ts-mutants of porcine influenza viruses: Pathway to live-attenuated vaccines in pigs?

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Wide spread occurrence and pathogenic potential of swine influenza A virus (swIAV) associated with respiratory diseases, cause considerable economic losses in pig production. Over the past decades in Europe, four pathogenic lineages (H1N1av, H1N2hu, H3N2, H1N1pdm/2009) emerged, some of them reassortant viruses between avian and human influenza viruses. New options to prevent respiratory symptoms in pigs by developing live vaccine candidates against infections with these four lineages are being explored. In this study, the focus is on the classical vaccine concept of temperature-sensitive (ts) live-attenuated influenza vaccines (ts-LAIV), which has yet to be evaluated in pigs. Recent field isolates of each of the four lineages have been cold-adapted (ca) through serial passaging at decreasing incubation temperature in MDCK-II and swine testicle cells. Full genome sequencing revealed multiple mutations in several gene segments compared to parental viruses. Growth kinetics established the ts-ca phenotype of the serially passaged viruses. The att phenotype will be assessed by experimental infections of mice and in the ultimate target species, pig. As swIAV have been critically involved in the development of at least the most recent human influenza pandemic virus, zoonotic potential of the vaccine virus candidates will be tested in the ferret as a human influenza model species.