

Title: Swine Influenza Epitope Validation

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Developing effective vaccines for highly variable viruses such as influenza represents a substantial challenge. In pigs, swine influenza A virus (IAV) is responsible for significant financial losses to pig farmers annually. Currently available vaccines confer limited protection against diverse circulating strains of the virus. To tackle this limitation, we applied immunoinformatics tools to identify short regions of the IAV genome (epitopes) that are highly conserved across representative strains and have the potential to induce broad protective immune responses. We designed and produced a DNA vaccine to deliver these epitopes. In a vaccination study, we observed immune responses specific to the predicted epitopes. These results confirm the capacity of our immunoinformatics tools to predict immunogenic T cell epitopes and demonstrate its potential for use in the design of universal influenza more broadly cross-protective vaccines for swine.