



KEYNOTE SPEAKER



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Topic:

Predictive Analytics in Animal and Related Populations

Abstract:

Over the last several decades, the way food animals are kept has considerably changed. The number of farms decreased, with simultaneous increase in the population size. Accompanied with general improvement in biosecurity; and in swine, separation of age groups to minimize frequency of contacts; these changes led to many health benefits. Some of them include increase in production efficiency and many aspects of food safety. However, frequent movement of animals between locations contributed, at least in part, to easier transmission of viral pathogens among distinct herds. Changes in herd demographics and in population size, and frequency of viral infections directly and indirectly contribute to the organization of veterinary services. A recent survey determined that among the viral diseases, porcine reproductive and respiratory syndrome virus (PRRSV), influenza A virus (IAV), and some porcine coronaviruses are among the top pathogens of concerns for veterinarians who practice swine medicine in North America. For many of these pathogens, partial genome sequence of the virus is an important information which contributes to decision making during management of clinical outbreaks. Such data could be used to attribute the outbreak source, and to forecast clinical impact of the pathogen in a population. Ultimately, this could inform design of infection and disease control practices. In our research group, we investigate approaches which could be used to predict clinical impact of specific viral genomes (e.g., PRRSV and IAV) at the population level, and assess the between-species transmission potential for influenza A viruses, including their zoonotic potential. In this presentation, I will be discussing some of the successes and challenges in investigating such questions using data-driven predictive modelling approaches.

References:

Keay S, Sargeant JM, O'Connor A, Friendship R, O'Sullivan T, Poljak Z. Veterinarian barriers to knowledge translation (KT) within the context of swine infectious disease research: an international survey of swine veterinarians. *BMC Vet Res.* 2020 Nov 2;16(1):416.

Melmer DJ, O'Sullivan TL, Greer A, Moser L, Ojkic D, Friendship R, Novosel D, Poljak Z. The impact of porcine reproductive and respiratory syndrome virus (PRRSV) genotypes, established on the basis of ORF-5 nucleotide sequences, on three production parameters in Ontario sow farms. *Prev Vet Med.* 2021 Apr;189.