RADIOIMMUNOASSAY AND OLIGONUCLEOTIDE MAPPING OF A/HswlN1 INFLUENZA VIRUSES ISOLATED FROM HUMANS AND ANIMALS

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In December 1983 three strains of influenza virus with Hswl haemagglutinin (HA) were isolated from humans in Alma-Ata (*1*). Later studies in Alma-Ata in 1984—1985 indicated a possible role of HswlN1 influenza viruses in the aetiology of acute respiratory viral infections (*2*).

The following influenza viruses have been compared in radioimmunoassay (RIA): A/Alma-Ata/1367, 1382, 1417, 1044, 1414, 1415, 247/84 (isolated from patients aged from 1.5 to 47 years during a seasonal outbreak of acute respiratory disease in November-December 1984); A/Pazardjik/Bulgaria/120/82 (isolated from children in Bulgaria); A/New Jersey/8/76 (isolated from a 19-year-old recruit in the U.S.A.); A/swine/Iowa/15/30 and A/duck/Alberta/35/76. Hyperimmune sera to viruses A/swine/15/30 and A/New Jersey/8/76 were successively adsorbed to viruses A/USSR/90/77 and A/PR/8/34 and subsequently cross-adsorbed with viruses A/swine/Iowa/15/30 and A/New Jersey/8/76. They were then analysed by indirect competitive solid phase RIA (sp-RIA) with immobilized homologous virus. The antigenic composition of HA of HswlN1 variants isolated in the U.S.S.R., Bulgaria and of the reference swine influenza virus were almost identical, but the antigenic composition of A/New Jersey/8/76 HA appeared different. It is known that the antigenic composition of the HA of both A/New Jersey/8/76 and A/Nevada/101/82 are more similar to the HA of A/swine/Wisconsin/1/67 (*3*). It was shown in sp-RIA that the antigenic composition of the HA of influenza virus strain H1N1 isolated from a wild duck (A/duck/Alberta/35/76) differed greatly from the HA of either A/swine/Iowa/15/30 or A/New Jersey/8/76.

Oligonucleotide mapping of the RNA segments encoding HA of the three strains showed a high degree of homology between the HA genes of A/swine/Iowa/15/30 and A/Alma-Ata/1417/84 viruses. Meanwhile, it revealed significant differences between HA genes of the A/New Jersey/3/76 virus and the A/Alma-Ata/1417/84.

The HA of recent Alma-Ata isolates is similar to that of earlier isolate A/swine/Iowa/15/30 which was serologically identical with the pathogen of the 1918 pandemia. The mechanisms of rigid conservation of the genetic information of these viruses and their recurrence are still unclear.

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