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Universal vaccination of H5N1 hemagglutinin

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The nature of influenza virus to randomly mutate and evolve into new types with diverse antigenic determinants is an important challenge in the control of influenza infection. Particularly, variations within the amino acid sequences of major neutralizing epitopes of influenza virus hemagglutinin (HA) hindered the development of universal vaccines against H5N1 lineages. Based on distribution analyses of the identified major neutralizing epitopes of hemagglutinin, we selected three vaccine strains that cover the entire variants in the neutralizing epitopes among the H5N1 lineages. HA proteins of selected vaccine strains were expressed on the baculovirus surface (BacHA), and the preclinical efficacy of the vaccine formulations was evaluated in a mouse model. The combination of three selected vaccine strains could effectively neutralize viruses from clades 1, 2.1, 2.2, 4, 7, and 8 of influenza H5N1 viruses. In contrast, a vaccine formulation containing only adjuvanted monovalent BacHA (mono-BacHA) or a single strain of inactivated whole viral vaccine was able to neutralize only clade 1 (homologous), clade 2.1, and clade 8.0 viruses. Also, the trivalent BacHA vaccine was able to protect 100% of the mice against challenge with three different clades (clade 1.0, clade 2.1, and clade 7.0) of H5N1 strains compared to mono-BacHA or inactivated whole viral vaccine. The present findings provide a rationale for the development of a universal vaccine against H5N1 lineages. Furthermore, baculoviruses displaying HA will serve as an ideal choice for a vaccine in prepandemic or pandemic situations and expedite vaccine technology without the requirement of high-level-biocontainment facilities or tedious protein purification processes.

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