Through these investments, CDC is transforming how the nation and world combat antimicrobial resistance. For example, CDC is: Visit the AR Investment Map The map currently shows fiscal year 2023 extramural funds that support CDC's antimicrobial resistance activities. CDC distributed the largest extramural portion of funding to support all 50 state health departments, several local health departments, and Puerto Rico, Guam, and the U.S. Virgin Islands. The map also includes fact sheets highlighting CDC's innovation work with partners to combat antimicrobial resistance. The information is updated yearly. CDC's investments in innovation to combat AR since 2016 include: CDC supports innovations and collaborations with investigators to identify and implement new ways to prevent antimicrobial-resistant infections and their spread. CDC supports innovative research to slow antimicrobial resistance through various funding mechanisms. In fiscal years 2016 through 2023, CDC awarded more than $52 million through Broad Agency Announcements to fight antimicrobial resistance. CDC funds awardees through a competitive selection process based on scientific needs and funds available and the awardees are typically announced each fall. The projects complement additional CDC antimicrobial resistance investments, collectively known as CDC's AR Solutions Initiative. Through these investments, CDC is transforming how the nation combats antimicrobial resistance at all levels. Development and Application of a National Pediatric Sepsis Event Surveillance Definition In this project, investigators will leverage their earlier experiences in developing and applying a national approach to sepsis surveillance in adults, as well as preliminary work developing pediatric sepsis surveillance definitions at the Children's Hospital of Philadelphia, to develop and validate an optimized pediatric surveillance definition and then apply it to electronic health record data from hundreds of U.S. hospitals to estimate total annual pediatric

sepsis cases and deaths in infants and children who are more than 30 days old. They will also develop a toolkit that hospitals can use to implement this definition to track sepsis cases in children. This work builds on the research priorities identified in 2019 by a CDC-convened group of pediatric sepsis experts and will be led by investigators at Harvard Medical School / Harvard Pilgrim Health Care Institute and the Children's Hospital of Philadelphia. The project team will partner with the Society for Critical Care Medicine Pediatric Sepsis Definition Task Force and include collaborators from Nemours Children's Hospital, HCA Healthcare, the Clinical Center at the National Institutes of Health, the University of Colorado, and Lurie Children's Hospital of Chicago. Development of a curated, international, antibiotic-resistant gonorrhea specimen bank Researchers will establish a CDC International Antibiotic-Resistant Gonorrhea Isolate Bank, which will include a diverse set of Neisseria gonorrhoeae strains based on geography, genomics, and antibiotic susceptibility profiles. Gonorrhea is a common sexually transmitted disease that can spread easily. N. gonorrhoeae has quickly developed resistance to each recommended treatment over time and gonorrhea is classified as an Urgent Threat in CDC's 2019 Antibiotic Resistance Threats Report. The CDC International Antibiotic-Resistant Gonorrhea Isolate Bank will provide complementary data to CDC's domestic specimens available through the Antibiotic Resistance Laboratory Network. These data will help experts understand the emergence and spread of antibiotic-resistant gonorrhea domestically and internationally and will be valuable in the development of treatment regimens, therapeutics, diagnostics, and prevention activities needed to combat this threat. Improving prevention, detection, and response to antibiotic resistant bacteria in Kenyan hospitals ICAP at Columbia University is being funded to develop a network of four hospitals in Kenya to improve their ability to detect bacterial infections, determine antibiotic resistance in the infections, assess antibiotic use and the prevalence of healthcare-acquired infections, and develop an antibiotic stewardship collaborative to

improve the use of antimicrobials at the hospitals. These activities are based on principles of quality improvement and use a variety of methods including laboratory evaluation, mentorship, and point prevalence surveys. ICAP will also support capacity of the National Public Health Laboratory in Kenya to detect and test for antimicrobial resistance. Current state of infection prevention and control (IPC) programs in Latin American hospitals Researchers will assess how national and healthcare facility IPC policies and guidelines are being adopted and implemented in hospitals across Guatemala, Panama, Ecuador, and Argentina. Latin American countries are facing a high burden of healthcare-associated and antibiotic-resistant infections. Findings will inform the development of a toolkit that other countries or facilities facing similar challenges can use to improve their IPC efforts and reduce the spread of infections. This research will build upon the latest knowledge by assessing current IPC practices, evaluating the healthcare worker perspective on IPC, and identifying challenges to implementing effective IPC in Latin American hospitals. Assessing Antibiotic Stewardship Practices in Non-US Healthcare Settings to Guide Implementation Efforts Investigators will develop a context-specific healthcare facility assessment tool to evaluate current antibiotic stewardship practices and needs across multiple institutions in various countries and regions globally. They will also perform qualitative interviews with key stakeholders to understand factors associated with successes and challenges in implementing antibiotic stewardship programs. Each of the three investigator groups, in collaboration with their partners and stakeholders, will focus on a different global region: Johns Hopkins University will work with partners in Latin America (Guatemala, Colombia, Panama, Ecuador and Argentina), University of Oxford and Duke University consultants will work with partners in South and South East Asia (Vietnam, Indonesia, Nepal and Thailand), and University of Pennsylvania will work with partners in Southeast Africa (Botswana, South Africa and Zimbabwe). This project will identify gaps in antibiotic stewardship programs and determine context-specific factors associated

with successful implementation of these programs to improve antibiotic use globally. Latin American A. fumigatus Azole Resistance Survey in 12 countries, 20 laboratories Researchers will conduct a survey of azole-resistant Aspergillus fumigatus throughout Latin America using the existing Latin American Medical Mycology Network (LAMMN). This survey will include air sampling using a citizen science approach—the involvement of the public in scientific research—with 20 coordinating LAMMN laboratories sending out and receiving specimen plates from the public. Researchers will isolate A. fumigatus and screen for resistance. The extent of resistance that is uncovered will help guide treatment and appropriate prevention measures. The genetic background of resistant strains will be determined and will help establish how resistance is spread. This information will build the basis of early and appropriate interventions to improve patient outcomes, reduce death, and lower health care costs, which are of special concern in countries with limited resources. Regional and global risk estimates for the emergence and persistence of MDR and XDR strains of enterobacterial human pathogens Researchers will determine the mobile genetic elements involved in the emergence of multi-drug resistant (MDR) Shigella sonnei and extensively drug-resistant (XDR) Salmonella Typhi. They will also look at the risk of spread for relevant antibiotic resistance genes. Researchers aim to develop bioinformatic pipelines (technology that helps store, analyze, and share biological data). This work will help understand when and where drug-resistant bacteria that are harmful to human health might emerge in the future. This study builds upon work supported by a previous BAA. Assessing Antibiotic Stewardship Practices in Non-US Healthcare Settings to Guide Implementation Efforts Collaborative project among Johns Hopkins University, University of Oxford with Duke University consultants, and University of Pennsylvania. See description under Johns Hopkins University. Investigating prevalence of multidrug resistance in Botswana – assessing relatedness using whole genome sequencing (IMPALA-TWO) Researchers will add to their work from a previous BAA award on multidrug-resistant Gram-negative

extended-spectrum cephalosporin-resistant Enterobacterales (ESCrE) and carbapenem-resistant Enterobacterales (CRE) to determine the genetic diversity of ESCrE and CRE in three regions of Botswana. Researchers will perform whole-genome sequencing on ESCrE and CRE isolates in order to describe the genetic mechanisms of resistance and evaluate relatedness between organisms. This study allows continued research to understand and compare colonization of ESCrE and CRE and lay the groundwork for the development of test strategies to decrease these drug-resistant bacteria in the area, and possibly globally. Assessing Antibiotic Stewardship Practices in Non-US Healthcare Settings to Guide Implementation Efforts Collaborative project among Johns Hopkins University, University of Oxford with Duke University consultants, and University of Pennsylvania. See description under Johns Hopkins University. Understanding co-infection with multidrug-resistant organisms among hospitalized patients with COVID-19 in U.S. Department of Veterans Affairs (VA) hospitals Researchers will develop a better understanding of the relationship between COVID-19 and antibiotic resistance among hospitalized patients to inform future care plans for patients. Researchers will focus on and identify: Carbapenem-resistant Enterobacterales surveillance in two intensive care units in India Globally, CRE is associated with a high death rate. In low- and middle-income countries, there are barriers in healthcare access, diagnostic testing, and treatment options, which lead to negative health outcomes for patients with CRE infections. In India, CRE is commonly found in healthcare facilities, but it is resource-intensive for healthcare facilities to monitor this threat. Researchers aim to find effective, feasible and sustainable way to implement screening for carbapenem-resistant Enterbacterales (CRE) in hospital systems in low- and middle-income countries where resources are limited. This research is important because creating a robust way to screen for CRE in low- and middle-income countries will provide data needed to inform infection prevention efforts and help healthcare facilities reduce death rates caused by CRE infections. Interrogating the

phylogenomics and mobilome of colonizing multidrug-resistant organisms (MDROs) in hospitalized patients and community-dwellers in Pakistan In this study, researchers will collect fecal waste (poop) samples and nostril and armpit swabs from seriously ill patients in hospitals in Pakistan. They will also collect samples from non-hospitalized people who live in the patient's home. Researchers will compare MDROs—including carbapenem-resistant Enterobacterales (CRE), extended-spectrum β-lactamase (ESBL)-producing Enterobacterales, methicillin-resistant Staphylococcus aureus (MRSA), and vancomycin-resistant Enterococcus (VRE)—to determine if there is a connection between the germs in patients and the germs found in household members. MDROs are often found in healthcare settings (e.g., surfaces and hospital plumbing systems), but it is not known if there is a link between these healthcare MDROs and MDROs in the community. By comparing the genetic relatedness of hospital MDROs with community MDROs, researchers will determine the inter-connectedness of spread between healthcare facilities and the community. This information is critical to direct and improve infection prevention strategies in the region to prevent spread. Integrated Food Safety Centers of Excellence One Health and Antimicrobial Resistance Projects CDC-designated Food Safety Centers of Excellence will lead collaborative One Health projects across states to explore antibiotic stewardship (improving antibiotic use), animal health, and animal ownership and their impact on antibiotic-resistant enteric (gut) infections in humans. These efforts will guide the development of educational interventions and materials for animal owners, caretakers, and veterinarians to prevent the spread of infections. Projects include: Effective treatments for chronic polymicrobial infections: Drug, dose & duration Researchers will use experimental model systems based on lungs that are infected by cystic fibrosis (CF) to test the effects of certain antibiotic drugs and their dosage and duration on antibiotic resistance (AR). People with CF suffer from life-long lung infections. Sometimes these infections can be caused by antibiotic-resistant germs, which are difficult to treat. Findings from this study will help

inform clinical decisions that balance CF treatment benefits with the risks of contributing to AR. This project builds on similar work Georgia Tech accomplished in 2017. Read about some of the first project's outcomes. Multicenter Impact of COVID-19 on Secondary Infections and Incidence of Hospital-onset Antimicrobial-Resistant (AR) and Fungal Organisms Researchers will describe the epidemiology and risk factors for secondary bacterial or fungal co-infections, and the subset associated with resistant organisms, in COVID-19 patients in intensive care units at three health systems in the Chicago area. These data will enhance current understanding of risk factors for secondary co-infections in COVID-19 patients as well as determine drivers of AR among these infections to support disease control and prevention strategies. introduction of antimicrobial resistant Salmonella species and bacterial reservoirs of transmissible antibiotic resistance genes into food animal populations through livestock and poultry feed, pet food and treats Researchers will examine livestock and poultry feed components, and pet treats of animal origin (e.g., pig ears) for potential presence of Salmonella species and other bacteria with antibiotic resistance genes. Researchers will compare any identified contamination of imported and domestically produced feed components and pet treats. Based on the study results, researchers will create livestock feed and pet treat biosecurity recommendations for specific imported and domestically produced feed components intended to prevent the introduction of Salmonella species and other bacteria with antibiotic resistance genes. Determining the Incidence of Secondary Aspergillus Infections in Influenza positive patients Researchers will establish a facility-level surveillance system for influenza-associated invasive pulmonary aspergillosis (IAPA), a concerning infection that can be caused by multidrug-resistant Aspergillus. This system will track laboratory and clinical data from patient medical charts. Analysis will determine the incidence of IAPA and other invasive mold infections among patients with influenza, and the associated patient characteristics, risk factors, and clinical outcomes. These infections are often reported as secondary infections in

patients with influenza but little is known about them. Prevalence of and risk factors for community-associated antibiotic-resistant Enterobacterales and genes Researchers will identify generally healthy people (no inpatient healthcare stay in previous year and no current antibiotic use) in a community to measure how commonly they carry certain germs in their gut and the risk factors that may have exposed them to those germs. Healthy people can carry antibiotic-resistant germs in their gut without being ill, but these germs can also cause serious infections in some circumstances or spread to others who are more vulnerable to serious infection. Researchers will ask participants to answer questions about a wide variety of possible exposures and collect stool samples to identify resistant bacteria. They will determine the full profile of all antibiotic resistance genes present in the stool samples and compare them to genes observed in healthcare, agricultural, and environmental settings. The germs include extended-spectrum beta-lactamase (ESBL)-producing Enterobacterales, carbapenem-resistant Enterobacterales (CRE), and antibiotic-resistant Escherichia coli (E. coli). Researchers will evaluate risk factors including use of antibiotics and other prescription pharmaceuticals, age, housing, water source, lifestyle factors (e.g., travel, companion animals), bacteria spread within households, and diet. Evaluating the targeted use of gown and gloves to prevent transmission of pathogens, including antibiotic-resistant organisms, within ventilator units in nursing homes Researchers will test the feasibility and impact of a new gown and glove strategy for healthcare providers in two nursing homes in Maryland to help prevent residents in ventilator units from getting Staphylococcus aureus, including both methicillin-resistant and methicillin-susceptible S. aureus (MRSA/MSSA), and carbapenem-resistant Gram negative bacteria, including Enterobacterales, Pseudomonas aeruginosa, and Acinetobacter species. Residents in ventilator units are at a higher risk of getting infections, including those caused by antibiotic-resistant germs. Healthcare workers in nursing homes care for many residents across different areas of the facility and can

spread germs from resident to resident, including high-risk residents within ventilator units, if not using personal protective equipment consistently and correctly and not cleaning their hands. This pilot study will help determine if a new gown and glove strategy can help prevent spread of germs. Secondary Infections and Antibiotic Resistance in Post-acute Care Patients with Recent COVID-19 Infection Researchers will determine the epidemiology and outcomes associated with COVID-19 infection encountered in the post-acute care setting. The focus will be on secondary infections, colonization (germs are present but no signs of infection), or infection with multidrug-resistant germs. Researchers will assess risk factors among patients with recent COVID-19 infection admitted to a long-term acute care hospital. This work will help answer questions regarding the long-term infectious outcomes associated with COVID-19. Clinical and molecular determinants of transmission of extended-spectrum beta-lactamase (ESBLs) in the community Researchers will study people with ESBL infections in the community to determine how often the germs spread within household settings and possible reasons for spread. Patients included in this study will have previously tested positive for an ESBL-producing Escherichia coli or Klebsiella species during a recent visit to an emergency department or outpatient practice. Researchers will evaluate the entire household over a two-month period starting as soon as possible after the patient is identified. They will collect stool samples from household members and pets and swab samples of common touch sites around the household. Other data collected will include: Examining the relationship between SARS-CoV-2 and antibiotic resistance genes within municipal sewage treatment facilities and the possible transmission to their employees Researchers will examine wastewater treatment plant (WWTP) systems to monitor for the presence of SARS-CoV-2 (the virus that causes COVID-19) and antibiotic resistance to better understand community spread of COVID-19 and antibiotic resistance. The COVID-19 pandemic has resulted in increased antibiotic prescribing to prevent and treat secondary bacterial infections, which could

drive significant changes in antibiotic resistance. WWTP systems have been identified as critical hubs for antibiotic resistance and may expose treatment plant workers to pathogens (germs). The results of the study will help CDC evaluate the performance of existing AR monitoring systems, inform guidance to protect utility workers, and establish a foundation for using municipal sewage as an indicator of community-wide viral infection burden. Evaluation of risk factors for the development of secondary bacterial and fungal co-infections, including antibiotic-resistant organisms, in COVID-19 patients in a regional healthcare system Researchers will describe the epidemiology of secondary resistant bacterial and fungal infections in hospitalized patients before and during the COVID-19 pandemic across socio-demographically diverse hospitals in the St. Louis area. The main objective of this work is to identify independent risk factors for secondary infections in patients with COVID-19, including socioeconomic status and race. These findings will offer insights on how best to protect and care for higher risk populations. Clostridioides difficile in the community setting: Identification of epidemiologic and microbiome-related risk factors for colonization and household transmission Researchers will study C. difficile among previous patients who have been discharged to their home. Data from this study will help identify epidemiologic and microbiome-specific risk factors for spread from the index case (first individual with infection) to their household contacts, including infection or colonization (germs are present but no signs of infection) of those contacts. The patients in this study tested positive for C. difficile in a specific healthcare facility during 2019 and were discharged home. Researchers will collect stool samples, as well as epidemiologic and behavioral risk factor data through interviews. Improving Environmental Control of Candida auris (C. auris) Contaminated surfaces and equipment in hospitals and long-term care facilities are a major source of C. auris transmission (spread) and outbreaks. Researchers evaluated the effectiveness of different products and methods used for C. auris disinfection, including commonly used liquid disinfectants and applications of UV

light for decontamination. Microbial bioburden of inpatient and outpatient areas beyond hospital patient rooms Contaminated environmental surfaces are an important potential source for spread of healthcare-associated pathogens (germs). Researchers will determine the frequency of environmental contamination in inpatient and outpatient areas beyond hospital patient rooms and investigate the potential for hands to acquire and transfer pathogens from contaminated surfaces and examine shedding of pathogens by patients in outpatient settings. Surveillance for Non-Ventilator Hospital-Acquired Pneumonia using Structured Electronic Clinical Data Researchers will provide valuable insights into the feasibility of widescale automated surveillance for non-ventilator hospital-acquired pneumonia (NV-HAP) using routine electronic health record data, deepening our understanding of treatment patterns and outcomes for NV-HAP, and allowing researchers to evaluate emerging NV-HAP prevention interventions. Structure and dynamics of Salmonella plasmids and their involvement in the dissemination of antibiotic resistance Researchers will identify and evaluate different structures and dynamics of Salmonella plasmids and how they spread antibiotic resistance. Group A Streptococcus Molecular Epidemiology and Ecology An active surveillance system for Group A Streptococci (GAS) pharyngitis has not existed in the U.S. since 2007. Researchers will develop an outpatient GAS surveillance network in five geographically distinct areas to better understand GAS burden and trends in the U.S. The Need for Epidemiology and Antibacterial Susceptibility Assessment of Otopathogens (infections in ears) causing Acute Otitis Media (AOM) in Children AOM is among the most common infectious diseases in children and is the most common bacterial infection in children for which antibiotics are prescribed. The researchers will examine effect of PCV13 (vaccine that protects against 13 pneumococcal bacteria) use on incidence of antibiotic-resistant pathogens causing otitis media in children. Evaluating Emergence of Resistance and Changes in Clinical Pathogens Following Introduction of Chlorhexidine Bathing Chlorhexidine gluconate (CHG) is a

broad-spectrum, topical antiseptic that is widely used in healthcare. Researchers will evaluate potential unintended adverse consequences of long-term CHG use, including emergence of CHG resistance, emergence of co-resistance to antibiotics, and shifts in frequency and distribution of microbial pathogens producing disease. Evaluating Changes in Skin Cultures and Skin Microbiome Due to Chlorhexidine vs. Soap Bathing in Patients Requiring Acute or Long-Term Care in Healthcare Facilities Previous studies and clinical trials of CHG bathing have demonstrated large reductions in infections and multidrug-resistant organisms. However, concerns exist about the unintended consequences of CHG bathing on the skin microbiome. Researchers will evaluate changes to the skin microbiome in patients in healthcare facilities following CHG use compared to soap bathing. Assessing human exposure to multidrug-resistant organisms in environmental waters in a Chilean community Researchers will examine what happens to humans when they are exposed to antibiotic-resistant pathogens in water from a Chilean community. Metabolomic validation of an intestinal microbiome disruption model Researchers at Washington University in St. Louis will be using a small laboratory system that resembles the human gut microbiome to look for markers of microbiome disruption from antibiotics. Using this information, they will develop and test a panel of markers that may be able to help clinicians understand their patients' risk for infection and may support development of new therapies and microbiome disruption diagnostics. The Leadership in Epidemiology, Antimicrobial Stewardship and Public Health (LEAP) Fellowship The LEAP Fellowship is a joint program of the Infectious Diseases Society of America, Society for Healthcare Epidemiology of America, and Pediatric Infectious Diseases Society. It is designed to provide select Fellows at infectious diseases training programs across the nation an opportunity for immersive experiences in healthcare leadership, antimicrobial stewardship and infection prevention, and the inner workings of public health departments. Assessing risk factors, clinical course, and microbiologic outcomes in patients infected with Shigella with

elevated ciprofloxacin MIC values using a population-based survey in California This project will provide needed information about the proportion of Shigella infections with decreased susceptibility to first line antibiotics such as ciprofloxacin and azithromycin. This project aims to assess the severity of illness and outcomes of those patients infected with Shigella with decreased susceptibility to these important antibiotics. The results of this project can may help inform treatment and prevention recommendations. Evaluation of barrier precautions for prevention of patient-to-patient transfer of healthcare-associated pathogens This study will identify routes by which germs spread and examine the effectiveness of different barrier precautions to prevent the spread of healthcare-associated infections from patient to patient. Predictors of antimicrobial exposure for application in the standardized antimicrobial administration ratio risk adjustment strategy Researchers will identify patient and facility level factors associated with antibiotic use that can be captured in electronic health records and can be used for benchmarking antibiotic use. Improving antimicrobial use at hospital discharge through a collaborative pharmacist-led transition-of-care intervention Patients are often prescribed antibiotics when they are discharged (when they are sent home from the hospital). This study aims to improve antibiotic selection and reduce excess length of antibiotic therapy by facilitating a team antibiotic prescription review supported by pharmacists at the time of discharge. Electronic direct-from-sample phenotypic antimicrobial susceptibility testing diagnostic for Neisseria gonorrhoeae The best approach to countering the spread of antibiotic resistant Neisseria gonorrhoeae is to treat patients quickly with effective antibiotics. ImpeDx Diagnostics, Inc. will develop a rapid system to provide phenotypic antibiotic susceptibility testing results for Neisseria gonorrhoeae directly from clinical samples in order to identify the preferred antibiotic for treatment of the individual, potentially reducing the time of infection, improving public health response, and reducing the incidence of antibiotic resistance. Campylobacter burden testing in dogs Researchers will determine the burden of

Campylobacter in dogs by sampling commercial breeding colonies and collecting information on antibiotic use to help better understand risks associated with the emergence of multidrug-resistant Campylobacter. Find out more about this project, including information about Campylobacter occurrence, antibiotic resistance, and use of antibiotics in breeding kennels. Barriers and facilitators for implementation of infection prevention practices for device care in high-acuity skilled nursing facilities: A human factors and systems engineering approach This study will evaluate how nursing home staff handle medical devices used during the care of residents, in order to identify best and most effective practices for minimizing harms from these devices. This research will identify implementation strategies to reduce infections and transmission of multidrug-resistant organisms among residents in skilled nursing facilities. A toolkit to enhance nursing antibiotic stewardship activities Researchers will develop and implement an antibiotic stewardship toolkit for nurses that focuses on improving assessment of penicillin allergy and culturing practices (urine and respiratory) based upon algorithms. Investigation of short and long term interventions to improve antibiotic prescribing in dentistry To improve antibiotic prescribing in dentistry, researchers will analyze insurance claim data to better understand prescribing by dentists, test a customized peer comparison message to the most frequent prescribers, and promote existing guidelines for prophylactic prescribing in dentistry. Development of reproducible, quantitative methods based on shotgun metagenome sequencing for assessment of risk of microbial transmission Using samples collected from a hospital, researchers will develop methods that will help others study the microbiome of the healthcare environment. This project will help healthcare providers ensure that facilities are safe. Candida auris, an emerging fungal pathogen of high concern Candida auris (C. auris) is an emerging, drug-resistant fungus that causes outbreaks of serious infections in healthcare settings. Patients who are colonized but not infected can transmit C. auris to others and are at risk of infection themselves. This study will help us better

understand factors that are associated with C. auris colonization in high-risk patients and the effectiveness of chlorhexidine bathing as a possible decolonization method. Genomic epidemiology of community-onset invasive USA300 MRSA infections Researchers will use whole genome sequencing (WGS) to examine historical methicillin-resistant Staphylococcus aureus (MRSA) clinical isolates from the Cook County Health and Hospitals System in Chicago, IL. The objective of this study is to use WGS along with epidemiologic data to better understand the spread of MRSA between healthcare and community settings, with an ultimate goal to identify potential interventions that can prevent infections. Metagenomic analyses study through simulated direct and indirect healthcare-related pathogen transmission events This project will evaluate and develop tools which can detect and follow the spread of specific bacteria and microbial communities between people and across surfaces in healthcare settings. Tracking hospital acquired infections using advanced metagenomics tools Researchers are working to streamline an existing sequencing method and develop new methods to track healthcare-associated infections as they spread in the healthcare setting. Prevalence of mcr-harboring Salmonella and Escherichia coli in food products, food-producing animals, and their environments in the Dominican Republic Researchers will collect samples from food, food animals, and the environment in the Dominican Republic and test for mcr genes, which can confer resistance against colistin, a critically important antibiotic. Researchers will examine the factors that contribute to the spread of these genes in the Dominican Republic to inform public health recommendations. A novel metric for benchmarking antibiotic use to inform outpatient stewardship Researchers will develop an evidence-based benchmark rate of antibiotic prescribing for children with acute respiratory tract infections. This metric will be applied to estimate how many adverse drug effects are associated with unnecessary antibiotic treatment. This study will also design an intervention to improve antibiotic prescribing for acute respiratory tract infections.

Antimicrobial use on crops and effects on antimicrobial resistant organisms and genes in the environment Researchers will establish field plots of tomatoes and treat these plots with organic fertilizers, herbicides, and antimicrobials. Following these treatments, samples from the plots will be analyzed to determine the kinds of antibiotic-resistant bacteria and genes that are present in these environments. Mitigating zoonotic transmission of Salmonella Heidelberg in the dairy calf production chain Researchers will assess the effectiveness of cleaning and disinfection methods to prevent the transmission of Salmonella Heidelberg through the dairy calf production chain. Researchers will develop and disseminate educational materials on cleaning and disinfection to livestock markets and veal calf production facilities to reduce the spread of Salmonella Heidelberg. Find out more about this project and how it informed mitigation strategies to reduce the spread of antibiotic-resistant bacteria among calves, people, and the environment. Antimicrobial stewardship education for calf producers Ohio State University will partner with calf producers to assess the impact of a farm antimicrobial stewardship plan on the quantity of antimicrobials used for disease treatment. The study will also measure changes in the presence and diversity of antimicrobial resistant genes in the environment before and after implementation of the stewardship plan. Find out more about this project, including how the project informed mitigation strategies to reduce the spread of antibiotic-resistant bacteria among calves, people, and the environment. Hospital and community burden of colonization due to multidrug-resistant gram-negative bacteria in Chile This project will determine the prevalence of and risk factors for carriage of multidrug-resistant gram-negative bacteria in communities and hospitals in Chile. This research will demonstrate how resistant bacteria spread and will help identify potential strategies that can help stop spread in South America. Comparison of commercial methods for molecular detection of Mycoplasma pneumoniae This study will evaluate the performance of commercially available diagnostic tests to detect Mycoplasma

pneumoniae, a common cause of respiratory disease, and to identify antibiotic-resistant infections. Rapid lateral flow assay for rapid diagnosis of coccidioidomycosis to reduce the unnecessary use of antibacterial drugs This project will study the impact of a newly developed rapid test to diagnose Valley fever (coccidioidomycosis), a fungal lung infection, in patients visiting Tucson, Arizona, emergency departments. A faster diagnosis can improve patient outcomes and reduce unnecessary antibiotic use. Combined surface sampling and quantitative microbial risk assessment modeling to optimize surface cleaning for targeted healthcare-associated infection reduction Germs can spread in healthcare settings on environmental surfaces. Researchers will use a combination of surface sampling and risk assessment modeling to characterize the effectiveness of different surface decontamination strategies to reduce the spread of germs and healthcare-associated infections. Strategies to reduce post-discharge invasive Staphylococcus aureus infection This study will evaluate what percent of Methicillin-resistant Staphylococcus aureus (MRSA) carriers being discharged from hospitals have a community-associated strain. Patients sometimes carry the germ without showing signs of it (colonization) and suffer infections from the strain later. This study will also assess what percent of patients carrying the community MRSA variant develop later infection within a year of discharge. Finally, this project will assess whether a repeated decolonization treatment can reduce post-discharge infections due to this strain. Design of a highly multiplexed targeted sequencing panel for the detection and characterization of antimicrobial resistance determinants from complex metagenomic samples This project will expand an approach that can analyze genetic data directly from stool samples to identify known antibiotic-resistant genes, a faster way than other testing methods. An efficient testing panel like this could improve outbreak detection and patient outcomes. Azole-resistant Aspergillus fumigatus strains from agricultural sites on the east and west coasts of the U.S. Aspergillus fumigatus causes deadly infections in immunocompromised patients, and strains have emerged in

the U.S. that are resistant to all azoles, which are the main antifungals used for treatment. Similar azole chemicals are used as agricultural fungicides to treat crops. Researchers will identify and isolate Aspergillus fumigatus samples from agricultural sites in multiple U.S. regions to better understand the emergence and sources of azole resistance. This study builds upon work supported by a previous BAA. New approaches to improve the efficiency, sensitivity, specificity and standardization of sampling, DNA isolation, shotgun library preparation, and microbiome DNA enrichment and analysis in healthcare settings Understanding what bacteria, viruses, and fungi (which together form a microbiome) exist in a healthcare environment and how they interact with each other and their immediate environment can help prevent and control infections. Researchers will develop protocols to detect microbes and characterize the microbiomes in healthcare settings using next-generation DNA sequencing. These methods will improve the sensitivity and efficiency of detection, while providing more information about the microbes than current methods. A novel metric for benchmarking antibiotic use to inform outpatient stewardship Researchers will validate a human gut model of healthy and 'disrupted' human microbiomes. These models will be used to determine how certain bacterial population can prevent infection by C. difficile and other multidrug-resistant organisms, and reestablish healthy gut microbiome function after receiving antibiotics. Transmission of antibiotic-resistant bacteria from patient-to-patient in the healthcare setting and the impact of contact precautions Researchers will study how antibiotic-resistant bacteria spread from patient to healthcare provider and from healthcare provider to patient. They will also evaluate the effectiveness of barrier precautions such as gloves and gowns. Longitudinal impact of prophylactic antibiotic use on the gut microbiota in healthy human populations This study will assess changes over time in the human gut microbiome in healthy patients undergoing elective surgery. Their ultimate goal is to develop measures that can assess microbiome health status that associate with important clinical outcomes, such as

acquisition of an antibiotic-resistant organism. Using complimentary in vitro and in vivo models of the human microbiome to study antibiotic-mediated disruption Researchers are testing more cost effective models that will look at the effects antibiotics have on the gastrointestinal microbiome. Enhancement and evaluation of metagenomics tools to identify and sequence whole genomes of Neisseria gonorrhea from clinical samples Researchers will develop improved laboratory methods to better detect drug-resistant gonorrhea directly from patient samples and create publicly available tools to analyze genetic antibiotic resistance data. Colonization with multidrug-resistant gram negative bacteria in Botswana This project will measure the prevalence of and risk factors for carriage of extended-spectrum beta-lactamase producing Enterobacterales (ESBL-EB) and "nightmare bacteria" carbapenem-resistant Enterobacterales (CRE) in inpatients, outpatients, and households in Botswana. This research will help us understand how these bacteria spread in healthcare facilities and communities and inform containment efforts in a country in Southern Africa. Metagenomic and whole-genome sequencing to define resistome evolution during antibiotic exposure and long-term acute care Researchers will characterize how antibiotics change the microbial communities living in patients' lungs and guts, as well as investigate the evolution of antibiotic resistance in Pseudomonas aeruginosa (a type of bacteria often found in the healthcare environment) during antibiotic treatment. Socio-ecological coupling of antibiotic resistance and the potential risk of human exposure to antibiotic-resistant pathogens in bioaerosols generated during wastewater treatment This study will measure the variability of antibiotic-resistant bacteria in bioaerosols (tiny liquid droplets in the air that can contain bacteria and viruses) generated during waste water treatment and evaluate the risk of exposure, colonization and infection to treatment plant workers. The study will compare antibiotic resistant bacteria found in employees working in wastewater treatment plants to those found in workers from drinking water treatment plants where exposure to antibiotic resistant bacteria is expected to be much lower.

Clinical and microbiologic outcomes in patients treated for multidrug-resistant Shigella infections in Dhaka, Bangladesh This study will look at clinical and microbiologic outcomes in patients treated for drug-resistant Shigella infections at a hospital in Dhaka, Bangladesh. Data from this study can be used to help determine antibiotic breakpoints (which help determine if an antibiotic will be effective on an infection) for drug-resistant Shigella. Novel interventions and approaches to mitigating carbapenemase-producing Gammaproteobacteria in healthcare premise plumbing Carbapenemase-producing Gammaproteobacteria, a class of bacteria that can be highly resistant to today's strongest antibiotics, may colonize (or live in) the premise plumbing systems of healthcare facilities. This project will investigate those factors that may influence colonization and growth of these organisms in sink drains and use a multifaceted approach to assess interventions designed to prevent the spread of these organisms from plumbing to patients. Critical barriers to antibiotic resistance during water reclamation and reuse Water reclamation and reuse uses advanced treatment methods to make treated wastewater safe for a variety of uses, like irrigation, cooling towers, reservoir augmentation, and aquifer recharge. This study will identify specific waste water reuse treatment methods that reduce antibiotic-resistant bacteria and genes by comparing wastewater samples throughout the treatment train of two distinct advanced treatment facilities. Identifying treatment approaches that reduce antibiotic resistance is important as water reuse becomes more widely adopted. Optimizing in-building disinfection of antibiotic-resistant opportunistic pathogens This study will evaluate the effectiveness of a variety of disinfection methods used in hospital plumbing systems to kill antibiotic-resistant bacteria and prevent evolution and spread of new resistant strains. The findings will provide helpful guidance to hospitals and similar facilities where disinfection is important to protect high-risk populations. Impact of early life antibiotic treatment in preterm infants on subsequent multidrug-resistant colonization and infection Researchers will use a mouse model to study the effects of

antibiotics on the microbiomes of infants C. difficile nucleic acid amplification test cycle threshold value associated environmental contamination (CONTAM Study) This study will look at the shedding of C. difficile by asymptomatic C. difficile carriers (patients who may carry C. difficile but do not show symptoms) and symptomatic patients with C. difficile infection among cancer (hematopoietic cell transplant and leukemia) patients admitted to the Siteman Cancer Center. In addition, the immediate surrounding patient care environments associated with these patients in the facility will be sampled to understand environmental contamination. This study will help determine if additional C. difficile infection prevention measures are needed for these patients. Cross-validation of human fecal minibioreactor arrays and humanized microbiota mice as complementary pre-clinical models of the gastrointestinal microbiome This project will evaluate in vitro and mouse models of human gut microbiomes to help create a pre-screening tool to evaluate potential therapies. Rapid assays to detect Neisseria gonorrhea antibiotic resistance at the point of care Investigators will develop and evaluate new diagnostics tools that can determine the antibiotics to which a patient's strain of gonorrhea is susceptible (slowed or killed). This fast and efficient test, once available, will help guide individual patient management and can be used to identify antibiotic-resistant strains of gonorrhea. It can also be used to support outbreak investigations of resistant gonorrhea in the community. Natural history of C. difficile colonization Researchers will use data to show how C. difficile germs spread and to develop more effective control measures. This project will grow our understanding of C. difficile colonization and infection. Prenatal antibiotic use and body weight in children The goal of this study is to examine the potential relationship between antibiotic use during pregnancy and pediatric weight problems. Computational methods for culture-independent disambiguation of wgMLST types in biological samples with multiple related bacterial strains Investigators will develop computational tools to differentiate and analyze different types of DNA mixed in one sample. This project will

help laboratories better understand the make-up of a mixture and its threat level. Antibiotic resistance in concentrated poultry feeding operations: Impacts on environmental waters This project will assess the types of antibiotic-resistant organisms in poultry houses, in addition to the amount of these organisms in a poultry house and further downstream in environmental waters. Researchers will also measure the amount of veterinary antibiotic residues in downstream environmental waters. Optimization of therapeutic strategies to manage polymicrobial CF lung infections: Clinical assessment Researchers will continue this project from last year to identify novel probiotic and antibiotic intervention strategies for patients with cystic fibrosis. The project will validate and improve new treatment strategies by implementing them in a small group of patients. The Leaders in Epidemiology, Antimicrobial stewardship and Public health, or LEAP, Fellowship are Infectious Diseases Fellowships to drive innovative education and approaches in antibiotic resistance, antibiotic stewardship and public health This project establishes a fellowship for infectious disease physicians to bridge clinical infectious disease and public health work in the areas of antibiotic resistance and antibiotic stewardship. Improved bioinformatics tools for detection and characterization of antimicrobial resistance in public health Researchers will develop a comprehensive gene and protein database and web-based resource that public health experts can use to quickly detect and identify antibiotic resistance genes as they emerge. Highly accessible system for infection control and antimicrobial stewardship in resource limited settings This project will modify a commercial cloud and mobile-based software platform, which integrates electronic patient data and local treatment guidelines, to support antibiotic stewardship and infection control in low- and middle-income countries. Investigators will translate the software to Spanish and use it in up to three medical sites internationally. Implementers will assess factors such as cost, clinical impact, and feasibility. Microbiome disruption and Enterobacterales dominance as a risk factor for sepsis in intensive care patients Antibiotics can change

the intestinal microbiome, which may increase the risk of sepsis. Researchers will extend previous CDC-funded work to assess intestinal microbiome disruption and dominance by the Enterobacterales order of bacteria as risk factors for sepsis. Rapid identification and analysis of transmission of the emerging pathogen Candida auris Researchers will validate a new rapid diagnostic platform to detect the multidrug resistant fungal pathogen Candida auris, and they will analyze C. auris transmission patterns in healthcare facilities by applying advanced genetic fingerprint methods. Perinatal antibiotics and weight gain in childhood Researchers will examine if antibiotics given to mothers immediately before birth, or to newborns right after birth, can increase the weight gain of children in the first 5 years of life. Preventing the dissemination of CRE from healthcare facilities into surface waters in the US (continuation request) The study will evaluate potential discharge of antibiotic resistant bacteria from hospital sewage and test a technology to prevent it. Understanding the microbiologic dynamics of Carbapenemase-producing organisms in hospital wastewater premise plumbing This project will track carbapenemase-producing organisms in healthcare facilities, in part by using a controlled sink lab to recreate a healthcare facility setting, to help guide facilities experiencing the transmission of these organisms from the healthcare environment or plumbing. The prevalence and diversity of antibiotic resistant bacteria in a mixed-use watershed Investigators will sample surface water to analyze it for human and agricultural waste and antibiotic-resistant bacteria. This project will help to determine how antibiotics, pathogens, and resistance elements move across environments and potentially pose a risk to human health. Considering homologous and non-homologous recombination in outbreak analysis Researchers are developing computational tool to improve analysis of bacterial DNA sequences, particularly from pathogen samples that are very closely related. Sentinel surveillance for Macrolide-resistant Mycoplasma pneumoniae at select sites in the U.S. Using samples from eight hospitals, researchers will determine the prevalence of macrolide

antibiotic resistance in Mycoplasma pneumoniae, how it spreads, and how it affects patients. Reducing antibacterial use in patients with coccidioidomycosis This project will study the delay in diagnosis of Valley Fever (coccidioidomycosis) in Tucson, Arizona where this disease is endemic (very common). To some clinicians, Valley Fever looks like community acquired pneumonia. The University of Arizona will collect the diagnostic codes for Valley Fever in its hospital computer system. Researchers will also analyze the health care cost due to delay in diagnosis and determine the unnecessary antibiotic usage for better antibiotic stewardship practices. Azole resistance in agricultural settings Researchers will collect and characterize azole-resistant fungal strains from agricultural and horticultural sites. Azoles are used to protect crops from fungi, but azole-resistant fungi can infect people and cause disease that is difficult to treat and can lead to death. Implementation of a novel strategy to prevent Staphylococcus aureus (SA) acquisition in community-based nursing homes to prevent invasive SA infection: Feasibility and pilot to guide a multicenter stepped wedge cluster trial Researchers will conduct a pilot study (small-scale study that helps design larger studies) on the use of additional gowns and gloves in nursing homes to prevent the spread of Staphylococcus aureus infections. Comparison of methods for detecting recombination in bacterial whole genome sequences Investigators will compare genome analysis methods that determine the source of genetic material. This project will help researchers to understand the relationships and transmission of antibiotic-resistant bacteria. Double blinded, randomized controlled Trial of Oral vancomycin versus placebo in hospitalized patients with diarrhea and stool toXin NEGative but nucleic acid amplification test positive for toxigenic C. difficile (TOX NEG trial) Researchers will assess the risks and benefits of C. difficile treatment compared to a placebo treatment. Researchers will determine the impact of oral antibiotics on the microbiome, antibiotic resistance, C. difficile, and colonization of a multi-drug resistant organism, healthcare environment contamination, duration of diarrhea, and outcomes.

Rectal microbiome disruption indices associated with acquisition of multidrug-resistant organism among subjects exposed to antimicrobials The project will identify characteristics of the microbiome that can predict which patients are at highest risk of acquiring multidrug-resistant organisms to develop novel strategies that can prevent people from acquiring drug-resistant bacteria. Barriers and facilitators for NHSN adoption in nursing homes The national study will determine the barriers of nursing homes to tracking C. difficile and multidrug-resistant organisms using CDC's National Healthcare Safety Network (NHSN), and what resources are needed to overcome these barriers. Surveillance of resistance gene carriage in patients with hematologic malignancies: A taxonomy-focused approach Researchers will work to understand the transfer of antibiotic resistance genes in Leukemia patients and what role the microbiome is playing. Evaluating the use of an adenosine triphosphate (ATP) bioluminescence assay to optimize hospital cleaning The study will evaluate the use of a new technology to measure and thereby optimize hospital room cleaning. Optimization of therapeutic strategies to manage polymicrobial cystic fibrosis lung infections The project aims to reduce the risk of lung infections in patients with cystic fibrosis by determining what protective alterations can be made to their microbiome. Preventing the dissemination of carbapenem-resistant Enterobacterales from healthcare facilities into surface waters in the U.S. The study will evaluate potential discharge of antibiotic-resistant bacteria from hospital sewage and test a technology to prevent it. Randomized controlled trial of Autologous microbiome reconstitution to prevent colonization by antibiotic-resistant bacteria A study in which stool will be collected from patients before they go to nursing homes. The stool will be re-administered to the patients after they receive antibiotics to restore their microbiomes and prevent drug-resistant infection. A randomized controlled trial of encapsulated fecal microbiota for vancomycin-resistant Enterococcus decolonization A study of fecal microbiota transplantation administered as a capsule to decolonize

patients with Vancomycin-resistant Enterococcus (VRE). Doctor-patient communication Researchers will study doctor-patient communication in acute care visits, including communications that may include educating patients about antibiotics. A comprehensive study of multidrug-resistant determinants and drivers in the fungal pathogen Candida glabrata A study to better define the genetic mechanisms and drivers fueling the emergence of drug-resistant fungal infections and validate a new diagnostic platform to rapidly identify resistant strains of Candida glabratra in the clinic and community. Unlocking the microbial ecology of environmental antibiotic resistance Researchers will target adapting molecular tools to improve understanding of the role of microbial communities in antibiotic resistance in the environment. A longitudinal assessment of the resistome among patients treated with intravenous-administered ceftriaxone The project will explore how selective pressure in the form of intravenous-administered ceftriaxone excreted into the gastrointestinal tract may lead to the emergence of antibiotic resistance in the gut microbiome, and whether specific intervention from SYN-004 (ribaxamase), the Company's clinical-stage beta-lactamase designed to protect the gut microbiome, may prevent the emergence of antibiotic-resistant organisms in the gut microbiome. Challenges and facilitators to standardized measurement of infections related to C. difficile and multidrug-resistant organisms in nursing homes The project will identify challenges and facilitators to implementing standardized measurement of C. difficile and other multidrug-resistant organism events in nursing homes. Resistance and genetics of community-acquired foodborne urinary tract infections The project will study the role of retail food as a potential source of multidrug-resistant Escherichia coli that cause community-acquired urinary tract infections among college-age women. A multifaceted intervention to improve prescribing for acute respiratory infection The project will evaluate behavioral approaches, audit and feedback, and peer-to-peer comparisons to reduce unnecessary antibiotic prescribing among physicians for adult and pediatric patients who come to

emergency departments and urgent-care centers with respiratory infections. Metagenomic shotgun sequencing to detect colonization, invasion, and transmission of multidrug-resistant organisms Investigators at Cincinnati Children's Hospital will use new methods to analyze the microbiome to precisely monitor colonization, infection, and transmission of multi-drug resistant bacteria. Improving antibiotic stewardship in long-term care through the UTIDecide Electronic Clinical Decision Support A project studying the use of an electronic clinician decision support tool to improve antibiotic use for urinary tract infections in nursing home patients. Nitric oxide releasing ultra-low fouling antibacterial intravascular catheters Researchers will be developing next-generation coatings to combat antibiotic-resistant bacteria in medical devices. Implementation of a C. difficile infection reduction bundle in acute care hospitals: Feasibility and pilot to guide a multicenter stepped wedge cluster trial A project to implement and assess a prevention bundle for C. difficile infection in acute care hospitals. Longitudinal impact of prophylactic antibiotic use on the gut microbiota in human populations The study will work to determine how the microbiome of surgery patients are impacted by antibiotics used before, during, and after orthopedic surgery. Detection and prognosis of colonization by Extended-spectrum Beta-lactamase (ESBL) producing Enterobacterales The project will develop of a diagnostic test to detect colonization and domination of the microbiome with ESBL-producing bacteria. Genomic insights into the origin and spread of antibiotic resistance in nursing homes The project seeks to apply genome sequencing to understand how antibiotic resistance spreads within and between healthcare facilities. Patient hand hygiene initiative A study on how improving hand hygiene of patients could prevent patients from becoming colonized or infected with drug-resistant bacteria. Preventing spread of carbapenem-resistant Enterobacterales among veterans through an automated tracking system An effort to develop and use a carbapenem-resistant Enterobacterales patient registry in the Veterans Affairs hospital system. Stool microbiome features to discriminate C. difficile

colonization and infection The study will apply microbiome analysis to define stool bacterial community types in patients who are colonized or infected with C. difficile in order to better understand non-C. difficile microbes, with the hope of improving our ability to diagnose, treat, and prevent C. difficile infection. Respiratory tract microbiome composition and risk for antibiotic-resistant lower respiratory infection during long-term acute care The study will comprehensively characterize respiratory tract microbiome composition and change during the course of prolonged mechanical ventilation in order to define bacterial community features associated with hazard for lower respiratory tract infection, particularly lower respiratory tract infection due to antibiotic-resistant pathogens. Targeted Reduction of Antimicrobials for Prevention of C. difficile Infection (TRAP-CDI) The study aims to compare the effectiveness of two antimicrobial use strategies for prevention of C. difficile infection in the hospital setting and to better understand the attitudes, social norms and beliefs of healthcare providers about C. difficile infection and antimicrobial stewardship. Impact of human and food animal wastes on antimicrobial gene abundance and Escherichia coli susceptibility patterns: A watershed approach The use of advanced genetic analyses to investigate how the spread of antibiotic-resistant genes in a river system is influenced by discharges of antimicrobials and human and animal wastes. Assessing the risk of acquisition of Carbapenemase-producing Enterobacterales from exposure to contaminated wastewater premise plumbing The study aims to understand the risk to patients posed by sink drains contaminated with drug resistant bacteria. Development of NHSN's AUR data and SAAR to support antibiotic benchmarking program among Vizient members The project will identify how to create and deliver antibiotic use data reports to hospitals. It will identify aspects of compelling reports that best help hospitals address inappropriate prescription practices. Enduring effects of early life antibiotic therapy on microbiota development and antibiotic resistance gene carriage in the preterm infant gut Investigators will research the long-term effects of early-life antibiotic therapy on

microbiota development and how that affects the mobility of antibiotic-resistances genes in the preterm infant gut. Prospective study characterizing fecal microbiome disruptions during and after receipt of antimicrobials The study will characterize the extent and duration of microbiome disruptions observed during and after usual courses of antimicrobials used to treat community-acquired pneumonia. Intestinal Metabolomic Factors affecting Clostridium difficile Colonization and Infection The study will lead a group of clinicians, chemists, and mathematicians to identify how diet, metabolism, and intestinal microbes interact to protect against C. difficile infection. Identification of microbial disruption indices predictive of colonization by multidrug-resistant Pseudomonas aeruginosa The study will track the microbiome of patients in intensive care units over time to predict risk of infection of multidrug-resistant Pseudomonas aeruginosa. CDC supports activities carried out by state and local health departments, partners, and investigators to combat antimicrobial resistance. CDC supports most of these activities through the Antimicrobial Resistance (AR) Solutions Initiative, and leverages investments from successful programs across the agency for maximum efficiency. These activities are funded through different mechanisms, some of which are listed below. CDC funding solicitation and award announcements change from year to year. Visit FedBizOpps to find current opportunities and exact deadlines throughout the Federal Government. Find the latest CDC antimicrobial resistance activities by state on the AR Investment Map. Antimicrobial resistance happens when germs like bacteria and fungi can defeat the drugs designed to kill them. Languages Language Assistance Languages Language Assistance