

Molecular tracking of enteric viral indicators in a swine production network

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In the swine industry, a complex network of exchanges exist between farms and slaughterhouses associated with transportation of pigs, but also frequent farm visits from animal health professionals which can multiply the risk for introduction and dissemination of microbial contamination. However, limited information is available concerning the distribution of enteric contamination within and between swine herds and slaughterhouses, especially regarding viral agents. The objective of this project was to evaluate the potential of specific enteric viruses as indicators of fecal contamination associated with the movement of vectors (vehicles of livestock transporters, veterinarians and animal nutritionists) between ten finisher swine farms belonging to the same network and a slaughterhouse over a one year period. On each farm, composite fecal samples and environmental swabbings (e.g. landing stages, front doors, fans and portable solid panels) were collected twice. Environmental samples (surfaces of truck tire tracks) on the slaughterhouse site during unloading of two separate animal shipments from selected farms were also collected. Finally, samples from each stakeholder's vehicle were also collected twice. For each sample, two enteric viral families (group A rotavirus and astrovirus) were targeted by RT-PCR and genetically characterized in order to assign a molecular fingerprint to each farm and stakeholder. Results demonstrate the presence of unique and sometimes novel viral strains on most farms, particularly for rotavirus, which allowed epidemiological monitoring between specific farms and the slaughterhouse through stakeholders such as the livestock transporters. Extensive genetic viral diversity detected at the slaughterhouse site suggests its potential implication in the propagation of viral contamination throughout the network. Results also point out the possible role of environmental fomites in the contamination process of pigs within farm sites. The implementation of new biosecurity measures or the strengthening of key measures already in place within the network is advisable in light of our results.