Animal Health (National Program 103) Annual Report for 2013

Introduction

Vision: The vision for ARS animal health research is to be a worldwide leader that delivers effective solutions to prevent and control animal diseases that impact agriculture and public health.

Mission: The mission of the Animal Health National Program (NP 103) is to conduct basic and applied research on selected diseases of economic importance to the United States livestock and poultry industries. The goals of the research mission are to produce knowledge and technology to reduce economic losses from infectious, genetic, and metabolic diseases. Cyril G. Gay and Eileen L. Thacker, National Program Leaders (NPL), Animal Health, manage the program.

The Animal Health National Program initiated the current five-year national program cycle Fiscal Year (FY) 2013. The Animal Health National Program currently includes 45 core research projects currently supported by 98 scientists located at 11 research sites throughout the country. The ARS research budget for the Animal Health Program FY 2013 was $61,917,200, reduced from $67,643,000 FY 2012.

The following scientists in NP 103 received prominent awards in 2013:

Oustanding Cross-Agency Team Award, Foreign Agricultural Service

Luis Rodriguez, Foreign Animal Disease Research Unit, Plum Island Animal Disease Center, Orient Point, New York, in recognition for outstanding collaboration in enhancing agricultural productivity and improving food security while opening markets to U.S. agricultural products in Pakistan.

Honor Award from the Secretary of Agriculture.

Mary Pantin-Jackwood, David Suarez, Erica Spackman, Patti Miller, David Swayne, Suzanne Deblois, Mark Freeman, Diane Smith, Scott Lee, Tim Olivier, and Kira Moresco, Southeast Poultry Research Laboratory, Athens, Georgia, and Amy Vincent, Kelly Lager, Alicia Janas-Martindale, and Leo Koster, National Animal Disease Center, Ames, Iowa, for outstanding group effort on preparedness activities for the H7N9 outbreak in China. The Secretary’s Honor Awards (SHA) are the most prestigious Departmental awards presented by the Secretary and recognizes exceptional leadership, contributions, or public service by individuals or groups who support the mission/goals of the United States Department Agriculture (USDA).

Research Results*:*

The following section of the report summarizes high impact research results addressing objectives in the current national program action plan.

H7N9 outbreak in China: Animal investigations and U.S. animal health preparedness activities

On March 29, 2013, the Chinese Center for Disease Control and Prevention completed laboratory confirmation of three human infections with an avian influenza A(H7N9) virus not previously reported in humans. By April 26, 2013, reports from the China Ministry of Agriculture indicated that the H7N9 virus had been confirmed in chickens, ducks, pigeons (feral and captive), and environmental samples in four of the eight provinces and in the Shanghai municipality, confirming that the source of human infections were poultry markets. The USDA set up a Situational Awareness Coordination Unit with a core team of subject matter experts and other USDA representatives, including the Animal and Plant Health Inspection Service (APHIS), the Agricultural Research Service (ARS), the Food Safety and Inspection Service, and the Foreign Agricultural Service. USDA and CDC worked collaboratively to understand the epidemiology of H7N9 infections among humans and animals in China. To date, there is no evidence of this strain of avian influenza A(H7N9) virus has entered the United States. ARS scientists at the Southeast Poultry Research Laboratory, Athens, Georgia, and the National Animal Disease Center, Ames, Iowa, rapidly conducted animal studies to characterize the virus pathogenicity and transmission properties of this virus in avian and swine species. Results from studies performed on poultry and pigs in ARS high-containment facilities indicated that chickens and quail showed no signs of illness but were shedding avian influenza A (H7N9) virus. Pigs infected with the H7N9 virus on the other hand did not amplify or shed the virus. This information was considered critical to prepare first responders in case this new and emerging virus reached the United States. ARS scientists also rapidly developed new diagnostic tests to ensure the virus could be quickly detected, and completed antigenic mapping studies to help identify virus isolates that could be used to develop a vaccine for poultry if needed.

A safe leaderless Foot-and-Mouth Disease vaccine platform with two negative markers for differentiating infected from vaccinated animals

ARS scientists at the Plum Island Animal Disease Center, Orient Point, New York, identified that the lead sequence, if removed, renders the Foot-and-Mouth disease (FMD) virus harmless to animals while still leaving it capable of growing in cell culture. This basic scientific information has contributed to our understanding of how the FMD virus amplifies, interacts with an animal host, evades the host defense mechanism, and how different parts of the virus genome function. Importantly, ARS scientists used this information to produce a new “leaderless” FMD vaccine virus. This vaccine is safer than current FMD vaccine technologies, which use naturally occurring (wild-type) virus, because the leaderless attenuated FMD vaccine virus does not cause disease in animals. This is a major milestone in vaccine technologies in that it will enable the safe production of FMD vaccines, eliminating concerns that FMD vaccine viruses might escape from a manufacturing plant and cause an FMD disease outbreak. This will be especially beneficial for FMD-free countries like the United States, providing the capability to rapidly manufacture millions of FMD vaccine doses without fear of vaccine virus escapes. In addition, the leaderless FMD vaccine has been genetically modified to include two negative markers to differentiate it from wild-type virus found in animals during a disease outbreak. A patent has been filed for this new technology, which is currently being developed in partnership with a multinational pharmaceutical company.

Complete genome sequences of new emerging Newcastle disease virus strains isolated from China

Five virulent Newcastle disease virus (NDV) strains were isolated from geese in China during 2010 to 2011. The complete sequences of two NDV strains and the sequences of the envelope glycoprotein genes (F and HN) of three other strains were determined. Phylogenetic analysis classified them into a new genotype, designated as genotype XII, which were genetically distinct from genotype VII, the predominant genotype responsible for most outbreaks of Newcastle disease in China in recent years. This is the first report of complete genome sequences of new emerging genotype XII NDV strains isolated from geese in China. This basic scientific information is critical to ensure current molecular diagnostic tests can detect emerging viruses that may migrate from China and pose a threat to the United States.

Complete Closed Genome Sequences of Mannheimia haemolytica Serotypes A1 and A6, Isolated from Cattle

Mannheimia haemolytica is a respiratory pathogen affecting cattle and related ruminants worldwide. *M. haemolytica* is commonly associated with bovine respiratory disease complex (BRDC), a polymicrobial multifactorial disease. ARS scientists at the U.S. Meat Animal Disease Center, Clay Center, Nebraska, and the Center for Grain and Animal Health, Manhattan, Kansas, completed the first two complete closed genome sequences of this important respiratory pathogen of cattle. This genome sequence information will enable the application of a new approach called reverse vaccinology where the complete identification of all the genes will allow the rational design of the next generation of highly effective vaccines.

Efficacy of BVD vaccines against HoBi like viruses

Recently a new group of viruses, known as HoBi like viruses, have been isolated from cattle in Brazil, Italy, and Thailand. HoBi like viruses are related to bovine viral diarrhea viruses (BVDV) and cause very similar diseases in cattle. Introduction of HoBi like viruses into North America could result in significant economic loss by cattle producers. There are no vaccines available for the prevention of infection of cattle by HoBi like viruses. ARS researchers at Ames, Iowa, performed studies to determine if cattle vaccinated using BVDV vaccines would be protected against infection with HoBi like viruses. It was found that cattle vaccinated against BVDV would have little or no protection against infection with HoBi like viruses. This suggests that new vaccines, specific for HoBi like viruses, need to be developed to control this emerging pathogen.

Determination of the genetic basis by which Haemophilus parasuis causes disease and development of more efficacious vaccines

Haemophilus parasuis is a bacterium that causes Glässer's disease in swine, a disease characterized by chronic debilitation and often death that costs the swine industry millions in losses annually. However, not all strains of the bacterium cause disease. To date, little is known about genetic differences among *H. parasuis* strains and the genetic factors that contribute to its ability to cause disease. ARS scientists at the National Animal Disease Center in Ames, Iowa, identified 10 strains of *H. parasuis* with varying ability to cause disease and then determined the DNA genomic sequence of these strains. Comparative genomic analysis of the different strains has identified several significant differences that likely contribute to the variability in disease caused by these strains. Subsequent studies have demonstrated that strains that don't cause disease can be used as vaccines against strains that do and are leading to improved vaccines against *H. parasuis* for pigs.

Development of a Brucella suis vaccine for feral swine

USDA continues to work to control brucellosis since it initiated an eradication program in the 1950's. However, persistence of Brucella in wildlife reservoirs (bison, elk, and feral swine) poses a risk for reintroduction to domestic livestock. New vaccines and diagnostics that can be applied to wildlife are needed. Brucellosis is not currently a problem in domestic swine. However, Brucellosis is common in the millions of feral pigs present in the United States. Surveillance has shown that up to 35% of some herds of feral pigs can be positive for Brucella. In addition, transmission from infected feral pigs, which shed the organism in their urine to cattle, has resulted in dairy herds in the South Eastern United States becoming positive for Brucella. Recent work by ARS scientists at the National Animal Disease Center, Ames, Iowa, has developed an experimental vaccine that has been shown to be protective against brucellosis in feral swine when administered orally or parentally. More work needs to be done to determine the optimal dose and efficacy data; however, this vaccine shows promise to reduce the risk of Brucella infection to humans and domestic livestock from feral swine.

Elimination of persistent infection and transmission risk following the re-emergence of Theileria equi in the United States

Theileria equi is a tick-borne disease of horses that can cause severe acute disease characterized by fever, anemia, hemoglobinuria, and in some cases death. Infected horses that recover from the acute disease become persistently infected for life. Disease caused by *T. equi,* called piroplasmosis, has been eradicated from the United States. In 2009, an outbreak of piroplasmosis occurred in Texas. Until recently, horses diagnosed with piroplasmosis were either euthanized or quarantined for life due to the persistence of infection. ARS scientists in Pullman, Washington, developed a treatment regimen using imidocarb dipropionate to eliminate *T. equi* from naturally infected horses and removed the risk of transmission of the pathogen to other horses. This allowed the horses to resume their previous lives and has facilitated international movement of horses between piroplasmosis infected countries and non-infected regions.

Determining the protective mechanisms for resistance and protection immunity to helminth infection in ruminants

Parasites are important economically to the cattle industry. Recently, it has been determined that many helminthes (internal parasitic worms) have increasingly become resistant to current drug control strategies. Understanding the protective mechanisms is critical to develop new strategies to control internal parasites. ARS scientists at the Beltsville Agricultural Research Center Laboratories, Beltsville, Maryland, characterized the transcriptome of parasite-resistant cattle using high-throughput technology. They identified cellular networks and biological pathways related to parasite resistance. In addition, three antimicrobials were identified that are likely involved in regulating host-parasite interactions. This information provides important insights into the immune regulation of host-parasite interactions and molecular mechanism of host resistance in cattle. This information facilitates applied breeding for parasite resistant animals and potentially vaccines that may confer protection against parasites.

Genome Sequencing of Ovine Isolates of Mycobacterium avium subspecies paratuberculosis provide insight into host association

Paratuberculosis (Johne's Disease) is a chronic progressive enteric disease characterized clinically by chronic or intermittent diarrhea, emaciation, and death. Johne's disease has worldwide distribution and economic impact on ruminant livestock production. The host responses to *Mycobacterium avium* subspecies *paratuberculosis* (MAP) are complex, so understanding the host-pathogen interactions will allow the development of new diagnostic tools and intervention strategies. Recent research by ARS scientists at the National Animal Disease Center, Ames, Iowa, found that goats and sheep are susceptible to MAP infection. Results of genome sequencing showed significant differences in the genome of cattle and sheep isolates of MAP. Using next-generation sequencing technology combined with optimal mapping, additional novel regions of difference between cattle and sheep MAP were determined. Tracking these differences allows understanding of differences in pathogenesis of Johne's disease between the two host species. This work will facilitate development of improved diagnostic assays more aligned with specific ruminant species that could have worldwide relevance in identifying infected animals and preventing production losses.