogen Surveillance
DODSR	Department of Defense Serum Repository
DRSi	Disease Reporting System internet
DTRA	Defense Threat Reduction Agency
E&A	Epidemiology and Analysis
EDC	EpiData Center
EI	Enteric Infections
EID	emerging infectious disease
ESSENCE	Electronic Surveillance System for the Early Notification of Community-based Epidemics
EUCOM	U.S. European Command
FHP	force health protection
FY	fiscal year
FVBI	Febrile and Vector-Borne Infections
GAO	Government Accountability Office
GCC	Geographic Combatant Command
GEIS	Global Emerging Infections Surveillance
GIS	Geographic Information Systems
GTD	Global Travelers' Diarrhea
H7N9	avian influenza A (subtype H7N9)
HAI	healthcare-associated infection
HAdV-B55	human adenovirus type 55
HAdV-11a	human adenovirus 11a
HIV	human immunodeficiency virus
HPV	human papilloma virus
IB	Integrated Biosurveillance
ICD-9	International Classification of Diseases, Ninth Revision
ICD-10	International Classification of Diseases, 10th Revision
ID	identification
IE	Office of Innovation and Evaluation

IHR	International Health Regulations
ILI	influenza-like illness
IPL	Institut Pasteur du Laos
JPEO-CBRND	Joint Program Executive Office for Chemical, Biological, Radiological, Nuclear Defense
LOE	line of effort
LRMC	Landstuhl Regional Medical Center
MDRO	multidrug-resistant organisms
MERS-CoV	Middle East Respiratory Syndrome Coronavirus
MHS	Military Health System
MRSN	Multidrug-Resistant Organism Repository and Surveillance Network
<i>MSMR</i>	<i>Medical Surveillance Monthly Report</i>
NAMRU-2	Naval Medical Research Unit No. 2
NAMRU-3	Naval Medical Research Unit No. 3
NAMRU-6	Naval Medical Research Unit No. 6
NATO	North Atlantic Treaty Organization
NCMI	National Center for Medical Intelligence
NECE	Navy Entomology Center of Excellence
NEPMU-2	Navy Environmental Preventive Medicine Unit 2
NHRC	Naval Health Research Center
NIH	National Institutes of Health
NMCPHC	Navy and Marine Corps Public Health Center
NMCPHC-EDC	Navy and Marine Corps Public Health Center-EpiData Center
NMRC	Naval Medical Research Center
OCONUS	outside the contiguous United States
OTSG-PVC	Office of the Surgeon General Pharmacovigilance Center
PCR	polymerase chain reaction
PHC-E	Public Health Command Europe
PTSD	Post-traumatic stress disorder
RI	Respiratory Infections
RME	reportable medical event
SMS	Surveillance Methods and Standards
SOUTHCOM	U.S. Southern Command
SSBP	Surveillance of Suicidal Behavior Publication
STI	sexually transmitted infections
TAMC	Tripler Army Medical Center
TBI	traumatic brain injury
USG	United States Government
USAFSAM	U.S. Air Force School of Aerospace Medicine
USACE	U.S. Army Corps of Engineers
USAMC	U.S. Army Medical Command
USAMRD-G	U.S. Army Medical Research Directorate–Georgia
USAMRD-K	U.S. Army Medical Research Directorate–Kenya
USAMRIID	U.S. Army Medical Research Institute for Infectious Diseases
USFK	United States Forces Korea
USINDOPACOM	U. S. Indo-Pacific Command
USU	Uniformed Services University of the Health Sciences
VE	vaccine effectiveness
WHO	World Health Organization
WRAIR	Walter Reed Army Institute of Research

## VISION

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To be the *central, integrated, customer-focused* epidemiologic and global health surveillance resource for the U.S. Armed Forces.

## MISSION

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To provide timely, relevant, and actionable, comprehensive health surveillance support to the Joint Staff, Combatant Commands and military Services in order to promote health and enhance Force Health Protection, Readiness and Lethality.

## CRITICAL FUNCTIONS:

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- Acquire, analyze/interpret, and disseminate health surveillance information and recommend evidence-based policy.
- Develop, refine, and improve standardized surveillance methods.
- Serve as a focal point for sharing health surveillance products, expertise, and information.
- Coordinate a global program of militarily relevant infectious disease surveillance.



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