influenza among pigs and over the past 13 years it appears that horses are the reservoir for influenza among horses.

For those of us who work with influenza infections in animals, especially "natural" host–parasite systems, e.g., swine, birds, and horses, the question of interspecies transfer is perplexing. Our field observations and serological studies have failed to show that human beings become infected when they are closely associated with animals with influenza infections. Observations by Czechoslovak workers indicate that transfer may occur from pigs to human beings. There is certainly a need to intensify our efforts to isolate influenza viruses from various animal species and to learn more about their natural history.

We are confronted with several problems in animal influenza systems, both in the laboratory and in the field, that deserve further definition. Several times in the foregoing discussions it has been suggested that new subtypes arise as a result of recombination in nature. This suggestion has been based on the success that several workers have had with recombination of influenza viruses in tissue-culture systems. Experiments are in progress in our laboratory to explore whether recombination of influenza viruses may take place in animals. To date we have not accumulated sufficient data to determine whether recombination has taken place. It is probable that the time of recombination and the conditions under which it may take place are extremely critical. There seems to be an infinite number of possibilities, but to select the correct one is a problem. We have been interested in studying persistent infections and whether recombination is more likely to occur under those conditions or in an acutely infected animal. We have also been interested in the effects of antibody on the course of infection and the conditions for recombination.

It is my opinion that many of our perplexing problems can be solved by more intensive use of swine and avian experimental model systems.

Studies of the Structure of the Influenza Virus Envelope

by H. A. BLOUGH [a]

Studies by J. M. Tiffany and myself, using the calculated amount of lipid found in the influenza virus envelope (A0/PR/8/34) have shown that there is twice as much lipid as can be accounted for by a bilayer of the Danielli-Davson-Robertson type. A more acceptable model is the lipoprotein-complex theory of membrane structure which suggests that lipids are bound specifically to apolar regions of the polypeptide by hydrophobic interaction. Models of the viral envelope were constructed of modelling clay and expanded polystyrene plastics. Fig. 1 represents a cross-section of several models containing the coiled internal nucleocapsid (rubber tubing). Fig. 1(a) shows a modified Wallach-Gordon bilayer; this was rejected since it does not account for all of the lipid. Fig. 1(b) is a modified Benson model with the addition of 2 intervening micelles of lipid between certain protein molecules; this was ruled out since one would anticipate an altered periodicity of surface projections. Fig. 1(c) shows a toadstool configuration that was ruled out on energetic grounds. The favoured configuration is the "inverted toadstool" shown in Fig. 1(d). An expanded model of this is shown in Fig. 2. The stem of the inverted toadstool is in contact with, and ionically bound to, polar groups of lipid in a micellar arrangement. The latter projects 10Å beyond the outer surface of the envelope and accounts for the spacing seen between the base of the spike and the envelope. The base of the toadstool consists of acyl chains (pipe-cleaners) hydrophobically bound to protein; this calculated amount of lipid bound hydrophobically is about 20%. Addition of lipid at the base of the toadstool may take place under conditions of high multiplicity of infection and could explain, in part, the pleomorphism of von Magnus-type virus.

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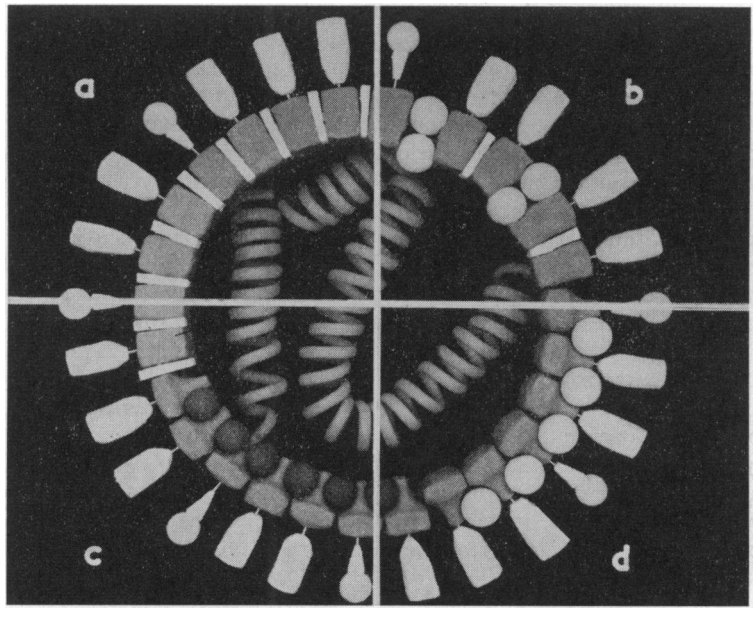
FIG. 1

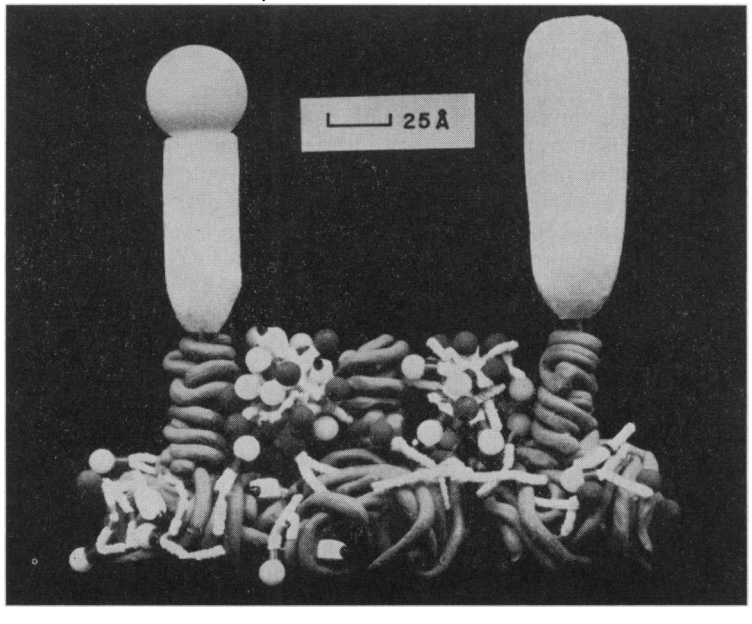
CROSS-SECTION OF INFLUENZA VIRUS ENVELOPE SHOWING 4 POSSIBLE CONFIGURATIONS FOR THE LIPOPROTEIN COMPLEXES [a]



[a] Surface projections represent haemagglutinin and neuraminidase (with terminal expanded polystyrene balls). The grey modelling clay represents envelope protein and the expanded polystyrene spacers represent bilayer (a) or micellar configurations.

FIG. 2

EXPANDED VIEW OF 3 INVERTED "TOADSTOOLS" (2 OF WHICH CARRY A SURFACE PROJECTION) [a]



[a] Modelling clay represents envelope protein: pipe-cleaners and plastics represent various lipid molecules. Single micelles of lipid (present in the upper ⅔ of toadstool) separate individual toadstools; lipid hydrophobically bound to toadstool protein is at the base.