Orbiviruses: A North American Perspective

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Abstract

Orbiviruses are members of the Reoviridae family and include bluetongue virus (BTV) and epizootic hemorrhagic disease virus (EHDV). These viruses are the cause of significant regional disease outbreaks among livestock and wildlife in the United States, some of which have been characterized by significant morbidity and mortality. Competent vectors are clearly present in most regions of the globe; therefore, all segments of production livestock are at risk for serious disease outbreaks. Animals with subclinical infections also serve as reservoirs of infection and often result in significant trade restrictions. The economic and explicit impacts of BTV and EHDV infections are difficult to measure, but infections are a cause of economic loss for producers and loss of natural resources (wildlife). In response to United States Animal Health Association (USAHA) Resolution 16, the US Department of Agriculture (USDA), in collaboration with the Department of the Interior (DOI), organized a gap analysis workshop composed of international experts on Orbiviruses. The workshop participants met at the Arthropod-Borne Animal Diseases Research Unit in Manhattan, KS, May 14–16, 2013, to assess the available scientific information and status of currently available countermeasures to effectively control and mitigate the impact of an outbreak of an emerging Orbivirus with epizootic potential, with special emphasis given to BTV and EHDV. In assessing the threats, workshop participants determined that available countermeasures are somewhat effective, but several weaknesses were identified that affect their ability to prevent and control disease outbreaks effectively.

Key Words: Bluetongue virus—Epizootic hemorrhagic disease—Vector—Vaccine—Diagnostic test—Epidemiology.

Introduction

Bluetongue (BT) and epizootic hemorrhagic disease (EHD) are noncontagious, insect-transmitted diseases of domestic and wild ruminants caused by related but distinct viruses. Both BT and EHD viruses cause hemorrhagic fevers in susceptible ruminants; however, BT is a disease of domestic livestock and certain species of wild ungulates, whereas EHD is principally a disease of wild ungulates. BTV is the prototype member of the genus Orbivirus, family Reoviridae (Mertens et al. 2004). All members of the Reoviridae share distinctive common properties, including segmented genomes of double-stranded RNA (dsRNA) and characteristic noneveloped, icosahedral virion morphology and structure. There are currently two subfamilies and some 16 distinct genera within the family Reoviridae, which includes pathogens of plants, crustaceans, fish, insects, reptiles, and mammals, including humans (King et al. 2012).

Some 22 distinct virus species of serogroups are within the genus Orbivirus, including BT virus (BTV) and EHD virus (EHDV). To date, 26 distinct serotypes of BTV have been described that all share common group antigens but are distinguished on the basis of serotype-specific virus neutralization assays (VNTs); at least seven serotypes of EHDV have been identified (Hofmann et al. 2008, Maan et al. 2011a, b, Savini et al. 2011). Variation among field strains of BTV, even those of the same serotype, is considerable, which reflects differences in the nucleotide sequence of each of the 10 distinct dsRNA segments of the BTV genome (Bonneau et al. 1999, Pritchard et al. 2004a, b, Balasuriya et al. 2008, Maan et al. 2010, Maan et al. 2012, Shirafuji et al. 2012, Shaw et al. 2013, Legisa et al. 2013). Genetic heterogeneity of field...
strains of BTV occurs as a consequence of both genetic drift and genetic shift, the latter as a result of reassortment of viral genes during mixed infections of either the vertebrate or invertebrate hosts of the virus (Bonneau and MacLachlan 2004, Coetzee et al. 2012a, b, Shaw et al. 2013). Variation in the sequence of individual genes occurs through a complex process of genetic drift and founder effect during alternating passage of BTV in its ruminant and insect hosts (Bonneau et al. 2001). These phenomena are also complicated by salivary gland and midgut barriers to infection and transmission by vector midges. Although less well characterized, similar variation also likely occurs among field strains of EHDV (Cheney et al. 1995, Cheney et al. 1996, Savini et al. 2011).

BT is principally a disease of certain breeds of sheep, although disease sporadically occurs in cattle and some species of wild non-African ruminants (Verwoerd and Erasmus 2004, MacLachlan et al. 2009, Verwoerd 2012). Epizootic hemorrhagic disease is principally a disease of deer, especially white-tailed deer, although disease sporadically occurs in other wildlife ruminant species and cattle (Hoff and Trainer 1978, Odiawa et al. 1985, Savini et al. 2011). Orbivirus infection of ruminants occurs throughout much of the temperate and tropical regions of the world, coincident with the distribution of specific species of hematophagous Culicoides (Diptera: Ceratopogonidae), biting midges that are the biological vectors of the viruses (Gibbs and Greiner 1994, Tabachnick 2004, Tabachnick 2010, MacLachlan 2011). BT typically occurs when susceptible sheep are introduced into areas where virulent strains of BTV circulate, or when virulent strains of BTV extend their range into previously unexposed populations of ruminants.

The global distribution of BTV generally has been between latitudes of approximately 40–50°N and 35°S. BTV was spread transiently into southern portions of Mediterranean Europe during the 20th century, but since 1999, multiple serotypes have invaded and spread throughout extensive portions of the continent, penetrating farther north than previously documented (Mellor and Leake 2000, Gomez-Tejedor 2004, Mellor et al. 2008, Rodriguez-Sanchez et al. 2008). During the recent European BTV-8 epizootic, for example, the virus spread throughout Western Europe (Purse et al. 2005, Toussaint et al. 2006, Purse et al. 2008, Wilson and Mellor 2008, Guis et al. 2012).

The global epidemiology of EHDV infection is less precisely defined than that of BTV, but the global range of EHDV is predicted to occur between latitudes 35°S and 49°N, coincident with the distribution of competent biting midge vectors (Savini et al. 2011). Unlike BTV infection, EHDV has not been described to date in Europe, although the virus occurs throughout extensive portions of Asia, Southeast Asia, Australia, Africa, and the Americas (Savini et al. 2011). BT has been recognized in the United States since at least the late 1940s; BTV serotype 10 (BTV-10) was first isolated and characterized in California during the early 1950s (McKercher et al. 1953), and BTV-11, -13, and -17 were identified later (Barber 1979). BTV-2 was first reported in Florida in 1982, and since 1998, some 10 additional serotypes of BTV have been isolated in the southeastern United States (Gibbs et al. 1983, Collisson et al. 1985, MacLachlan 2011). BTV-1 was detected in the southeastern United States in 2004 from a white-tailed deer isolate (Johnson et al. 2006). Additionally, BTV-2, which was long considered to be confined to the extreme southeastern United States, was recently isolated from cattle in California (Mecham and Johnson 2005, MacLachlan et al. 2013, Gaudreault et al. 2014). In a similar manner, EHDV-1 and -2 also have been present in the United States since the 1950s, but new serotypes (EHDV-6) have been introduced as recently as 2006 (Allison et al. 2010). The continual risk of virus introductions into areas with naïve livestock and wildlife populations, as well as the expanding distribution of the Culicoides vector into northern latitudes due to warming climates, makes BT and EHD a constant threat to livestock producers.

Both BTV and EHDV are considered animal pathogens worldwide, and new viral strains are continuously emerging that may cause severe disease outbreaks; however, not every susceptible animal species will show disease following infection with all strains of these viruses. The differences in clinical outcomes depend on the susceptibility of animal hosts and on the pathogenic potential of strains of the viruses. Hence, the World Organization for Animal Health (Office International des Epizooties, OIE) pragmatically defines cases of BTV and EHDV as infection with these viruses, with or without clinical signs. The basis of differences in species susceptibility is not known and virulence determinants of Orbiviruses are not described. Comprehensive disease control strategies will require investing in basic research to determine these unknown aspects of the virus–host interaction.

The viruses that cause BT and EHD are also of concern to livestock producers in North America because of: (1) The repeated and consistent emergence of new serotypes of unknown virulence, (2) increased reports of clinical disease in cattle, and (3) increased spread and adaptation to new geographical areas. Accordingly, the United States Animal Health Association (USAHA) passed Resolution 16 in October of 2012 requesting the United States Department of Agriculture (USDA) and the United States Department of Interior (DOI) to organize a diverse panel of experts, including industry stakeholders, university and federal researchers, and federal and state regulatory agency representatives, to determine research needs and identify and prioritize intervention strategies.

In response to USAHA Resolution 16, USDA, in collaboration with DOI, organized a gap analysis workshop composed of international experts on Orbiviruses. The workshop participants met at the Arthropod-Borne Animal Diseases Research Unit in Manhattan, Kansas, May 14–16, 2013, to assess the available scientific information and status of currently available countermeasures to effectively control and mitigate the impact of an outbreak of an emerging Orbivirus with epizootic. Special emphasis was given to BTV and EHDV.

In assessing the threats, workshop participants determined that available countermeasures are somewhat effective, but several weaknesses were identified that affect the ability of countermeasures to effectively prevent and control disease outbreaks. In the long term, the workshop participants determined that implementing the critical research studies is fundamental to addressing the extensive gaps in our scientific knowledge base. Importantly, this research is paramount to advancing the development of effective countermeasures. The complete report from the gap analysis workshop can be accessed at the following internet website: http://go.usa.gov/BJ5F.
Author Disclosure Statement

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References


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