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Nucleotide sequences of influenza A virus RNA segment 7: a comparison of five isolates

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The nucleotide sequences of RNA segment 7 from influenza viruses A/WSN/33 (N), A/WS/33 (W), A/FW/1/50 (F), A/Singapore/1/57 (S), A/Port Chalmers/1/73 (P), and mouse-adapted A/Port Chalmers/1/73 (M) were determined directly from virion RNA by dideoxy primer-extension sequencing[1] and they are compared to that of A/Udorn/72 (U) determined previously[2]. Nucleotide numbering starts at residue 1 at 3' end of virion RNA segment 7. Untranslated regions, residues 1-25 and 1007-1027 were not determined. The table shows nucleotide differences; those causing coding changes are stippled. Amino acid changes in the M_1 and M_2 proteins between A/Udorn/72 and other strain(s) are also shown.

Ntd #	Strains U	N	W	F	S	P M	aa # & change	Ntd #	Strains U	N	W	F	S	P M	aa # & change	Ntd #	Strains U	N	W	F	S	P M	aa # & change
31	c	t	t	t	t	c		331	a	g	g	g	g	a		785	c	t	t	t	c	c	
37	g	a	a	a	a	a		373	a	a	a	a	g	a		791	t	c	c	t	t	t	
55	t	c	c	c	c	t		394	a	a	a	a	a	g		794	t	c	t	t	t	t	
70	t	c	c	c	c	t		406	c	t	t	c	t	c		795	g	a	a	g	g	g	28 V-I**
94	g	g	g	g	g	a		427	g	g	g	g	g	a/g		800	t	a	a	c	c	t	
100	g	a	a	a	a	g		454	c	a	a	a	c	c		803	g	a	a	a	g	g	
124	t	a	a	t	t	t		463	g	g	g	a	g	g		805	g	a	a	g	g	g	31 S-N**
127	a	g	g	g	g	a		469	t	c	c	c	t	t		815	g	a	g	g	g	g	
136	a	c	c	c	c	a		502	c	t	t	t	t	c		819	t	t	t	c	t	t	
147	c	t	c	c	c	c/t	41 A-V*	503	a	c	c	a	a	a		866	c	t	t	t	t	c	
169	a	a	a	a	a	t		514	g	g	g	g	g	a		872	a	t	t	t	c	a	
175	a	a	a	a	a	t		524	g	a	a	a	a	g	167 A-T*	873	t	c	c	c	t	t	54 P-L*
205	g	a	a	a	g	g		532	c	t	c	c	c	t		874	t	g	g	t	t	t	54 P-R#
211	t	t	t	c	t	t		544	a	c	c	a	a	a		879	g	a	a	a	a	g	56 E-K**
214	a	g	g	g	a	a		568	g	a	a	g	g	g		882	c	t	t	c	c	c	57 H-Y**
241	a	g	g	a	a	a		610	a	g	g	g	g	a		888	c	t	t	c	c	c	
274	c	t	t	c	c	c		619	g	a	a	a	a	g		917	a	g	g	a	a	a	
277	c	t	t	t	c	c		637	g	t	t	g	g	g	205 E-D*	920	t	a	a	a	a	t	
286	t	c	c	t	t	t		638	g	a	a	g	g	g	206 V-I*	958	g	a	a	g	g	g	82 S-N**
289	g	a	a	g	g	g		670	a	g	g	a	a	a		970	c	t	t	c	c	c	86 A-V**
309	g	a	a	g	g	g	95 R-K*	677	g	a	a	g	g	g	218 A-T*	977	c	t	t	t	t	c	
328	a	g	g	a	a	a		697	c	c	c	a	g	c	224 S-R*	978	a	g	g	a	a	a	89 S-G**
								712	a	a	a	g	a	a		991	g	a	a	a	g	g	93 S-N**

* = M_1 aa; ** = M_2 aa; + = M_2 aa strain F; # = M_2 aa strains N & W

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