Trends and Patterns of Influenza Virus Circulation in Ontario Swine Herds

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ABSTRACT

The ecology of influenza in North American swine populations was stable and dominated by circulation of classical swine H1N1 virus until the 1990s; when a new lineage of H3N2 viruses emerged. This lineage was characterized by a unique combination of internal genes (TRIG cassette) that allowed easy adoption of two genes encoding external proteins, resulting in emergence of different recombinants. This original triple-reassortant H3N2 (rH3N2) virus emerged in Canada in 2005. An event that marked a considerable change in attitudes toward influenza surveillance in Canada was the detection of pandemic H1N1 (pH1N1) in a swine herd in Alberta during the early phase of the 2009 pandemic in people. On one side this resulted in heightened interest towards influenza surveillance in swine by animal and public health authorities, and on the other side, the actual surveillance and testing for influenza decreased. The surveillance that did occur during 2009 and later in different Canadian provinces indicated that diversity of influenza viruses circulating in swine is high (Nfon et al., 2011). As an example, a majority of the H1N1 viruses that circulated in Canadian pigs in 2009 had two external genes originating from the classical swine H1N1 virus, and the TRIG cassette from the trH3N2 viruses. The second most common group of H1N1 viruses was the pandemic H1N1 virus, followed by recombinants between the seasonal H1N1 human influenza and rH3N2 viruses. Similarly, different recombinants of H3N2 viruses have been reported. As an example, Tremblay et al. (2011) reported recombinant H3N2 virus that had all internal genes originating from pH1N1, and HA and NA genes from trH3N2. Similarly, in Ontario turkeys, Berhane et al. (2012) reported different recombinant virus that had combination of genes from the pH1N1 and trH3N2 viruses. Circulation of seven different reassortant viruses between the pH1N1 and endemic influenza viruses was also reported in the US pigs (Ducatez et al., 2011). The interest of public health authorities was sparked again during summer of 2012 when some of these recombinant H3N2 viruses, declared as variant H3N2 (vH3N2) started infecting people who had long-term exposure to swine during pig shows. All this data indicate that influenza is becoming a more complex infection. One of the obvious questions is whether a set of dominant influenza variants will emerge, or the ecology will continue to be dominated by constantly emerging reassortment viruses. This has implications for management of this infection, and monitoring its trends. During this presentation, large scale trends and seasonality of influenza will be discussed, data coming from virological surveillance will also be presented, and results obtained through simulation modeling will also be commented on. The data reported in the scientific literature, as well as the data obtained through the current ongoing Ontario projects will be discussed.

REFERENCES

