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Complete nucleotide sequence of gene segment 8 encoding non-structural protein NS2 of SA bluetongue virus serotype 10

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The sequence of the double stranded RNA gene segment S8 of bluetongue virus serotype 10 (SA BTV 10) has been determined. It is the first reported sequence of a gene encoding a non-structural single-stranded RNA (ssRNA) binding protein (1) in the Orbivirus genus of the family Reoviridae. SsRNA binding proteins for rotavirus (2) and reovirus (3) have also been described. However, unlike σNS of reovirus and NCVP4 of rotavirus, BTV NS2 is phosphorylated and the possibility of autophosphorylation has been raised (4).

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   1 gttaaaaatccttgagtcA TGGAGCAAAAGCAACGTAGA TTTACTAAAAACATTTTTGT TTTGGATGCAAATGCTAAAA CACTATGCGGACGGATCGCA
 101 AAGTTGAGTTCGCAACCGTA CTGTCAGATTAAAATTGGAA GAGTAATAGCTTTTAAACCT GTCAAGAATCCGGAACCTAA AGGATACGTGCTAAATGTTC
 201 CAGGACCTGGTGCGTACAGA ATTCAGGATGGACAGGATAT CATTAGCTTGATGTTGACAC CACATGGAGTTGAAGCGACA ACGGAAAGATGGGAAGAGTG
 301 GAAGTTTGAGGGTGTTAGTG TGACACCAATGGCTACTAGG GTACAACATAACGGTGTGAT GGTTGATGCTGAGATTAAGT ATTGCAAAGGGATGGGAATT
 401 GTACAACCATATATGCGGAA CGATTTTGATCGGAATGAGA TGCCCGATTTGCCAGGTGTG ATGAGGTCAAATTACGATAT TCGCGAATTGCGCCAGAAGA
 501 TTAAAAATGAACGAGAGTCA GCGCCACGGCTTCAGGTTCA AAGCGTGGCGCCAAGGGAAG AGTCGCGCTGGATGGATGAT GATGAAGCAAAGGTGGACGA
 601 AGAGGCTAGAGAAATGATCC CGGGAACTAGCAGATTGGAG AAGCTGCGTGAAGCGAGAAG CAACGTTTTTAAGGAGGTGG CAGCTGGGATTAATTGGAAT
 701 CTGGATGAGAAAGATGAAGA AGATGGAGATGAACGAGAGG ATGAGGAGCGGGTGAAGACC CTGAGTGATGATGATGAGCA AGGTGAGGATGCGAGTGACG
 801 ATGAACACCCAAAGACTCAT ATAACTAAGGAATACGTTGA AAAGGTTGCAAAACAGATTA AACTGAAGGATGAACGATTC ATGAGTTTGTCAAGCGCTAT
 901 GCCTCAAGCGAGCGGCGGAT TTGATCGCATGATTGTTACA AAGAAGCTTAAATGGCAGAA CGTACCACTATATTGTTTTG ATGAATCATCGAAAAGGTAT
1001 GAGTTGCAATGTGTGGGTGC GTGTGAGCGTGTTGCTTTTG TCTCTAAGGACATGAGCTTG ATCATATTGCGGTCGGCGTT TAGGCGCTTGtgaccgcgtg
1101 gttaggggggattttacac ttac
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A complete segment 8 gene was cloned into pBR322 (5). This gene (containing the 5' and 3' terminal conserved sequences) was recloned into the Bluescribe vector and sequenced in both directions according to standard Sanger dideoxy sequencing protocols. The sequence is 1124 base pairs in length and contains a single open reading frame which codes for a protein of 357 amino acids. The protein has a molecular weight of 41 153 Daltons and a net charge of -4 at pH 7.0. The C'terminal half of the protein is relatively hydrophilic - amino acids 234-294 constitute a very prominent region of hydrophilicity. Analysis of the amino acid sequence has revealed that NS2 does not contain the highly conserved sequence motifs which are characteristic of the catalytic domains of all known protein kinases (6). Therefore, it is unlikely that NS2 has kinase activity.

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