



8^e Symposium du CRIPA

21-22 mai 2015

Affiche

First report of kobuvirus detection in swine in the province of Quebec

Nantel-Fortier, N.¹, Letellier, A¹, Lachapelle, V.¹, L'Homme, Y¹, Brassard, J^{1,2}

¹ Faculty of Veterinary Medicine, University of Montreal

² Agriculture and Agri-Food Canada

Kobuvirus, a non-enveloped and single-stranded positive RNA virus, is a member of the *Picornaviridae* family. Kobuviruses are detected in a variety of animal species including humans. Its prevalence in swine is reported over the world, but its role as an agent causing diarrhea in animal is still unclear. To date, no data is available regarding the presence of kobuvirus on Quebec farms. The aim of this study was to investigate the presence of kobuvirus in swine farms belonging to a single integration system in Quebec. The association of kobuvirus infection in piglets and diarrhea was also evaluated. In this study, rectal swabs from piglets with diarrhea (n=70) and clinically healthy (n=133) were sampled on four occasions during growth: at 1, 5, 12 and 20 weeks of age (n=606). Fecal samples from their sows (n=85) and surface swabs and composite samples from pens were also collected (n=286). Detection of kobuvirus in samples was performed using

conventional RT-PCR and sequencing was used to confirm. A total of 61 farm visits were made and 85% of them had at least one kobuvirus-positive sample. In nursery, 39 % of the piglets excreted kobuvirus in their feces. This prevalence increased to 72 % during post-weaning and decreased to 47 % and 16 % at 12 and 20 weeks of age respectively. The peak excretion was observed at 5 weeks of age ($p<0.001$). An increase of kobuvirus detection in environmental ($p<0.0001$) and surface swab samples ($p<0.02$) was also observed at the same period. A significant correlation was established between sows and their 1 week old piglets, when both were positive to the virus ($p<0.002$). Vertical transmission of kobuvirus is strongly suspected. No significant association between diarrhea and kobuvirus infection was demonstrated in the present study. Future phylogenetic analysis will allow a better understanding of the route of transmission from mother to offspring and will also assess the genetic diversity of strains present in the swine production system.