The complete nucleotide sequence of genome segment 7 of bluetongue virus, serotype 1 from South Africa

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The complete sequence of genome segment 7, of bluetongue virus, serotype 1 South Africa (BTV1SA), which encodes the serogroup-specific antigen, VP7 (1), was determined from a full length cDNA clone synthesized using terminal oligonucleotides as primers (2). Genome segment 7 from BTV1SA is the same length as the corresponding segment from BTV10 (3), 1156 nucleotides with an open reading frame of 349 amino acids. Comparison of the two clones at the nucleotide level revealed an homology of 88.9%. The homology at the amino acid level was 98.3% identity and 98.9% similarity (including conservative changes).

REFERENCES

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                        M  D  T  I  A  A  R  A  L  T  V  M  R  A  C  A  T  L
1     GTTAAAAATCTATAGAGATGGACACTATCGCTGCAAGAGCACTTACTGTGATGCGAGCATGTGCTACGCT

        Q  E  A  R  I  V  L  E  A  N  V  M  E  I  L  G  I  A  I  N  R  Y  N
71    TCAAGAAGCAAGAATTGTGTTGGAAGCTAACGTGATGGAGATACTGGGGATAGCAATCAACAGATATAAT

       G  L  T  L  R  G  V  T  M  R  P  T  S  L  A  Q  R  N  E  M  F  F  M
141   GGATTAACTTTACGAGGGGTGACGATGCGCCCGACCTCATTGGCGCAGAGAAATGAGATGTTTTTTATGT

      C  L  D  M  M  L  S  A  A  G  I  N  V  G  P  I  S  P  D  Y  T  Q  H  M
211   GTTTAGATATGATGCTGTCCGCGGCTGGGATAAACGTAGGACCGATATCTCCAGATTATACCCAACATAT

        A  T  I  G  V  L  A  T  P  E  I  P  F  T  T  E  A  A  N  E  I  A  R
281   GGCTACAATTGGTGTACTAGCGACGCCAGAGATACCTTTTACAACGGAAGCGGCGAATGAGATTGCTCGC

       V  T  G  E  T  S  T  W  G  P  A  R  Q  P  Y  G  F  F  L  E  T  E  E
351   GTGACTGGGGAGACTTCGACGTGGGGGCCAGCCCGTCAGCCTTATGGTTTCTTCCTTGAAACTGAGGAAA

      T  F  Q  P  G  R  W  F  M  R  A  A  Q  A  A  T  A  V  V  C  G  P  D  M
421   CCTTCCAGCCCGGACGTTGGTTCATGCGTGCCGCCCAAGCAGCAACTGCGGTAGTGTGTGGTCCGGATAT

        I  Q  V  S  L  N  A  G  A  R  G  D  V  Q  Q  I  F  Q  G  R  N  D  P
491   GATTCAAGTGTCACTGAATGCTGGAGCAAGAGGAGATGTGCAGCAGATATTTCAGGGTCGTAACGACCCC

       M  M  I  Y  L  V  W  R  R  I  E  N  F  A  M  A  Q  G  N  S  Q  Q  T
561   ATGATGATATATCTAGTTTGGAGAAGAATTGAAAACTTCGCGATGGCGCAGGGTAACTCACAGCAAACTC

      Q  A  G  V  T  V  S  V  G  G  V  D  M  R  A  G  R  I  I  A  W  D  G  Q
631   AAGCAGGCGTGACTGTTAGCGTTGGTGGAGTAGATATGCGGGCGGGGCGTATCATAGCGTGGGATGGACA

        A  A  L  H  V  R  N  P  T  Q  Q  N  A  M  V  Q  I  Q  V  V  F  Y  I
701   GGCTGCTCTACATGTGCGCAATCCAACACAACAGAATGCGATGGTTCAGATACAGGTCGTGTTCTACATT

       S  M  D  K  T  L  N  Q  Y  P  A  L  T  A  E  I  F  N  V  Y  S  F  R
771   TCTATGGATAAGACCTTAAATCAATACCCTGCCTTGACTGCTGAAATCTTTAATGTTTATAGCTTCAGAG

      D  H  T  W  H  G  L  R  T  A  I  R  N  R  T  T  L  P  N  M  L  P  P  I
841   ATCACACATGGCACGGGCTTAGAACGGCTATACGCAACAGAACTACACTGCCGAATATGCTGCCACCCAT

        F  P  P  N  D  R  D  S  I  L  T  L  L  L  L  S  T  L  A  D  V  Y  T
911   CTTTCCACCAAACGATCGAGATAGTATCCTGACTCTTTTGCTTTTGTCTACGCTTGCTGATGTTTATACT

       V  L  R  P  E  F  A  M  H  G  V  N  P  M  P  W  P  L  T  A  A  I  A
981   GTTTTAAGACCTGAGTTCGCGATGCACGGCGTAAACCCAATGCCTTGGCCGCTCACAGCTGCTATTGCAC

      R  A  A  Y  V  *
1051  GCGCCGCCTATGTGTAGTCCACTTAGCACGGGTGTGGGTTACATATGCGGTGTGTCGGTTGTGGGATATA

1121  TGTGACCCATTCAAACGTCTCTTAGATTACACTTAC
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