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Besvarelse vedr.

▸ Coronavirus i danske husdyrpopulationer og i vilde dyr

Bestilling

- En redegørelse for hvad vi ved om corona-virus i husdyr-populationer (i verden, med relevans for danske husdyrpopulationer) og andre dyrepopulationer i Danmark. Inklusive omtale af zoonotisk potentiale.

Svar

▸ Introduction

Coronaviruses (CoVs) are a diverse group of large, enveloped, RNA viruses in the family *Coronaviridae*, order *Nidovirales*. The viruses have single-stranded, positive-sense RNA genomes of about 28-30 kb (these are the largest known RNA virus genomes). The virus particles (95-190 nm) are characterized by the presence of projections on the virus surface, comprised of the spike protein. These viruses infect many different mammalian hosts and also birds.

Certain CoVs can cause severe diseases in animals, birds and humans. For example, the SARS (severe acute respiratory syndrome) and MERS (Middle East respiratory syndrome) epidemics in humans have generated considerable interest in the coronaviruses. The new epidemic in Wuhan, China, is caused by another coronavirus. This virus is distinct from, but most closely related to, a SARS-like virus from bats. In addition, the widespread incidence of disease in the USA, in pigs, caused by the porcine epidemic diarrhea virus (PEDV) recently resulted in severe economic losses; about 7 million young pigs died there in the course of one year (2014) due to this infection. Various countries in Europe have also had some cases of PEDV in recent years but not of the same severity as in the US.

Characteristics of coronaviruses

The coronaviruses are divided into 4 different genera: the alphacoronaviruses (e.g. PEDV), betacoronaviruses (e.g. the SARS and MERS viruses plus the Equine coronavirus (ECoV)),

gammacoronaviruses (e.g. infectious bronchitis virus, IBRV) and deltacoronaviruses (e.g. porcine deltacoronavirus). Examples of members of each genus are listed in the Table.

Some of these viruses primarily cause respiratory disease (e.g. IBRV) while some cause enteric infections (e.g. PEDV) and some cause both respiratory problems and diarrhea (e.g. SARS virus and the bovine coronavirus (BCoV)). Transmission of virus through aerosols and by the fecal-oral route can occur with the same virus. It is believed that the widespread occurrence of the porcine respiratory coronavirus (PRCV), a naturally occurring variant of TGEV with an internal deletion within the S gene that results in altered tissue tropism, has led to protection of pigs against the closely related transmissible gastroenteritis virus (TGEV).

New outbreaks of disease often seem to be associated with the jump of a virus from one host species to another (e.g. to humans). This seems to underlie the SARS epidemic. SARS-like viruses have been detected in horseshoe bats and also in the civet cat. The Wuhan coronavirus is also believed to have spread from animals; the natural host has not yet been established and any intermediates in the spread to humans are also undefined but bats are possible sources. It should be emphasized that zoonotic transmission of coronaviruses seems to be a rare event and has only been documented for a few betacoronaviruses.

Recombination between different coronaviruses is known to occur. For example, the genome of the swine enteric coronaviruses (SeCoV) has the gene encoding the “spike” protein derived from a PEDV virus in a backbone that is from TGEV. The recombination can result in a new virus with characteristics that are different from the two parental viruses. Closely related SeCoVs have been detected in several European countries.

Many different coronaviruses have been detected in bats, which are considered a natural reservoir for alpha- and betacoronaviruses. It appears that delta- and gammacoronaviruses have avian reservoirs.

Coronaviruses in Denmark

Well-known alphacoronaviruses that infect pigs, such as PEDV and TGEV, have never been identified in Denmark (see Table). However, recent studies have identified more than 5 distinct alphacoronaviruses from screening of fecal material collected from 5 different species of bats within Denmark (out of 17 known species present in the country). Note the analysis of these different viruses was based on the sequencing of a small fragment (ca. 200 nt) out of the complete genome (ca. 28,000 nt). However, complete genome sequences for three of these viruses are now known and this has confirmed their classification. Elsewhere, betacoronaviruses have been identified in bats, including within other European countries.

Equine and bovine coronaviruses, together with the porcine haemagglutinating encephalomyelitis virus, are betacoronaviruses, along with the SARS and MERS viruses. The equine coronavirus (ECoV) can infect both horses and donkeys. Normally, the mortality is low, but higher levels have been observed in young animals and miniature horses. ECoV has mainly been identified in cases of enteric disease and is predominantly a disease of adult horses.

Additionally, a few detections of ECoV from the respiratory tract of horses suffering mild respiratory disease have been made. The main clinical signs of ECoV are anorexia, lethargy, fever and diarrhea. Moreover, clinical signs of neurological disease have been related to the presence of ECoV, and the symptoms are believed to be caused by a hyperammonaemia-associated encephalopathy.

Bovine coronaviruses are widespread in cattle globally and are also prevalent in Denmark. The virus causes respiratory- and enteric diseases in calves and occasionally severe hemorrhagic diarrhea in adult cattle.

Infectious bronchitis virus is a gammacoronavirus that causes acute, highly contagious respiratory infections in young birds and egg drop in adult poultry (Egg Drop Syndrome). The virus is widespread globally including in Denmark where it is controlled by vaccination.

Canine coronaviruses (CCov1 and CCov-2) are widespread in dogs globally causing enteric and respiratory diseases in young dogs, respectively. Similarly, feline coronavirus (FeCV) is widespread resulting in a subclinical enteric infection in cats. This virus can expand its cell tropism and infect macrophages resulting in a fatal systemic disease termed feline infectious peritonitis (FIP).

The occurrence (or not), in Denmark, of various different coronaviruses is summarized in the Appendix table. This list is not meant to be exhaustive but to give some examples.