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The CEIRR Risk Assessment Pipeline Executive Report:

Assessment of the Pandemic Potential of Swine A(H1) 1B.2 Influenza Viruses

Prepared by The CEIRR Risk Assessment Pipeline

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Priority for Risk Assessment and Risk Mitigation: High

Executive Summary: H1 1B.2 influenza A viruses are prevalent in swine on multiple continents, have a high degree of genetic and antigenic diversity, evade human antibody immunity to influenza, and share key traits with human-adapted viruses. Continued monitoring of their prevalence and informed implementation of biosecurity measures are needed to limit human exposures. Additional research on transmission between swine and humans, evolution of current lineages, and the extent and limits of population immunity will help clarify pandemic risk from this group of viruses.

Background: The hemagglutinin (HA) of influenza A virus allows the virus to enter cells and is the major target of protective immune responses. The swine A(H1) 1B.2 influenza viruses derive their HA from human seasonal influenza viruses that circulated prior to the 2009 pandemic. Since related viruses have not spread in humans since 2009, most individuals born since 2009 have not been exposed to this HA. Swine A(H1) 1B.2 viruses therefore present a pandemic concern because of declining population immunity and the presence of an HA protein known to be able to support infection and spread in humans.

Properties of the Virus | Genetic diversity

- Independent introductions of human seasonal H1N1 viruses into swine between 1980 and 2009 seeded distinct lineages. Currently, the swine A(H1) 1B.2 viruses comprise at least seven antigenically distinct clades, with differing geographic distributions. Two clades (1B.2.1 and 1B.2.2) have circulated in the US since the early 2000s.
- CEIRR surveillance revealed that swine A(H1) 1B.2 viruses circulating in Chile also stem from two separate introductions into pigs in the 1990s and have HA and NA genes that are genetically divergent from IAVs reported elsewhere in the world.
- In the US, the HA of 1B.2 viruses sampled from pigs between January 2024 and January 2025 showed substantial diversity, with 39 different diversity groups represented when a 99% similarity threshold was applied.
- In the US, 1B.2 HA and NA genes were detected in 29 distinct genetic backgrounds between 2009 and 2024.

Properties of the Virus | Receptor Binding

The HA of swine A(H1) 1B.2 lineage viruses have α2,6 receptor specificity. This specificity is important for spread in humans. The receptor binding specificity of these strains is, however, much broader than that of human H1 strains.

Properties of the Virus | Transmission

- Swine H1 1B.2 viruses spread readily by an airborne route among ferrets, which are the primary animal model used to evaluate influenza virus transmission. To model humans that have been previously infected with modern seasonal influenza viruses, transmission was tested in ferrets with immunity to a human H1N1 virus. Swine A(H1) 1B.2 viruses overcame this immunity to transmit through the air to 50%-100% of exposed ferrets.
- Using a swine-to-ferret experimental transmission model, a swine A(H1) 1B.2 virus transmitted to only one of four exposed ferrets.

Attributes in the Human Population | Human Infection

- Between January 2024 and January 2025, four human cases of infection with swine H1 1B.2 lineage influenza A viruses were detected (three in the US and one in Brazil).
- Since 2010, 11 human infections with 1B.2 viruses have occurred in the US.

Attributes in the Human Population | Population Immunity

- Serological data indicate that elderly individuals and young children lack protective antibodies against the swine H1N2 viruses detected in Chile.
- For most swine H1 1B.2 strains from the US, antibodies that could reduce infection were typically not detectable in serum from humans.
- For one swine H1 1B.2 strain from Spain, antibodies that could reduce infection were detectable in serum from most humans tested.
- Vaccination with the seasonal influenza vaccine does not increase antibody titers to swine H1 1B.2 viruses