

***Streptococcus equi* subspecies *zooepidemicus* across species in Canada**

Streptococcus equi zooepidemicus is normally thought of as an opportunistic pathogen of horses. Intermittently, cases occur in other species with differing presentations. Based upon an interdisciplinary discussion with a small group of CEZD members and experts from linked networks; the summary below describes some of the case presentations seen in Canada.



- A severe mortality event due to *S. zooepidemicus* was recently reported in Manitoba swine ([O. Costa and Lage 2019](#)). Sudden death due to septicemia occurred at several locations in Canada and the US. ([USDA 2019](#)). No human infection or disease has been related to these events.
- Whole genome sequencing indicates that the bacteria in linked cases in this event are clonal and that there is no clear linkage to cases in other species. ([Chen et al, 2019](#)) Multilocus sequence typing Identifies this isolate as ST194
- The current cases have been controlled with autogenous vaccination and treatment.
- Historical cases (just one case in each of 2001 and 2002) have been seen in Quebec in individual animals displaying respiratory and reproductive signs.
- Coinfection with various pathogens occurred in recent cases in Manitoba and historical cases in Quebec. (PRRS, Influenza, *Bordetella* or *Pastuerella*)



- *Streptococcus equi zooepidemicus* is the most common opportunistic pathogen of the [respiratory tract](#) of horses and a common cause of [bacterial abortion](#) (Merck Veterinary Manual online, 2020)
- Disease occurs occasionally everywhere horses are found. The highest number of isolates of *Streptococcus equi zooepidemicus* reported by veterinary laboratories across Canada originate from horses.
- An unusual case of sudden death of a group of mares with *S. equi zooepidemicus* recently occurred in Saskatchewan.



- Cats are not thought to be a primary host for this agent. Animals from shelter and hoarding situations have presented with middle and inner ear infections in British Columbia, Ontario and Quebec.
- Virulence factors associated with strains (ST173) identified In British Columbia have been identified and are pathogenic to both cats and dogs . ([Britton et al, 2018](#))



- Dogs are not thought to be a primary host for this agent, disease occurs sporadically. Dogs may appear healthy and then die suddenly with severe upper respiratory tract infections and hemorrhagic pneumonia.
- There is no clear trigger for severe disease occurrence.
- Small clusters of animals may be affected, and some dogs appear to be carriers of the bacteria only.
- Occasionally a lack of response to treatment occurs, even when the bacteria are susceptible to antibiotics.
- The bacteria has been isolated from dogs in Saskatchewan, Ontario and Quebec, with clinical disease reported from Ontario.
- Cases of fatal pneumonia in dogs have been reported in the literature from many countries including [Korea](#), [United States](#), [UK](#), [Norway](#).



- A few isolates have been identified from Ontario and Quebec bovines, but no information is available on whether clinical disease was present.
- Dairy cows may have mastitis associated with this agent.



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- Human infection with *Streptococcus zooepidemicus* is an unusual event; rarely infection with this agent can lead to severe disease.
- When cases do occur, they tend to be associated with direct contact with horses or from consumption of unpasteurized milk and cheese
- Case reports of human infections in Canada have been reported in [Halifax](#) and [Quebec](#).

Cross species similarities and differences

The only commonality notable across species is that animals exhibiting severe disease often are housed in higher density situations, or have undergone stressful events. It is also important to note that cases in individual animals also occur. The appearance of more severe disease across species does not appear to be linked to a specific bacterial strain or virulence factor at this time.

Human cases are currently extremely rare, and insufficient evidence is present to make any linkages with human disease and other species, beyond what is known about individual cases. Known risk factors include contact with horses and consumption of unpasteurized dairy products.

Conclusion

Insufficient information is available to speculate about whether an emerging trend exists across species. Going forward, MLST and whole genome sequencing can provide more specific information to identify linkages between cases. Epidemiological similarities and environmental parameters that influence emergence are not immediately obvious.