RESEARCH ABSTRACT

SWINE HEALTH

Title: Advances in Vaccine Design: Developing A Cross-conserved Influenza Vaccine for Swine **- NPB #13-121**

Investigator: Anne S. De Groot

Institution: Institute for Immunology and Informatics, University of Rhode Island

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Scientific Abstract:
Computer-driven algorithms enable accelerated vaccine design for emerging pathogens. iVAX is an integrated set of epitope-driven vaccine (EDV) design tools that is based on the EpiMatrix algorithm and has been extensively validated for human vaccine design. Comparable tools for the development of vaccines for food animals are not available. We used the pocket profile method to create T cell epitope-prediction matrices (PigMatrix) for porcine MHC (Swine Leukocyte Antigens, SLA). These new matrices were integrated into iVAX so that this comprehensive suite can be used to design EDV for pathogens affecting swine. For this study, we developed matrices for common class I and II SLA alleles and predicted 28 cross-conserved class I and 20 class II epitopes from seven circulating IAV.

Multi-epitope DNA vaccines encoding strings of class I and II epitopes separately were produced and pooled for intramuscular injection into pigs. Peptides induced specific recall responses as evidenced by IFN-γ production upon exposure to pooled peptides, demonstrating their immunogenicity and validating the SLA matrices. Pooled peptides induced similar recall responses as whole inactivated virus (WIV) used as antigen. Moreover, epitope-specific recall responses in DNA vaccinated pigs were equivalent in magnitude to WIV-induced responses in pigs immunized with quadrivalent inactivated vaccine (FluSureXP®). In other words, a reduced set of cross-conserved peptides (48), predicted using immunoinformatics tools, induced a similar IFN-γ response as four inactivated viral strains. In terms of viral loads, neither the DNA vaccine nor the commercial vaccine was protective against intranasal challenge with A/California/04/2009 (H1N1). From the T cell epitope perspective, the results are advantageous and demonstrate the potential of immunoinformatics tools for prediction of porcine T cell epitopes. We are now in a position to dissect the responses induced by individual epitopes to better understand the mechanism of action and potentially improve current available vaccines.