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USE OF ANTIGENIC CARTOGRAPHY IN VACCINE SEED STRAIN SELECTION

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Important Findings

This study revealed antigenic differences between circulating H5N1 viruses and the H5 viruses used in poultry vaccines. Considerable antigenic variation was also observed within and between H5N1 clades. These observations have important implications for the efficacy and long-term use of poultry vaccines.

Significance of Findings

Human influenza A viruses are classic examples of antigenically variable pathogens that have a seemingly endless capacity to evade the host's immune response. The viral hemagglutinin (HA) and neuraminidase (NA) proteins are the main targets of our antibody response to combat infections. HA and NA change continuously to escape from humoral immunity, a process known as antigenic drift. As a result of antigenic drift, the human influenza vaccine is updated frequently. The World Health Organization (WHO) coordinates a global influenza surveillance network that routinely characterizes the antigenic properties of circulating strains by the hemagglutination inhibition (HI) assay to select new seed viruses for such vaccine updates.

To facilitate a quantitative interpretation and easy visualization of HI data, a new computational technique called "antigenic cartography" was developed. Since its development, antigenic cartography has been applied routinely to assist the WHO influenza surveillance activities. Until recently, antigenic variation was not considered a serious issue for influenza vaccines for poultry. However, because of the diversification of the Asian H5N1 lineage since 1996 into multiple genetic clades and subclades, and because of the long-term use of poultry vaccines against H5 in some parts of the world, this issue needs to be readdressed.

Additional Information

Antigenic cartography is a new computational technique that facilitates a quantification and visualization of virus phenotype data, "Antigenic maps" are simple visualizations of HI data, in which distances represent antigenic similarities between viruses (Fig. 1).

Antigenic variation of avian influenza viruses represents a new challenge for the development and application of poultry vaccines. It has become clear that different vaccine seed strains may result in variable vaccine efficacy against infection with different viruses of the same subtype. The most optimal vaccine seed strain may even vary for different vaccination campaigns, as the antigenic properties of the circulating field strains have been shown to vary temporally, geographically, or even by host species and poultry production sector. Moreover, since vaccination generally represents only one strategy out of the many measures employed to prevent, manage, or eradicate avian influenza, appropriate monitoring programs for the effectiveness of the vaccine and the potential emergence of antigenic drift variants need to be implemented.

Although dealing with the antigenic variation of avian influenza appears to be a serious challenge, a blueprint for a successful action plan is already available. The WHO-coordinated global influenza surveillance network has been effective in tracking the antigenic evolution of human influenza viruses for many years and generated appropriate vaccine seed strains when needed. In this network, national reference laboratories assemble virus collections for antigenic characterization from a variety of sources of virus isolates in the country. Strains of interest are shared with global reference laboratories to ensure a thorough, coordinated, and integrated analysis of the antigenic properties of the strains that circulate around the world. New vaccine seed strains are then generated by the network as the need emerges. For the avian influenza field, a similar strategy may be envisaged. Such a coordinated network would likely be more successful, efficient and cost-effective than ad-hoc or local monitoring programs. This is particularly important as we rely on high quality serological data for antigenic characterization, and demand ultimate proof of effectiveness of vaccine seed strains in expensive and time-consuming vaccination-challenge experiments in poultry. As a welcome side effect, such a coordinated global avian influenza surveillance network would facilitate more close interactions—and integration—with the WHO-coordinated human influenza surveillance network, fitting in beautifully with the one world, one health initiative.

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