H1N1 G4 swine influenza T cell epitope analysis in swine and human vaccines and circulating strains uncovers potential risk to swine and humans

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Abstract

Pandemic influenza viruses may emerge from animal reservoirs and spread among humans in the absence of cross-reactive antibodies in the human population. Immune response to highly conserved T cell epitopes in vaccines may still reduce morbidity and limit the spread of the new virus even when cross-protective antibody responses are lacking. We used an established epitope content prediction and comparison tool, EpiCC, to assess the potential for emergent H1N1 G4 swine influenza A virus (G4) to impact swine and human populations. We identified and computed the total cross-conserved T cell epitope content in HA sequences of human seasonal and experimental influenza vaccines, swine influenza vaccines from Europe and the United States (US) against G4. The overall T cell epitope content of US commercial swine vaccines was poorly conserved with G4, with an average T cell epitope coverage of 35.7%. EpiCC scores for the comparison between current human influenza vaccines and circulating human influenza strains were also very low. In contrast, the T cell epitope coverage of a recent European swine influenza vaccine (HL03) was 65.8% against G4. Poor T cell epitope cross-conservation between emergent G4 and swine and human influenza vaccines in the US may enable G4 to spread in swine and spillover to human populations in the absence of protective antibody response. One European influenza vaccine, HL03, may protect against emergent G4. This study illustrates the use of the EpiCC tool for prospective assessment of existing vaccine strains against emergent viruses in swine and human populations.

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