Predicting swine flu vaccine efficacy: Assessing T cell epitope cross-conservation in vaccine and field strains

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Objective

When swine influenza vaccine and circulating strains are poorly matched, vaccine-induced antibodies may not protect but highly conserved T-cell epitopes may still have a disease-mitigating effect. The conservation of T cell epitopes between vaccine and novel swine influenza A virus (IAV) strains is highly variable and may explain the variability in vaccine efficacy. Methods for estimating the degree of epitope conservation between vaccines and outbreak strains are needed. Here, we examine the extent of class I and II T cell epitope conservation of a T cell-directed DNA vaccine among 2017 swine IAV isolates by immunoinformatics methods.

Methods

Twenty-eight class I and 20 class II epitopes in the prototype vaccine are published (Gutierrez et al. 2016). We obtained 182 2017 H1N1, H1N2 and H3N2 swine IAV genomes from the Influenza Research Database. Two immunoinformatics algorithms were used to evaluate conservation of vaccine epitopes among 2017 swine IAV isolates: T cell epitope content comparison (EpiCC), and JanusMatrix (JMX). Pairwise comparisons between prototype and circulating strains were conducted with EpiCC to analyze overall vaccine epitope cross-conservation; an epitope-by-epitope assessment was conducted using JMX.

Results

We observed epitope content variability across proteins and subtypes. The prototype vaccine had the highest EpiCC epitope cross-conservation (93% for class I and 87.1% for class II) in 2017 H1N1 viruses. Higher EpiCC scores are thought to be associated with greater protection by vaccines against challenging strains (Gutierrez, et al 2017). Internal proteins are well conserved across all subtypes, indicating internal proteins might contribute to vaccine efficacy. On the individual epitope level, two of the seven class I epitopes sourced from H1N1 M and one H3N2 HA epitope were absent in 2017 isolates.

Conclusions

These complementary immunoinformatics methods suggest that the prototype vaccine could stimulate CD4 and CD8 T cells that recognize epitopes in 2017 strains and contribute to protection. These approaches can be applied to analyze other viral vaccines.

Total : 2099/2100 characters