



5^e Symposium du CRIP

**Mercredi 16 mai & jeudi 17 mai 2012
à la Faculté de médecine vétérinaire
de Saint-Hyacinthe, Québec, Canada**

Présentation par affiche (poster)

Identification of vectors and viral contamination sources within a network of swine farms and a slaughterhouse

Virginie Lachapelle¹, Julie Brassard², Ann Letellier^{1,3}, Philippe Fravallo¹, Yvan L'Homme⁴

¹CRSV, GRESA, Faculté de médecine vétérinaire, Université de Montréal; ²Agriculture et Agroalimentaire Canada; ³GREMIP, Faculté de médecine vétérinaire, Université de Montréal; ⁴Agence canadienne d'inspection des aliments

Due to their importance in the livestock industry and long-term domestication, pigs are regarded as a large zoonotic reservoir of pathogens for humans. However, there is a knowledge gap in regard of the diversity, pathogenicity and prevalence of many swine enteric virus families. In addition, there is limited information concerning the different sources of viral contamination within and between swine herds. The objective of this project is to identify and characterize specific viral families associated to vectors (selected stakeholders such as animal transportors, veterinarians and nutritional technicians) and sources of introduction and spread of these selected agents within a functional network. In this study, the network of interest was composed of 10 swine farms and a single slaughterhouse situated in the province of Quebec, Canada. A total of 4 enteric viral families (rotavirus, astrovirus, hepatitis E virus and Torque Teno virus) were targeted by molecular techniques and when possible, genetically characterized in order to link a molecular fingerprint for each farm and stakeholder. The results demonstrate the presence of unique and sometimes novel viral strains on most farms, particularly for rotavirus, which underscores a potential for epidemiological monitoring between all farms and the slaughterhouse through various stakeholders. Preliminary results also suggest paths of contamination through specific vectors but also substantial differences in the potential role played by some in the contamination process. Moreover, the results have brought to light a wide variety of group A rotavirus strains, some of which share genetic proximity to human strains, suggesting a common evolutionary history and/or zoonotic potential. The implementation of new biosecurity measures or the strengthening of key measures already in place within the network are emerging in light of our results.