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Origin of the virus or ...a rose by any other name...

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Since several decades have passed since the last major influenza pandemic, many influenza experts believed another such event was imminent. The world has been on high alert since the 1997 emergence of highly pathogenic avian influenza H5N1 in Asia. This heightened awareness has resulted in enhanced influenza surveillance, and in the spring of 2009, the first cases of a novel influenza virus were identified in Southern California. The CDC identified the virus as an influenza A H1N1 virus of swine influenza virus lineage. On June 11, 2009, influenza experts were proven correct, when the World Health Organization declared the H1N1 influenza pandemic.

There is no doubt that just the name pandemic induces fear, but we should remember that pandemic, clearly defined, merely describes the occurrence of a disease in all parts of the globe. It does not indicate virulence or severity; it is merely an epidemiologic term. So, by definition, pandemics can be mild or severe in the illness and death they cause, and the severity of a pandemic can change over the course of that pandemic.¹

Epidemiology aside, the origins of the pandemic influenza virus of 2009 need to be clearly understood, especially by swine veterinarians, because we represent the few scientifically trained individuals who understand pork production, disease, and public health. The 2009 Pandemic H1N1 influenza virus is called Swine Flu not only by the media, but by many researchers and scientists in various publications scholarly or otherwise. The battle over the name has been lost because one cannot deny that the genetic makeup of the virus is truly comprised of influenza viruses previously identified in pigs in North America, Europe, and Asia.² Calling the virus Swine Flu is genetically correct and simple, but it implies that there is a direct link between pigs and humans associated with the current pandemic OR that pigs and people are concurrently ill in the same locations. The negative implications of such a name as Swine Flu are lost on human medical professionals, public health officials, and the like. They care little that pork producers or indeed any animal agricultural industry may suffer. And so, we trudge on. We look at the science behind the matter and hope that common sense will prevail. We do our best for our clients, our students, our families, our friends, and the pigs.

To understand the origins of any influenza A virus, you must know the following. Influenza virus is an enveloped, segmented, single-stranded, negative-sense RNA virus belonging to the family Orthomyxoviridae.³ The family consists of 4 genera – influenza A virus, influenza B virus, influenza C virus, and thogotovirus.³ Swine influenza virus (SIV) is an influenza A virus. Influenza A viruses cause disease in animals, birds, and humans.⁴ Influenza B viruses cause disease only in humans. There is evidence that pigs in the UK and China have been exposed to influenza B virus because they have been shown to possess antibodies against influenza B virus, but there has never been an influenza B virus actually isolated from a pig.^{5,6} There is also a report of influenza B virus infection in a marine mammal.⁴ Influenza C viruses are very rare but can infect humans, dogs, and swine but there is no evidence that influenza C viruses are circulating and causing disease in pigs today.^{5,7,8} Because swine influenza is caused by influenza A virus, this genus will be discussed in detail here.

There are eight RNA gene segments to the influenza A virus genome.³ These eight genes are responsible for the translation of 10 viral proteins³ and apparently, for some human, equine and avian influenza viruses, 11 viral proteins.^{9,10} Two of the genes – hemagglutinin (HA) and neuraminidase (NA) - encode for surface glycoproteins that project from the viral envelope and, because they possess distinct antigenic properties and nucleotide gene sequences, are used to subtype influenza viruses into 16 HA types (1 – 16) and 9 NA types (1 – 9).³ Influenza A viruses are then named by their HA and NA type, (e.g. H1N1) and are often given “strain” names that include their genus or type, host species if other than human, location of isolation, arbitrary laboratory number, and year of isolation (e.g. A/Swine/Iowa/15/1930).

Within each subtype, there are numerous variants that arise due to genetic drift (mutations within each gene) and genetic shift (reassortment of genes between viruses infecting that same host cell). Due to genetic shift and drift and the susceptibility of the pig to infections by influenza viruses of human, mammalian, and avian origin, the influenza viruses currently circulating in pigs today are triple reassortant viruses.¹¹ Triple reassortant influenza

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A viruses are those with viral genes from more than one origin. These triple reassortant influenza A viruses are well established in pigs and have a propensity for continuous change. In the case of the 2009 H1N1 pandemic virus, the virus has accumulated changes in several genes that make it capable of spreading easily from human to human and from human to pig. Why those changes occur, when they occur, and where they occur can not be definitively identified, but many speculate. Speculation can have a negative impact, just as a simple name did.

Regardless of the epidemiology, the origin, and the implications, it is clear that continued research of influenza transmission, both from pigs to people and vice versa, is needed. There is more involved in interspecies influenza transmission than mere proximity and contact. Further research into the factors that play a role in human and swine influenza infection is necessary in order to better define the existing gateways that facilitate or the barriers that prevent inter-species transmission. The emergence of the novel H1N1 influenza A virus in the spring of 2009 will hopefully spur on further research regarding the transmissibility and spread of influenza viruses between populations of humans and animals.

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