Understanding the Impact of Porcine IAV-S

Influenza A viruses, belonging to Orthomyxoviridae family, contains a genome of eight single-stranded RNA segments. With this many genome segments, simultaneous infection can yield novel gene combinations via genetic "reassortment."

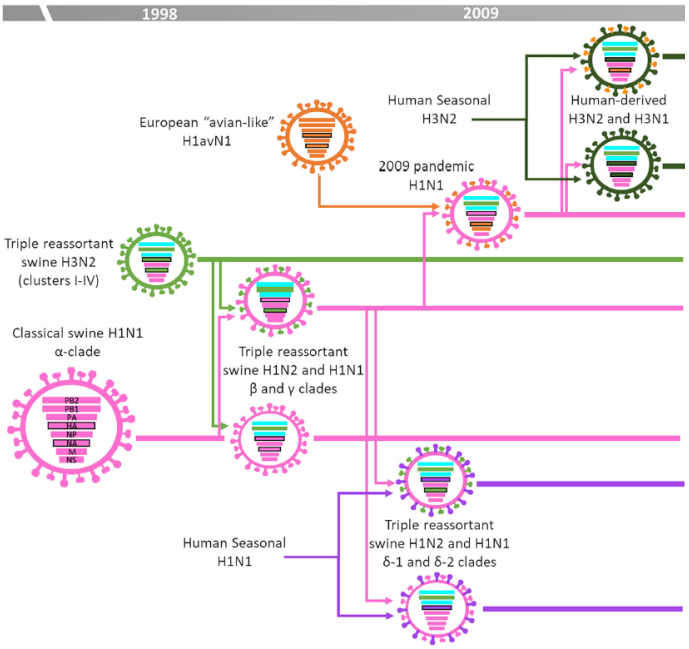
Influenza A viruses cause acute respiratory infections in swine that result in significant economic losses for the global swine industry. Currently, there are three different subtypes of Influenza A worldwide: H1N1, H3N2, and H1N2 (Mancera Gracia et al, 2020).

During the early 2000s, the US swine population encountered human-seasonal H1 and N2 genes via reassortment. The antigenically distinct H1 viruses, classified as clades d-1 and d-2, marked a departure from the "classical swine" lineage. In a landmark development, the novel "H1N1 pandemic strain" emerged in 2009. The "H1N1 pandemic strain" rapidly spread within the human population and also found a foothold within the North American swine population, embodying the intricate interplay between zoonotic and animal health dynamics.

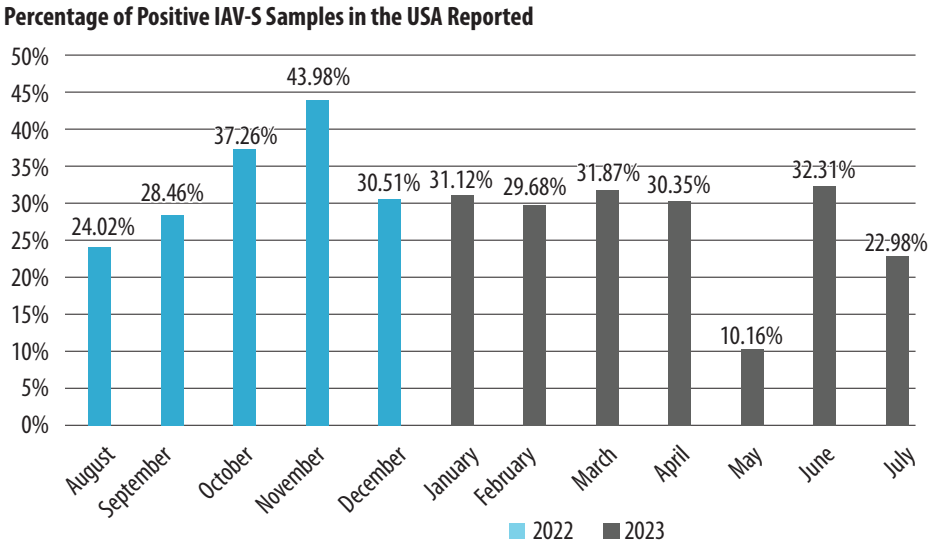
Even though the colder temperatures of winter bring increases in spikes of IAV-S in swine herds, it is still a relatively abundant virus reported monthly by Swine Health & Information Center (SHIC) (Figure 2).

Impact on Swine Herd Production

Even within a naive pig group, clinical manifestations may only manifest in a minority of individuals. Co-infection with other viruses and bacteria paints a graver picture of morbidity and mortality, often accompanied by pronounced economic repercussions. Simultaneous infections with other swine diseases or affliction in late-pregnant sows can plunge herds into substantial health challenges, as documented by Fablet et al. (2012). Concomitant infection with Mycoplasma hyopneumoniae, for instance, can magnify H1N1's clinical impact, as highlighted by Deblanc et al. (2013). Research by Wesley et al. (2004) found that gilts naturally exposed to H3N2 SIV during late gestation (D 80-82) resulted in a 22% stillbirth rate, compared to the ideal target of 5-7%.



▲ **Figure 1.** The evolution of IAV-S in the USA swine herds over time (adapted from Qui et al., 2015).



◄ **Figure 2.** Percentage of positive IAV-S samples submitted as reported by the SHIC monthly disease monitoring reports in the USA *(https://www.swinehealth.org/domestic-disease-surveillance-reports/)*.

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