EQUINE

Equine Herpesvirus-1

A single-nucleotide polymorphism (A(2254) or G(2254)) in the DNA polymerase gene of equine herpesvirus 1 (EHV-1) has been linked to the neuropathogenic phenotype which induces equine herpes myeloencephalitis (EHM). Based upon this, a real-time PCR assay to distinguish potentially neuropathogenic from non-neuropathogenic EHV-1 strains was described in 2007. With some limitations, this assay was useful for typing purposes, but lacked the sensitivity to be used for combined detection and typing purposes. Recently, a second generation assay was described to accomplish this (1). Both the original and the new assay were then compared in terms of performance on a combination of archived isolates and clinical specimens. The results showed that the new assay had greater sensitivity and typing accuracy than the previous one and, as such, will be a valuable tool for the differentiation between neuropathogenic and non-neuropathogenic strains of EHV-1.

Equine influenza

Equine influenza A with the molecular signature H3N8 is endemic in Europe and North America and outbreaks are of major economic significance to the equine industry worldwide. The main potential initiators of such outbreaks are the subclinically infected vaccinated horses. The diagnostic method of choice is real-time RT-PCR for virus detection and the hemagglutination inhibition test for antibody level quantitation (2).

Equine influenza A (H3N8) virus infection is an important cause of respiratory disease in horses worldwide. Vaccination with commercial inactivated vaccines is efficacious, but protection against heterologous strains and duration of immunity are limitations of this vaccine type. It has recently been demonstrated (3) that a DNA vaccine expressing the hemagglutinin protein of equine H3N8 influenza virus generates homologous and heterologous immune responses, and protects against clinical disease and viral replication by homologous H3N8 virus in horses. Needle-free delivery was found to be as efficient and effective as conventional parenteral injection.
Equine rhinitis viruses

The results of serological surveys have shown that equine rhinitis viruses A and B (ERAV and ERBV) are common equine respiratory viruses found worldwide. Until now virus isolation has been the main laboratory method to detect the presence of equine rhinoviruses in diagnostic samples. Recently, PCR-based methods have been developed to detect equine rhinoviruses and differentiate between them (4). The authors indicated that a larger number of clinical specimens will need to be tested before each assay is adequately validated for the detection of ERAV and/or ERBV in clinical samples.

Neonatal infections of foals

Slovis et al. (5) recently investigated the prevalence of 9 infectious agents in Kentucky foals between the ages of 2 days and 17 weeks. The foals were either clinically normal or had symptoms of gastrointestinal disease. Real-time PCR was used to analyze the samples for equine rotavirus, equine coronavirus, Clostridium difficile toxin A & B, Neorickettsia risticii, Clostridium perfringens alpha toxin, Lawsonia intracellularis, Rhodococcus equi, Cryptosporidium spp., and Salmonella spp. Whereas 34.6% of the samples contained equine rotavirus, Lawsonia was not detected at all. Co-infections with different agents were diagnosed significantly more frequently in the group with GI problems.

Equine coronavirus in adult horses

Equine coronavirus (ECoV) has long been recognized as a viral agent inducing intestinal infections in young foals. More recently equine coronavirus has also been implicated in disease of older horses. Pusterla et al. (6) described clinical, hematological and fecal PCR results from 161 horses involved in outbreaks at four separate boarding facilities between November 2011 and April 2012 in the States of CA, TX, WI, and MA. All four outbreaks involved primarily adult horses. Fifty-nine horses developed clinical signs with 12–16 sick horses per outbreak. The main clinical signs reported were anorexia, lethargy and fever. Four horses from 3 different outbreaks were euthanized or died due to rapid progression of clinical signs. Common hematological abnormalities were neutropenia and/or lymphopenia. Eighty 6% of horses with abnormal clinical signs tested PCR positive for ECoV. In contrast, 93% healthy horses tested negative. The authors concluded that ECoV is associated with self-limiting clinical and hematological abnormalities in adult horses.

BOVINE

Bovine neurotropic astrovirus

Pathogens causing CNS disease in cattle include bovine herpesviruses 1 and 5 (BoHV-1 and BoHV-5), lyssavirus (rabies), ovine herpesvirus 2 (sheep-associated malignant catarrhal fever), Listeria monocytogenes, Histophilus somni, Escherichia coli, Salmonella spp., Chlamydophila spp., Neospora caninum, amoebas, and prions (BSE). Linlin et al. (7), using a state-of-the-art next
generation sequencing approach, identified a novel astrovirus which was genetically related to ovine astrovirus from brain tissue from a young adult crossbreed steer with acute onset of neurologic disease. Subsequent analysis of 32 archived bovine encephalitis cases identified an additional cases in which bovine astrovirus was detected by PCR and *in situ* hybridization. The microscopic lesions consisted of widespread neuronal necrosis, microgliosis, and perivascular cuffing preferentially distributed in gray matter and most severe in the cerebellum and brainstem, with increasing intensity caudally down the spinal cord. Bovine astrovirus-specific RNA was detected in the cytoplasm of affected neurons within the spinal cord, brainstem, and cerebellum.

**PORCINE**

**Porcine Epidemic Diarrhea**

Porcine epidemic diarrhea virus (PEDV) is induced by a coronavirus and was initially described by Pensaert in Belgium. PED is also circulating in Asia. The virus emerged in the US at the end of April 2013. Affected farms, initially in Iowa but subsequently in other swine-producing states, experienced diarrhea and vomiting in all age groups. The mortality rate in suckling piglets was as high as 90–95%. Very similar to transmissible gastroenteritis (TGE), another coronavirus, pigs with PED had severe villous atrophy but tested negative for porcine rotaviruses and TGEV. Particles with coronavirus morphology were detected in fecal specimens by negative staining electron microscopy. Coronavirus sequences were amplified from RNA extracts in a pan-coronavirus RT-PCR assay. Whole genome sequencing has now shown that the sequence identity of 2013 U.S. PEDV to all known PEDV strains is between 96.6 and 99.5%. Based upon the very close temporal association of the disease outbreaks and the very high degree of sequence homology between positive samples obtained at unrelated farms a common source of virus initiating the US outbreak has been suggested (8).

**Variant H3N2 swine influenza virus**

A new swine influenza A virus, designated H3N2 variant (H3N2v) was first detected in the US in 2011. This new influenza virus has acquired the matrix (M) gene from the pandemic Mexican 2009 (pdm09) influenza (H1N1) strain. It has been speculated that the acquisition of the M gene from the 2009 human strain can enhance the transmissibility of these strains from swine to humans and potentially also between humans. In 2011, 12 human cases of infection with H3N2v influenza viruses were reported in 5 states.

The first case of variant H3N2 influenza infection in Michigan was reported in August 2012. The child had recent exposure to swine at the Ingham County Fair, experienced mild illness and was not hospitalized.

In August 2013, the Michigan Departments of Community Health (MDCH), and Agriculture and Rural Development (MDARD), along with the Berrien County Health Department (BCHD) identified one case of H3N2v in a child who was a swine exhibitor at the Berrien County Youth Fair. The child was not hospitalized and was considered to have contracted H3N2v after
exposure to swine at the fair. A sick pig from the fair tested positive for Influenza A at DCPAH. Samples were referred to NVSL and H3N2v virus was detected in these samples.

ARBOVIRUSES

In 2012, a total of 627 cases of West Nile virus infection were reported in horses. As of September 25, 2013, the nationwide number of positive equine cases was at 157. Only two equine cases have been detected in Michigan in 2013 thus far.

Nationwide, as of September 25, the number of equine cases of EEE infection in 2013 was at 139. One case was diagnosed in Michigan in 2013 so far. The national 2012 tally of eastern equine encephalitis cases in horses was 209. No equine cases were diagnosed in Michigan in 2012.

Epizootic hemorrhagic disease has affected Michigan deer since 1955. In 2012 the disease was really devastating. Die-offs occurred in 30 counties across the southern half of the Lower Peninsula with 14,898 fatalities reported.

REFERENCES


