Universal Human and Swine Influenza Vaccine

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Technology description

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This technology provides universal centralized influenza vaccine candidate genes against all known human and swine influenza strains (102 gene sequence in total). A universal vaccine for influenza has become a high priority and there are several efforts being pursued to achieve this goal. UNL researchers applied an epigraph approach to create novel synthetic influenza immunogens that are designed to provide the greatest degree of vaccine coverage of all influenza strains. The epigraph immunogens provide substantially greater advantages over the single mosaic and consensus approaches by using a multi-immunogen cocktail vaccine strategy. A major advantage to the epigraph approach is the ability to design multiple epigraph genes that will maximize vaccine coverage (Figure 1).

Figure 1: The design of universal influenza vaccine genes.

A. Strain-specific antigens only target the strain they were designed from and few closely related variant strains. B. Compared to strain-specific antigens, centralized consensus antigens were created using all known and unique influenza genes only, which represents all evolved sequences equally while biases toward the predominant circulating strains. C. Using the same gene dataset, Mosaic antigens were created through the Mosaic Vaccine Designer program from the Los Alamos National Laboratories Tool Suite and were computationally analyzed for optimal potential T cell epitope coverage. D. The same dataset was submitted to the Epigraph software suite where a 3 antigen cocktail was created. All the vaccine antigens were analyzed phylogenetically and found to localize either to the center of the phylogenetic tree, or, in the case of consensus and mosaic proteins, to the two main influenza clusters with a recombinant covering the minor cluster, in the case of the epigraph vaccines.

About NUtech Ventures

NUtech Ventures is the non-profit technology commercialization affiliate of the University of Nebraska–Lincoln. Our mission is to facilitate the commercialization and practical use of innovations generated through the research activities at the University of Nebraska.

Application area

Human and Swine Flu Vaccine

Advantages

Analysis based on all known unique HA sequences extracted from all known human and swine influenza gene data after getting rid of repeats
No bias towards common strains
Bias towards predominant circulating strains
Employing consensus centralization, Mosaic and Epigraph strategies
Optimized coverage of potential T cell epitopes (PTE)
Wide protection – these vaccine genes cover 96% of existing human and swine influenza strains

Institution

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