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Complete nucleotide sequence of the simian rotavirus SA11 VP4 gene

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A full length cDNA clone of simian rotavirus SA11 gene 4 was constructed from two partial clones. The nucleotide sequence was determined by the dideoxy chain termination method. The cDNA clone of 2362 nucleotides has a single open reading frame (bases 10-2337) of 776 amino acids, coding for a polypeptide of 86,775 MW. Comparison of the predicted amino acid sequence of SA11 VP4 with other rotavirus strains (Table) shows that this sequence differs markedly from one previously published for SA11 (1). The latter is closely related to the C486 bovine strain and is therefore almost certainly derived from a bovine virus. The trypsin cleavage sites noted for other rotavirus strains are conserved (2).

VP7 Serotype	I		III			IV	V
	WA(3)	RV5(4)	UK(2)	C486(5)	SA11fM(1)	RRV(6)	OSU(7)
SA11	70.6%	70.9%	74.6%	81.4%	83.0%	88.4%	82.2%
SA11fM	70.2%	70.4%	73.8%	97.0%		84.5%	81.6%

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GGCTATAAAATGGCTTCGCTCATTTATAGACAATTGCTCACGAATTCTTATACAGTAGATTTATCCGATGAGATACAAGAGATTGGATCAACTAAATCAC 100
AAAATGTCACAATTAATCCTGGACCATTTGCGCAAACAGGTTATGCTCCAGTTAACTGGGGACCTGGAGAAATTAATGATTCTACGACAGTTGAACCATT 200
GCTGGATGGGCCTTATCAACCAACGACATTCAATCCACCAGTCGATTATTGGATGTTACTGGCTCCAACGACACCTGGCGTAATTGTTGAAGGTACAAAT 300
AATACAGATAGATGGTTAGCCACAATTTTAATCGAGCCAAATGTTCAGTCTGAAAATAGAACTTACACTATATTTGGTATTCAAGAACAATTAACGGTAT 400
CCAATACTTCACAAGACCAGTGGAAATTTATTGATGTCGTAAAAACAACTGCAAATGGAAGTATAGGACAATATGGACCATTACTATCCAGTCCGAAATT 500
ATATGCAGTTATGAAGCATAATGAAAAATTATATACATATGAAGGACAGACACCTAACGCTAGGACAGCACATTATTCAACAACGAATTATGATTCTGTT 600
AATATGACTGCTTTTTGTGACTTTTATATAATTCCTAGATCTGAAGAGTCTAAATGTACGGAATACATTAATAATGGATTACCACCAATACAAAATACTA 700
GAAATGTTGTACCATTATCGTTGACTGCTAGAGATGTAATACACTATAGAGCTCAAGCTAATGAAGATATTGTGATATCCAAGACATCATTGTGGAAAGA 800
AATGCAATATAATAGAGATATAACTATTAGATTTAAATTTGCAAATACAATTATAAAATCAGGAGGGCTGGGATATAAGTGGTCAGAAATATCATTTAAG 900
CCAGCGAATTATCAATACACATATACTCGTGATGGTGAAGAAGTTACCGCACATACTACTTGTTCAGTGAATGGCGTTAATGACTTCAGTTTTAATGGAG 1000
GATATTTACCAACTGATTTTGTTGTATCTAAATTTGAAGTAATTAAAGAGAATTCATACGTCTATATCGATTACTGGGATGATTCACAAGCATTTCGTAA 1100
CGTGGTGTATGTCCGATCGTTAGCAGCAAACTTGAATTCAGTTATGTGTACTGGAGGCAGCTATAATTTTAGTCTACCAGTTGGACAATGGCCTGTTTTA 1200
ACTGGGGGAGCAGTTTCTTTACATTCAGCTGGTGTAACACTATCTACTCAATTTACAGATTTCGTATCATTAAATTCATTAAGATTTAGATTTAGACTAG 1300
CTGTCGAAGAACCACACTTTAAACTGACTAGAACTAGATTAGATAGATTGTATGGTCTGCCTGCTGCAGATCCAAATAATGGTAAAGAATATTATGAAAT 1400
TGCTGGACGATTTTCACTTATATCATTAGTGCCATCAAATGATGACTATCAGACTCCTATAGCAAACTCAGTTACTGTACGACAAGATTTAGAAAGGCAG 1500
TTAGGAGAACTAAGAGAAGAGTTTAACGCTTTGTCTCAAGAAATTGCAATGTCGCAGTTAATCGATTTAGCGCTTCTACCATTAGATATGTTCTCAATGT 1600
TTTCTGGCATTAAAAGTACTATTGATGCTGCAAAATCAATGGCTACTAATGTTATGAAAAAATTCAAAAAGTCAGGATTAGCGAATTCAGTTTCAACACT 1700
GACAGATTCTTTATCAGACGCAGCATCATCAATATCAAGAGGTTCATCTATACGTTCGATTGGATCTTCAGCATCAGCATGGACGGATGTATCAACACAA 1800
ATAACTGATATATCGTCATCAGTAAGTTCAGTTTCGACACAAACGTCAACTATCAGTAGAAGATTGAGACTAAAGGAAATGGCAACACAAACTGAGGGTA 1900
TGAATTTTGATGATATATCAGCGGCTGTTTTGAAGACTAAGATAGATAAATCGACTCAAATATCACCAAACACAATACCTGACATTGTTACTGAAGCATC 2000
GGAAAAATTCATACCAAATAGGGCTTACCGTGTTATAAACAACGATGATGTGTTTGAAGCTGGAATTGATGGAAAATTTTTTGCTTATAAAGTGGATACA 2100
TTTGAGGAAATACCATTTGATGTACAAAAATTCGCTGACTTAGTTACAGATTCTCCAGTAATATCCGCTATAATTGATTTTAAAACACTTAAAAATTTGA 2200
ACGATAATTACGGCATTACTAAGCAACAAGCATTTAATCTTTTAAGATCTGACCCAAGAGTTTTACGTGAATTCATTAATCAGGACAATCCTATAATTAG 2300
AAATAGAATTGAACAACTGATTATGCAATGCAGGTTGTGAGTAATTTCTAGAGGATGTGACC                                       2362
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