REPORT OF THE COMMITTEE ON BLUETONGUE AND RELATED ORBIVIRUSES

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The Committee met on October 3, 2010 at the Adams Mark Hotel, Buffalo, New York, from 1:00 – 5:20. There were 20 members and 17 guests present. James Maclachlan and William Wilson, Chairperson and Vice-chairperson, respectively, introduced the meeting. There was discussion of the previous year's resolution that the USAHA support efforts to remove the serotypes of BTV that have been identified since 1998 in the Southeastern United States from the Department of Homeland Security's select agent list.

Presentations

An update on Bluetongue in Europe 2011: Vaccines, reassortants and new serotypes

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Although bluetongue virus is distributed around the world, not all of the 26 serotypes are found in each geographic region. This has led to the proposal that different BTV strains have adapted, in order to be transmitted by their local *Culicoides* vector species and there may therefore be genetic factors that limit the emergence and spread of 'exotic' BTV strains. However recent events have demonstrated that BTV can emerge into new geographic regions, with multiple exotic strains detected in the USA, Australia and for the first time across the whole of Europe.

Sequencing and molecular epidemiology studies have provided evidence for the existence and/or introduction of different BTV strains into Europe, almost every year since 1998, including serotypes 1, 2, 4, 6, 8, 9, 11, 16 and an entirely novel serotype BTV-25. These viruses which belong to both eastern and western topotypes have entered Europe via at least four distinct routes: from the east into Greece; from North Africa into Italy and the western Mediterranean islands; From Morocco into Iberia, and (via an unknown mechanism) from sub-Saharan Africa directly into northern Europe.

Most of these strains were transmitted and became established in the Mediterranean region where the local distribution of *C. imicola* suggests that it represents the primary vector. Indeed most of the BTV strains that have entered Europe failed to spread out of this zone. However BTV-1, BTV-6 (vaccine strain), BTV-11 (vaccine strain) and most notably BTV-8, which belongs to a western topotype, were all transmitted successfully in northern Europe, beyond the range of *C. imicola.* This indicates the presence of alternative vector species, possibly members of the *C. obsoletus* and *C. pulicaris* groups that are abundant in most of Europe. BTV has recently been isolated from adults of both species suggesting their potential for direct involvement in BTV transmission and highlighting the risk that exists for further spread of BTV into central and northern Europe. BTV-9 also spread to the Balkans, beyond the range of *C.imicola*, but failed to reach northern Europe, suggesting that other vectors, or other environmental, climatic or geographic factors may be involved in the spread of these viruses.

The northern European outbreak caused by BTV-8 was first detected in August 2006 in the Maastricht region of the Netherlands, as a result of clinical signs of the disease in sheep.

Subsequent investigations have indicated that it probably started in Belgium a few weeks earlier. The virus also spread at a low level into Germany, northeast France and Luxemburg. The initial source of the infection and its route of arrival into the region are unknown. However, 2006 was the hottest summer on record in northern Europe with temperature in Maastricht up to 6.5 degrees hotter than previously recoded. The outbreak was initially quite mild and was primarily spread in cattle. Belgium only lost approximately 100 sheep to the BTV-8 outbreak in 2006. The BTV-8 virus survived through the winter reappearing from May 2007 onwards in many locations across the region that had been affected in 2006. This was despite the absence of detectable cases of transmission during the winter, and resulted in a continuation of the outbreak that was far more severe than in the first year. During the late summer Belgium alone lost over 20,000 animals killed by the disease (mainly sheep) with case fatality rates of ~30%. This represents ~ 20% of the national flock.

Severe clinical disease was seen in sheep with high levels of case fatalities. Cattle were also affected with a low level of fatalities but more significant losses in productivity, including abortion, stillbirth and teratogenic effects. most notable of these is the dummy calf syndrome, where development of the cerebral hemispheres was completely inhibited (Wouda et al 2008) .

During 2007-8, approximately 30% of calves born to cows that had been infected with BTV-8 during pregnancy in the UK, were also infected in *utero* and were PCR positive for BTV at birth. This may provide a possible overwintering mechanism for the virus.

During 2007 the second year of the BTV-8 outbreak In Germany, was over 100 times more severe than in 2006. Massive levels of infection were detected in during the early part of 2008 (with >2033 infected farms), reflecting transmission during the late 2007. However in the later stages of 2008, there was clear evidence for a 'burn-out' zone with very few cases, simply because most of the surviving animals were now immune.

There was also an explosion of BT outbreaks in other Northern European countries including the first ever spread of the virus to the UK during August (first detected in September 2007) France reported ~20,000 new farms infected with BTV-8 during 2008 year and ~2000 farms with BTV-1 (mainly in the south-west). There were also 54 animals (8 farms) detected with both BTV-1 and 8 giving an opportunity for the exchange (reassortment) of genome segments, and emergence of novel virus strains, containing genome segments from both parental strains.

There appeared to be ~ 4 years to the BTV-8 outbreak in Europe: Year 1 - low level initial spread (mainly in cattle), low mortality; Year 2 - high level spread in cattle and sheep very severe, with most deaths occurring in this 2nd year; Year 3 - most animals had been exposed at this stage and had already sero-converted, so there were fewer susceptible animals and fewer cases; Year 4 - fewer sources of infection remain (due to lower levels of infection in year 3) and most animals were still immune. This provides an opportunity for eradication, and perhaps explains why some outbreaks (e.g. those in Greece) had been self-limiting within 4-5 years.

By vaccinating against BTV-8 UK authorities hoped to go directly from the first to the last of these 4 years, without the major losses seen on mainland Europe during 'year two'. During 2008, vaccination with the inactivated BTV-8 vaccines was completely successful in the UK, with no further insect transmitted cases being detected. Indeed the vaccination campaigns against BTV-8 (and BTV-1) were spectacularly successful across the whole of Northern Europe with France dropping from 38,000 cases in 2008 to 83 in 2009 and only a single case in 2010. Northern Europe now appears to be free of BTV, although vaccination has now largely stopped and there is a high turnover in ruminant animals (approximately 20% per year) which will restore the naïve animal population within a few years. Although the European BTV-8 may be gone from the North, it was also spread to southern European countries and to Israel. Events in Europe highlight the capability of local *Culicoides* populations to transmit BTV and indicate a risk of further outbreaks.

Although live attenuated vaccines had previously been used to combat multiple BTV types in Southern Europe (as the only vaccines then available) and they had helped prevent clinical disease in the vaccinated animals, these live viruses had also contributed to the genetic pool of BTV in the region, leading to both onward transmission and reassortment with field strains. There is also evidence that the live vaccines could cause a certain level of clinical diseases in fully naïve animals, although experience in the field suggest that this may be reduced in animals that already have some immunity to other serotypes.

Further threats and reassortants

The outer surface of the BTV capsid is composed of two proteins, VP2 and VP5 (which are encoded by Segments 2 and 6 [Seg-2 and Seg-6] of the BTV genome). These proteins have evolved to escape recognition by host antibodies and are therefore more variable than the other virus proteins. Sequence analysis of Seg-2 / VP2 show that they control BTV serotype and have provided a basis for molecular epidemiology studies, as well as new generations of diagnostic assays by conventional and real-time RT-PCR. 24 distinct clades of Seg-2 were detected that correlate perfectly with virus serotype (Maan S, et al 2008). Molecular comparisons of Seg-2 can therefore be used to identity BTV serotype more rapidly and more accurately than by conventional serological methods. These techniques, which now form the primary diagnostic assays for BTV serotype, were originally used to identify the exotic strains that have spread into Europe and the USA. These studies have also provided a basis for the identification of two novel BTV types: BTV-25 (from goats in the Toggenburg region of Switzerland, and adjoining regions of Germany and Italy) and BTV-26 (from sheep in Kuwait).

BTV-4 has been endemic in Recent Morocco and Spain for several years but unlike BTV-1 failed to spread to northern Europe. However recent reports indicate that recent strains of BTV-4 from Morocco in 2009/2010 have an increased virulence in cattle. Full genome sequence analyses of BTV-1, 4 and 8, show that the latest Moroccan strain of BTV-4 is a reassortant containing only three of the original genome segments from the earlier BTV-4, with the remaining segments from BTV-1 and 8 (both of which had previously spread to northern Europe). It is considered possible that this new strain of BTV-4 may therefore have acquired the ability to spread, and could potential pose as new threat to northern Europe. The ability of these viruses to grow in *Culicoides* vectors is currently being assessed.

Conclusions

- The use of inactivated vaccines helped to eradicate BTV-1 and 8 from Northern Europe
- However, once the naïve population has been restored, a future introduction of BTV may cause a new outbreak.
- The use of live vaccines in Southern Europe protected against clinical disease but did not eradicate the virus, contributing to virus transmission and reassortment (new strains)
- Most BTV strains in southern Europe did not spread north (including BTV-4), possible due to an inability to be transmitted by northern European vectors?
- The reassortment of BTV-4 with BTV-1 and BTV-8 in Morocco and Southern Spain has generated new strains that may represent further threats to Northern Europe.
- Better molecular typing assays is identifying new serotypes (including BTV-25 and 26).
- The threat to Europe remains from further BTV incursions and outbreaks caused by other orbiviruses and other arboviruses

Acknowledgements

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References:

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USDA APHIS bluetongue surveillance activity

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The US Department of Agriculture has developed a Climate Change Science Plan and encouraged its member agencies to identify approaches to better understand the effects of climate change on natural and managed ecosystems specifically mentioning the surveillance of pests and disease including epidemiological characteristics. The plan also encourages the development of science based information and tools.

APHIS Veterinary Services has chosen to analyze existing bluetongue and EHD virus related data to determine if there are climate related factors that are affecting the distribution of those diseases in the United States. We are utilizing a data set that has been aggregated over the last 30 years and have had good cooperation from agencies that have collected the information.

We intend to analyze the distribution of virus/vector as evidenced by positive isolations of blue tongue or EHD virus to determine if temporal distribution trends exist and then utilize various analysis techniques to determine possible associations with climatic or environmental characteristics. The results of the analysis should indicate if sufficient data is available to identify trends or if additional surveillance for disease or vectors is necessary. If sufficient, and associations with climatic and environmental characteristics can be established, recommendations for periodic monitoring of the associated characteristics will be made as an additional method for pre-emptive awareness of the potential for increased spread of these diseases.

Anthropogenic and metereological drivers of BTV infection in California

Christie Mayo

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Bluetongue is an economically important arboviral disease of ruminants that is transmitted by hematophagous *Culicoides* midges. In light of dramatic recent changes in the

global distribution of bluetongue virus (BTV), the goals of this study were to re-evaluate the prevalence of BTV infection of cattle, abundance of *Culicoides* midges, and BTV infection rates of *Culicoides* midges on individual dairy farms in California. A serosurvey of adult dairy cattle confirmed that BTV infection is prevalent throughout much of the state, although the coastal northwestern region remains free of infection and prevalence varies markedly among farms in the remainder of the state. Intensive entomological sampling was performed for one year on 4 farms in the northern Central Valley of California using three trapping methods (CO_2 traps with UV light, CO_2 traps without UV light, animal baited aspirations). The entomological surveillance showed that the abundance of *Culicoides* midges was markedly different and coincided with the prevalence of BTV infection of sentinel cattle on each farm. Mean maximum and minimum temperatures and other meteorological parameters were similar on all 4 farms, thus we speculate that particular management practices were responsible for both the increased midge abundance and prevalence of BTV infection of cattle at individual farms. Specifically, it is concluded that variation in vector abundance at individual farms most likely is the result of lagoon waste-water and irrigation management practices, leading to higher BTV infection rates among livestock held on farms with more waste-water lagoons and greater acreage of land for waste-water application.

The second portion of this project was to examine the seasonal BTV infection rates of *C. sonorensis* midges to develop estimates of risk for BTV transmission to sentinel cattle at each farm. BTV infection rates were remarkably lower amongst female *C. sonorensis* midges collected by CO_2 traps with UV light than among midges collected by either animal- baited aspirations or in CO_2 traps without light. Analysis of BTV-infected midges using serotype-specific quantitative reverse-transcriptase polymerase chain reaction (qRT-PCR) assays confirmed that BTV serotypes 10, 11, 13 and 17 are all present in the region, but that midge infection rates and the number of BTV serotypes circulating differed markedly among individual farms. Furthermore, more serotypes of BTV were present in midges than sentinel cattle at individual farms where BTV circulated, and the virus was detected at each farm in midges before it was detected in cattle. Findings from this study confirm the importance of using sensitive surveillance methods for both midge collection and virus detection in epidemiological studies of BTV infection, which is especially critical if the data are to be used for development of mathematical models to predict the occurrence of BTV infection of livestock.

Improving surveillance of *Culicoides sonorensis* with more efficient light traps

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In North America, *Culicoides sonorensis* is thought to be the main disease vector of Bluetongue and Epizootic hemorrhagic disease viruses. Surveillance for *Culicoides* is predominantly conducted with light traps baited with carbon dioxide and ultraviolet light. However, laboratory studies have not been conducted to determine the optimal wavelength or color of light that is maximally attractive. *Culicoides sonorensis* photo attraction was evaluated using a cloverleaf arena illuminated by visible and ultraviolet light from LEDs. Light intensities were equalized for red, green, blue and ultraviolet LEDs before testing. More *Culicoides* were attracted to the UV light than the other three colors, which confirmed field experiments, and past *Culicoides* trapping experience. However, these experiments also reviled interesting perturbations to the UV attractions trend based on narrow UV wavelength analysis, unequal light intensities, and insect physiological state. In summary, ultraviolet light is maximally attractive to *Culicoides* and remains the best visual attractant in light traps for surveillance and insect monitoring purposes.

Whole genome sequence analysis of field strains of bluetongue virus

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The Arthropod-Borne Animal Diseases Research Unit (ABADRU) has adapted the published single primer ligation - whole genome amplification protocol that allows the whole bluetongue and epizootic hemorrhagic disease virus genome to be amplified without prior sequence knowledge and submitted to high-throughput DNA sequencing. This technology was applied to bluetongue virus serotype 3 isolates from Florida, Arkansas, Mississippi, Central American and the Caribbean basin. Although the dataset is not complete the analysis is consistent with hypothesis that these viruses were introduced from the Central America and the Caribbean basin. There was also evidence of gene reassortment among US serotypes with the newly introduced virus serotypes. At this time, the newly introduce serotypes of Bluetongue have been isolate only in the South Eastern United States.

Increased incidence of EHDV in Texas

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Texas' current drought is the most severe one-year drought on record. August 2011 was the hottest month in Texas history. The average temperature was 88.1 F (31.2 C), breaking the previous record of 87.1 F (30.6 C) set the month before. In San Angelo, Texas, the record for warmest month was set three times in three months from June to August, according to the National Weather Service. June to August was the driest summer on record, with only 2.44 inches of precipitation. The Epizootic Hemorrhagic Disease (EHD) cases from 2009 consisted of the three circulating serotypes of the virus 1, 2, and 6 as determined by RT-PCR. In 2010 and 2011 an increase in EHD cases have been confirmed as EHD.

Pathogenesis of BTV-8 in white-tailed deer

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World-wide there are at least 26 serotypes of bluetongue virus (BTV), a complex non-enveloped virus in the family Reoviridae, genus *Orbivirus*. Bluetongue (BT) is an arthropod-borne disease of cattle, sheep, goats, and deer and is transmitted by *Culicoides* biting midges. In 2006, bluetongue serotype 8 (BTV-8) invaded north-western Europe resulting in the largest BT outbreak ever recorded. This BTV strain differs from other BTV strains in many aspects; competent vector(s), transplacental and oral transmission, and severity in cattle. In the U.S., white-tailed deer (*Odocoileus virginianus*) are the sentinel wildlife species for re-emerging BT outbreaks of our domestic serotypes (BTV-2, 10, 11, 13, 17). To determine their susceptibility to the European strain of BTV-8 BTV-seronegative deer were inoculated with IAH-collection BTV-8 NET2007/01. Two deer were sham inoculated to serve as uninfected controls and housed with infected animals to verify the inability of this virus to spread by direct contact transmission. Body temperatures and clinical signs were recorded daily. Peak clinical disease was seen between 8-15 days post inoculation and included fever, upper and lower respiratory distress, swelling of the tongue and

face, oronasal discharge, loss of appetite, lethargy, depression, loss of balance and death. Periodic blood samples, as tested for BTV RNA by real time PCR, were positive by as early as day 3, peaking from 8-12 days, and persisting for up to 28 days when the study was ended. Serum samples, as tested for BTV antibodies by competitive ELISA, showed antibody responses as early as day 8, peaking between 12-21 days with high antibody titers for the duration of the experiment. At the time of necropsy, gross pathology included petechial hemorrhages of the liver, intestinal hemorrhages, and indications of bacterial pneumonia in the lungs. Necropsy tissue samples as tested by real time PCR for BTV RNA, showed a widely disseminated infection including liver, spleen, kidney, adrenal gland, mandibular and mesenteric lymph nodes, lung, heart, and intestine. Results suggest that if BTV-8 is accidentally or intentionally introduced into the U.S., our white-tailed deer would be very susceptible and would serve as significant virus amplifying hosts for subsequent insect transmission to livestock.

USDA/APHIS/VS National Veterinary Services Laboratories

Bluetongue virus (BTV) and epizootic hemorrhagic disease virus (EHDV) isolations/PCR positives

Calendar year 2010

Bluetongue virus or RNA was detected in 11 samples submitted during calendar year 2010. The positive bluetongue virus isolation and polymerase chain reaction (PCR) test results from submissions to the National Veterinary Services Laboratories (NVSL) in 2010 are listed in Table 1.

Table 1. BT virus isolation (VI) / PCR positives, Calendar year 2010

State	*No.*	*Species*	*PCR*	*VI*
CA	4	Cattle	Positive	BTV-10
CA	2	Cattle	Positive	BTV-11
FL	4	Sheep	Positive	BTV-1
FL	1	Deer (SCWDS*)		BTV-12

*Southeastern Cooperative Wildlife Disease Study, Athens, GA

During calendar year 2010, 4 samples tested positive for EHDV by virus isolation and/or PCR. The positive EHDV isolation and PCR test results from submissions to the National Veterinary Services Laboratories (NVSL) in 2010 are listed in Table 2.

Table 2. EHDV isolation (VI)/ PCR positives, Calendar year 2010

State	*No.*	*Species*	*PCR*	*VI*
FL	1	Deer	Positive	EHDV-2
IL	1	Deer	Positive	EHDV-2
LA	1	Deer isolate		EHDV-2
MO	1	Deer	Positive	EHDV-2

Calendar year 2011 (January 1– September 27)

As of 27 September 2011 bluetongue virus has been identified in two samples: BTV-17 was isolated from a cattle blood sample from California and BTV-11 was isolated from North Carolina deer tissue. In the same time period, EHDV-2 was isolated from nine deer tissue samples from the following: Washington DC, Florida (2), North Carolina (2), New York (2), Oklahoma, and South Dakota. EHDV-6 was isolated from one South Dakota deer. EHDV has also been identified by RT-PCR in one additional Florida deer (virus not isolated), two additional North Carolina deer (virus isolation in progress), and one additional New York deer (autolyzed tissue, no virus isolation).

2011 Bluetongue Serology Proficiency Test

Fifty-two laboratories participated in the 2011 bluetongue (BT) proficiency test. The panel consisted of 20 ruminant serum samples. The passing score was zero or one sample missed. Of the 52 laboratories participating in the 2011 BT proficiency test, 50 agreed with each other and with NVSL on the positive/negative bluetongue antibody status of all 20 samples. Two laboratories missed one sample. Laboratories approved to conduct official (export) bluetongue serology are listed on the website: http://www.aphis.usda.gov/animal_health/lab_info_services/approved_labs.shtml

SCWDS Update: Hemorrhagic Disease and *Culicoides* sp. Surveillance

Mark Ruder, Joseph Corn, Daniel Mead, and David Stallknecht
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An overview of epizootic hemorrhagic disease viruses (EHDV) and bluetongue viruses (BTV) isolated by SCWDS during the 2010 and 2011 transmission seasons was presented. During 2010, 14 viruses were isolated from the 85 virus isolation attempts made, representing 21 states and 7 species (59 white-tailed deer, 19 mule deer, 1 key deer, 3 elk, 1 unknown cervid, 1 cow, and 1 sheep). Table 1 lists virus isolates.

During the summer and early fall of 2011, SCWDS has received numerous reports of suspected hemorrhagic disease in free-ranging white-tailed deer populations. As of September 30, 2011, there have been 37 viruses isolated after 84 virus isolation attempts, representing 19 states and multiple species (76 white-tailed deer, 4 mule deer, 2 elk, and 2 unknown cervids). Table 2 lists the viruses isolated thus far in 2011.

In addition, an update on surveys for *Culicoides* species in the Southeastern United States was provided. These surveys have been conducted since 2007 as part of a Cooperative Agreement for Exotic Arthropod Surveillance with USDA-APHIS-VS. Surveys have been conducted in Florida, Georgia, Alabama, Mississippi, Louisiana, Arkansas, and Texas. Survey sites in AR, MS, FL, and TX included premises where historically non-endemic BTV or EHDV serotypes had previously been detected. Contents of light traps are processed and *Culicoides* sp. identified at SCWDS. During November 2007 – September 2011, traps were set for 4,456 trap nights at 224 premises in 111 counties throughout the Southeastern US. A total of 145,121 *Culicoides* biting midges have been recovered from the traps, with 49 species identified to date. Exotic *Culicoides* sp. have not been identified, but identification of most of the insects collected is pending. Possible range expansions of *C. insignis* and *C. alachua* have been detected. Presently, field collections and identification of *Culicoides* sp. collected are underway in Alabama, Florida, and Mississippi and will continue at these locations in 2012.

TABLE 1: A list of the 14 viruses isolated from a total of 85 individual animal submissions made to SCWDS during 2011.

2010 Hemorrhagic Disease Diagnostics
Virus Isolations
Southeastern Cooperative Wildlife Disease Study

STATE	COUNTY	MONTH	SPECIES	VIRUS
ALABAMA	Geneva	Jul.	WTD[c]	EHDV-2
		Jul.	WTD[c]	EHDV-2
	Covington	Jul.	WTD[c]	EHDV-1
		Jul.	WTD[c]	EHDV-1
		Jul.	WTD[c]	EHDV-1
		Nov.	WTD[c]	EHDV-2
ARKANSAS	Jefferson	Aug.	WTD[c]	EHDV-6
FLORIDA	Lee	Jul.	WTD[c]	BTV-12
	Dixie	Sep.	WTD[c]	EHDV-2
MARYLAND	Anne Arundel	Aug.	WTD	EHDV-2
NEW JERSEY	Salem	Sep.	WTD	EHDV-2
NEW MEXICO	Torrance	Oct.	elk[c]	EHDV-2
	Torrance	Sep.	elk[c]	EHDV-2
NORTH CAROLINA	Person	Sep.	WTD	EHDV-2

[c] captive animal
WTD = white-tailed deer

The Arthropod-borne Animal Diseases Unit: research program update and current status
Dr. D. Scott McVey
USDA, ARS, Arthropod Borne Animal Diseases Unit, Manhattan, KS

To accomplish the continuing research mission of the Arthropod Borne Animal Diseases Unit (ABADRU) in solving major endemic, emerging, and exotic arthropod-borne disease problems in livestock, the Unit has completed the move to Manhattan, KS. The ABADRU is one of five units at the Center for Grain and. Animal Health Research (CGAHR). The ABADRU is doing BSL-2 research at CGAHR and has operational cell culture and insectary laboratory units at the Center. The ABADRU has also begun BSL-3 laboratory and animal work at the new Biosecurity Research Institute at Kansas State University. An insect-secure laboratory will be available for animal research projects late in 2011. The ABADRU has three 5-year project plans under two ARS National Research Programs; Animal Health NP103 and Veterinary, Medical, and Urban Entomology NP 104. These plans include research on bluetongue virus (BTV; exotic and domestic), vesicular stomatitis virus (VSV), and Rift Valley fever virus (RVFV). Research progress to date for exotic BTV include a susceptibility study of white-tailed deer with BTV serotype 8 isolate originally isolated in The Netherlands. Research progress to date for RVFV includes vector competence studies, animal infection model studies, production of BSL-2 diagnostic assays including qRT-PCR, ELISA, and immunohistochemistry. The ABADRU has recruited a new research leader and veterinary medical officer (Dr. D.S. McVey), a new field entomologist (Dr. L. Cohnstaedt), a new Molecular Entomologist (Dr. D. Nayduch) and is recruiting an additional veterinary medical officer. The ABADRU continues to have the highest level of funding in its history, thanks to additional funding sources such as Department of Homeland Security, ARS Office of International Research Projects, and the Department of State Biosecurity Engagement Program. Additionally, the lab has the largest number of national and international collaborations in its history, and continues

Committee Business

The Committee did not propose any new resolutions for this year. The Committee recommended an update to their mission statement, to replace “bovine retrovirus” with “related viruses of livestock.” The revised statement reads as follows:

“The purpose of the Committee on Bluetongue and Related Orbiviruses is to assemble scientific data on bluetongue and related viruses of livestock that can be formulated into recommendations for national and international regulatory policies.”