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## **Pork industry intensification and the changing ecology and epidemiology of swine-origin influenza**

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The 2009 swine-origin influenza virus A subtype H1N1 (S-OIV) pandemic resulted in an alarming increase in pediatric influenza mortality. According to phylogenetic analyses, each segment of the S-OIV genome derives from swine influenza lineages circulating primarily in pigs for at least a decade before the pandemic emerged. Considerable genetic and antigenic stability had characterized most swine influenza virus isolates in North American for 80 years before the emergence of the primary progenitor of S-OIV, the triple reassortment swine flu virus first identified in U.S. pig herds in 1998, which became established throughout North America and generated further reassortment viruses and sporadic human infection. Changes in industry structure and husbandry practices that may have played a role in this shifting dynamic are explored. Identifying and resolving conflicting priorities between veterinary and public health professions can bolster the One Health vision and may help prevent the emergence and spread of pathogens with pandemic potential.