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Citation	Japanese Journal of Veterinary Research, 42(1), 34-34
Issue Date	1994-06-17
Doc URL	http://hdl.handle.net/2115/2464
Type	bulletin (article)
File Information	KJ00002377692.pdf



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ANTIGENIC VARIATION AMONG EQUINE H3N8 INFLUENZA VIRUSES

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Since the first isolation of equine H3N8 influenza virus in 1963, viruses of this subtype have been circulating among horses worldwide. Although antigenic drift of the H3 hemagglutinin (HA) of equine influenza viruses has been suggested, the extent of variation is not fully understood. To provide detailed information on the antigenic variation among equine influenza viruses, 20 H3N8 influenza virus strains isolated from horses in different areas of the world during the period 1963–1992 were analyzed antigenically. The panel of monoclonal antibodies (McAbs) used for the analysis consisted of those recognizing at least 7 different epitopes on the HA molecule of A/equine/Minami/1/63 (H3N8) influenza virus.

The results indicate that (1) equine H3N8 viruses show antigenic drift with the year of isolation, (2) different antigenic variants cocirculate among horses, (3) compared with human strains, the extent of antigenic variation of the HA of equine H3N8 viruses is low and (4) some McAbs that bind to the HA and neutralize viral infectivity did not inhibit hemagglutination of the virus as shown with avian influenza viruses, supporting the notion that equine influenza viruses were derived from avian viruses.

To assess the immunogenicity of different equine H3N8 influenza viruses, including vaccine strains and recent isolates, antisera of mice vaccinated with each of these viruses were examined by neutralization and hemagglutination-inhibition tests. The results indicate that selected recent isolates from horses should be recommended for use as vaccine strains.