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Nucleotide sequence comparison of the genome of two 17D-204 yellow fever vaccines

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The genome of the attenuated 17D-204 yellow fever vaccine is a single stranded RNA composed of 10862 nucleotides. The sequence derived from the 17D-204 strain supplied by the American type culture collection (ATCC) was first published by Rice et al. (1). Independently, we have cloned the genome of the Pasteur 17D-204 vaccine. Partial sequences were reported (2,3). We have now completed the sequence by the classical method (4). The variations between the ATCC and Pasteur substrains are summarized in the Table. When possible, the changes were checked by sequencing overlapping cDNAs and the genomic RNA, using specific oligodeoxynucleotides (5,6). They were also compared with the published sequence of the virulent Asibi virus from which the 17D vaccine was derived (7).

Nucleotide	Protein	ATCC		PASTEUR			
		cDNA nt	aa	cDNA nt	aa	RNA nt	aa
2309	E	T*	Phe	T*,C	Phe,Leu	U*	Phe
6529	NS 4A	C	Phe	T*	Phe	–	–
6758	NS 4A	G	Val	A,A*	Ile	A*	Ile
6874	NS 4A	A*	Ser	G,A*	Ser	A*	Ser
7319	NS 4B	G*	Glu	A,A	Lys	–	–
7695	NS 5	A	Asp	G,A*	Gly,Asp	A*	Asp
9605	NS 5	G	Asp	A*	Asn	A*	Asn
10454	3'NCR	G		A*		–	
10722	3'NCR	G*		A		–	

Table : Differences at the nucleotide and amino acid level in the genome of the ATCC (1) and Pasteur 17D-204 yellow fever vaccines. * indicates that the base is present in the sequence of Asibi virus; - no data by sequencing; NCR : non coding region.

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