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Application of new molecular tools to assess virus viability in production animals

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“There has been an increasing pressure on the livestock sector to meet the growing demand for high-value animal protein.” Taken from the FAO’s Global and regional food consumption patterns and trends. It is widely accepted that climate/environmental shocks, growth in human population, the modern food system, and disruptions in the food chain are the biggest threats to global food security. Persistent viral infections routinely impose an inconvenient, always costly but thankfully not all too often catastrophic outcome on our modern food system. Managing viruses is key for all concerned if our objective is to meet the ever-growing demand to high-value animal protein. Whether it’s the impact influenza A virus (IAV) has on the avian or swine industries, Porcine reproductive and respiratory virus (PRRSV) on the swine or Deformed wing virus (DWV) on honey bees in both the honey and pollinator sectors - the negative impact and damaging cost to the individual producer, country and global economy cannot be overstated.

The overarching research objectives of my lab is to develop molecular-based research tools, rooted in both the Life Sciences and Veterinary Medicine, to provide a mechanistic understanding as how to best intervene or mitigate the negative impact viruses may have on food animals and associated organisms in the modern food system. This is especially important as no global set of standardized analytical procedures at commercial or research laboratories exist to facilitate and accurately measure potential viable virus contamination in feed ingredients, complete feed, and even fomites. As a result, there is high uncertainty of the extent of virus contamination and the true risk it poses to the food production industry. Moreover, inactivation kinetics of viruses are often generalized and erroneously inferred based on the absence of sound real-world data or in some cases data based on unvalidated surrogate systems. Many prevalent and very familiar viruses, such as IAV and PRRSV, that repeatedly plague production systems,

should on paper be some of the easiest viruses to kill and thus eliminate. Here I discuss the benefits of using new cost-effective molecular tools into routine diagnostic assays to produce a more reliably measure of viability to complement or in some cases negate the need for infectivity data.