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VIRUS RESEARCH

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GENETICS AND PATHOGENICITY OF NEGATIVE STRAND VIRUSES

Abstracts of papers presented at the 7th International Meeting on Negative Strand Viruses

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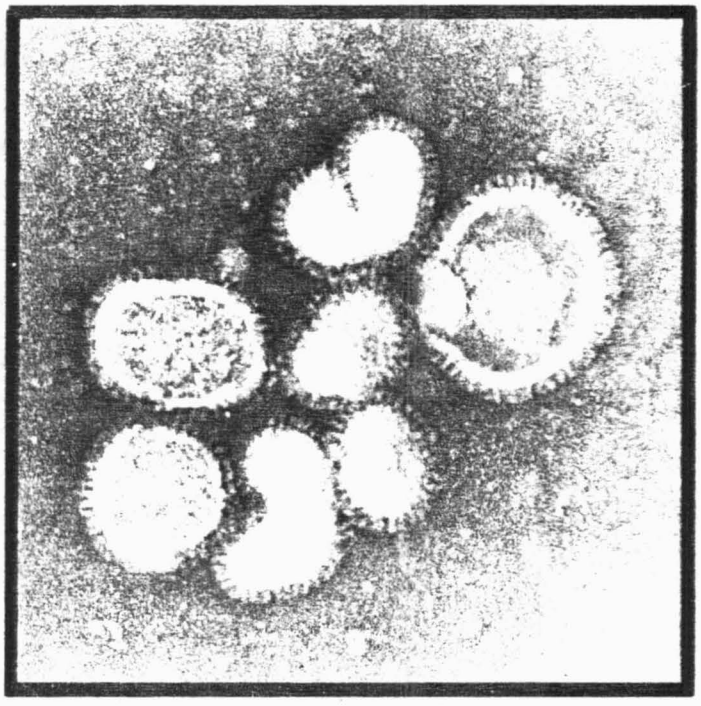
18–23 September 1988



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VIRUS RESEARCH

An International Journal of Molecular and Cellular Virology

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Cover illustration: Fowl Plague virus. Mixture of intact particles and particles partly penetrated by stain after partial digestion with phospholipase C. Magnification X 202,000. Photograph courtesy C.J. Smale, Pirbright.

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MATHEMATICAL MODELLING APPROACH FOR REVEALING PHYLOGENETIC RELATIONSHIPS BETWEEN ANTIGENICALLY RELATED AVIAN PARAMYXOVIRUSES (PMV)

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Within avian PMV group numbering to date 9 antigenic serotypes, diverse multidirectional antigenic interconnections have been found being displayed by both hemagglutination and neuraminidase inhibition tests. A combinatorial mathematical model published recently (Rishe & Lipkind, 1987) described the complicated antigenic relationships including phenomenon of the one-way asymmetric cross reactivity. Further development of the mathematical model resulted in elaborating approach for revealing the ancestry between the compared antigenically related viruses. This permitted the construction of a phylogenetic tree based on computer-assisted combinatorial consideration (theory of trees). Treatment of the serological cross reaction data involving all the avian PMV serotypes and based on combinatorics or provisional triples ("parent-child-grandchild") has revealed 12 triple combinations (from the whole total of 788 possible ones) which satisfied the postulated criteria of ancestry. Although an individual triple alone does not tell which member of the triple (serotype) plays the role of parent, child and grandchild the above global analysis of the whole totality of all the data provided for only one probable solution. The analysis revealed definite phylogenetic connections between the members of the avian PMV group which has not yet been properly established taxonomically.

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ANTIGENIC VARIATION ON THE INTERNAL PROTEIN OF MEASLES VIRUS : IDENTIFICATION AND EXPRESSION OF THE INDIVIDUAL EPITOPES IN BACTERIA

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Measles virus is a childhood infection. The severity of the disease may differ in various regions. Although measles is considered as a monotypic virus, recent observations have suggested problems with vaccination. To investigate this, we isolated a number of measles virus strains from Africa and France. We examined them with a bank of monoclonal antibodies against the two glycoproteins (haemagglutinin and fusion) and two internal proteins (nucleoprotein and matrix). The only antigenic variation was on the nucleoprotein. Three distinct epitopes were identified with the nucleoprotein monoclonal antibodies. One was found on all strains, whereas the other two varied. To define these epitopes, we cloned the nucleoprotein gene into the PRIT vector and expressed it as a fusion protein in E. Coli. All three epitopes could be identified by Western blotting on the recombinant protein. Deletions of the nucleoprotein gene were used to produce fragments which were subsequently expressed in E. Coli and examined for the presence of the three epitopes. We have shown that the two variable sites are at the C-terminus of the protein (a.a. 457-480 and 519-525), whereas the non-variable site was closer to the N-terminal end (a.a. 122-150). The preparation of antigenic probes, as shown here, will enable a more detailed study of the epidemiology of measles and its associated infections.