

Multiple Sequence Alignment and Phylogenetic Tree Construction of Viral Protein 2 of Bluetongue virus

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Abstract

Bluetongue is a non contagious disease of animals and spread by the biting midges. Bluetongue disease is mild in goats and severe in sheep as sheep is the primary host of bluetongue virus. There are several clinical symptoms of Bluetongue disease have been found in ruminants like fever, viraemia, sore muzzle, facial oedema, hyperaemia and congestion, erosion of mucous memberane, haemorrhages, vascular permeability. The bluetongue virus is hypervariable in nature therefore there are 24 serotypes of bluetongue virus are well recognised with three newly proposed serotypes BTV 25 from Switzerland and BTV 26 from Kuwait and BTV 27 from France. Therefore, there are 27 different serotypes of BTV have been identified according to the specificity of interactions between neutralizing antibodies and the virus outer capsid, the VP2 protein. Bluetongue has a serious economic impact on dairy and wool industry mainly due to high morbidity, mortality and mandatory trade barrier on the movement of BT infected livestock and germplasm. Bioinformatical tools like Clustal X and Clustal Omega are promising and helpful in the construction of phylogenetic tree to check the evolutionary relation among all 24 serotypes of BTV and alignment of the many sequences through Multiple sequence Alignment.

Keywords : BTV, VP2, MSA, FASTA, NCBI, CLUSTAL X, CLUSTAL OMEGA

Bluetongue is a highly infectious vector born viral disease and it is a disease of wild and domestic animals (ruminants). Bluetongue is a non contagious disease of animals and spread by the biting midges (Sperlova, A. and Zendulkova, D. 2011). Bluetongue disease is mild in goats and severe in sheep as sheep is the primary host of bluetongue virus. Cattle act as reservoir of bluetongue virus (Browne, 1971). There are several clinical symptoms of Bluetongue disease have been found in ruminants like fever, viraemia, sore muzzle, facial oedema, hyperaemia and congestion, erosion of mucous memberane, haemorrhages, vascular permeability (OIE, 2014). The bluetongue virus is hypervariable in nature therefore there are 24 serotypes of bluetongue virus are well recognised with three newly proposed serotypes BTV 25 from Switzerland and BTV 26 from Kuwait and

BTV 27 from France. Therefore, There are 27 different serotypes of BTV have been identified according to the specificity of interactions between neutralizing antibodies and the virus outer capsid, the VP-2 protein (Roy *et al.* 1992; Maan *et al.* 2011; Bumbarov, V. 2012; Zientara *et al.* 2014; Chand *et al.* 2015). In India 22 serotypes have been reported of Bluetongue virus (Prasad *et al.* 2009). Bluetongue virus belongs to family Reoviridae and genus Orbivirus (Tabachnick *et al.* 2009). Bluetongue has a serious economic impact on dairy and wool industry mainly due to high morbidity, mortality and mandatory trade barrier on the movement of BT infected livestock and germplasm. BT is evolving into newer challenges and poses ever increasing threat to associated environment. Unnatural host like canines have in the past contracted BT infections. Many species of

AGJ83602.1
ABB71704.1
AGJ83652.1
AGJ83612.1
ABB71694.1
AKV60674.1
AAB30550.1
AGW27481.1
ABB71700.1
AGC83563.1
AGJ83472.1
AGJ83512.1
AEP22601.1
CAE51109.1
AKV60616.1
AKV60677.1
AGJ83462.1
AGJ83592.1
AKV60678.1
AL151285.1
AMD77980.1
AGJ83582.1
AKV60675.1
AGW27457.1

SPMFINARLRLTHEGASIRKTD...
APFDTKYKITEETIANAKN...
SPMFINAKLRHAGEIATR...
APMFINARLKITKEIEAQA...

AGJ83602.1
ABB71704.1
AGJ83652.1
AGJ83612.1
ABB71694.1
AKV60674.1
AAB30550.1
AGW27481.1
ABB71700.1
AGC83563.1
AGJ83472.1
AGJ83512.1
AEP22601.1
CAE51109.1
AKV60616.1
AKV60677.1
AGJ83462.1
AGJ83592.1
AKV60678.1
AL151285.1
AMD77980.1
AGJ83582.1
AKV60675.1
AGW27457.1

LVQNVNVSQRGLVLSAFP...
IIRSSNDANRKSFEYFP...
LIQKSDGPERLDVLRNF...
VIRRVTKGRLEAISRE...

AGJ83602.1
ABB71704.1
AGJ83652.1
AGJ83612.1
ABB71694.1
AKV60674.1
AAB30550.1
AGW27481.1
ABB71700.1
AGC83563.1
AGJ83472.1
AGJ83512.1
AEP22601.1
CAE51109.1
AKV60616.1
AKV60677.1
AGJ83462.1
AGJ83592.1
AKV60678.1
AL151285.1
AMD77980.1
AGJ83582.1
AKV60675.1
AGW27457.1

QQQRQSSVFAYISQRDD...
MRQRQTSLHKTLDDP...
LEQRQSAVFEHLNKQDD...
KRQEQSAYKHILANLAD...

AGJ83602.1
ABB71704.1
AGJ83652.1
AGJ83612.1
ABB71694.1
AKV60674.1
AAB30550.1
AGW27481.1
ABB71700.1
AGC83563.1
AGJ83472.1
AGJ83512.1
AEP22601.1
CAE51109.1
AKV60616.1
AKV60677.1
AGJ83462.1
AGJ83592.1
AKV60678.1
AL151285.1
AMD77980.1
AGJ83582.1
AKV60675.1
AGW27457.1

AIPMVLFDTE-IKIPVEV...
SVPVLIYSOG-LMIWPA...
SVPVLIYGD-IKIPVEV...
SVPILYADT-LWFLPVE...

AGJ83602.1
ABB71704.1
AGJ83652.1
AGJ83612.1
ABB71694.1
AKV60674.1
AAB30550.1
AGW27481.1
ABB71700.1
AGC83563.1
AGJ83472.1
AGJ83512.1
AEP22601.1
CAE51109.1
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AKV60677.1
AGJ83462.1
AGJ83592.1
AKV60678.1
AL151285.1
AMD77980.1
AGJ83582.1
AKV60675.1
AGW27457.1

PELHEGLEHQTHTPSD...
DQDW--ESLKQYKHP...
PDLHEGLEHQTHTPKI...
GYAP--ESEIEFDFPK...

AGJ83602.1
ABB71704.1
AGJ83652.1
AGJ83612.1
ABB71694.1
AKV60674.1
AAB30550.1
AGW27481.1
ABB71700.1
AGC83563.1
AGJ83472.1
AGJ83512.1
AEP22601.1
CAE51109.1
AKV60616.1
AKV60677.1
AGJ83462.1
AGJ83592.1
AKV60678.1
AL151285.1
AMD77980.1
AGJ83582.1
AKV60675.1
AGW27457.1

EYMNTRMSQGGVNI...
NYMRTDIFKGGIKN...
EYTKTKISQGGVDS...
EYFLNTTIYLGNIQ...
NYMKTIISEGGVNL...

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AGJ83602.1  DKLEPQIRAEQVLSKYYYSRRHVLGVISISVSDGGLK-VYSSGIVRHRLCEKSIKLYKC
ABB71704.1  DLAEQPHRISKALFEFHVDRDHRVGIASISISRNQDVT-THSQGIVKVELLKKNILRHQF
AGJ83652.1  DNDVMQIRSEQAISRYYSRRHIAGVWISICISQDGGK-AYSTGIVKHRICEKSLKLYKC
AGJ83612.1  DRVSAGYRCDKLSRFPLSLDLHGRGIVILSVSKSRAIS-AYSEGIVSHRLCKKINVLGFTC
ABB71694.1  DRVPAARLRCDRLLRFPLSAQHLKGIWVIQINEEGGFD-VYTEGIVTHRVCCKSLKHKVC
AKV60674.1  DRVDAAHRCNRLRARFPLSAVHLKGIWVLSIAKDRTVK-AYTEGIVTHRLCKKINVLGFTC
AAB30550.1  DKLEPHTRSEQIVSRVYYSRKHCTGIVSVTVGQNSQLR-VHTSGIVKHRVCDKFLKHKC
AGW27481.1  ERVPASIRASRIKLRFPPLSVKHLKGIWVIQIDEEGKFT-VYSEGIVSHRICKKINLKYKC
ABB71700.1  DKLDPQVRSEQLSKYYYSRRHICGVAVSVGQEGQLQ-VYSTGIVRHRICEKSIKLYKC
AGC83563.1  DVVPYSVRRERISRFPLSKHRLGIALIADRNQKVS-VQTEGIVTHRLCKKINLKYKC
AGJ83472.1  GRGSASDCVRRATRLRYIQRHIRGVSVVSLRDGVIN-TYSEGIKAMLCSEKSVLKMYH
AGJ83512.1  DKLEPHRSEQVSKYYYSRRHICGVAVSVGQEGQLQ-VYSSGIVRHRVCEKFLKLYKC
AEP22601.1  ALTSPQLRIDKIKRRFPLSSDHLKGIWVQISVRPDTFS-VVTQGIVKHRVCKKTLKLYKC
CAE51109.1  DKLSPSQHAARAKRRFKGTQYIDVIVLQMKRPLGVSVSEKHSKIKVCRNRLNYDH
AKV60616.1  TLVGADVRIKIRRRFPLSAKHLKGIWVQISVHPRTFS-VTTGIVKHKVCKKTLKLYKC
AKV60677.1  DKISPAQHAARAKRRFRGTREYVNDVIVLQMKRPGTVGNVSEKHSKIKVCRNRLNYDH
AGJ83462.1  NKVSAYVRCNRLRARFPLSSIHRLGIALITIGKINRMD-AYTEGIVSHRICKKINVLGFTC
AGJ83592.1  GKGASDCVRRTRKRLRYIQHHRGVSIVISLSDGSIIN-TYSEGIKATLCKSVLKYSY
AKV60678.1  DLVEPQLRISRVMDYFKHVSEHRVAVSISIRNGDVS-TYSRGIVHVELLKKINLKYKC
ALI51285.1  DKLEPQIRSEQIVNYYYSRRHISGVVSIQVNGGQLK-VHSMGITRHRICKKINLKYKC
AMD77980.1  DVVPLSVRRERISRFPLSRHVKGIALISVDRNQKVS-VQTEGIVTHRLCKKINLKYKC
AGJ83582.1  DVVPATVRKERILMRFPPLSARHLRGIALITIDRDKVH-VQTEGIVSHRICKKINLKYKC
AKV60675.1  DVQVPOVQVCEALRRFPYTYREIYHDIWIVIQVGRPELKVQMKRGTSTKVKVCRNRLNYDH
AGW27457.1  SLVDSINRDIKIKRRFPLSHRHLRGIVQISVRPDTFG-VTTGIVKHKICKKTLKLYKC
    
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AGJ83602.1  KTIILIRMPGHVFGNDELMTKLLNI
ABB71704.1  RVALLKVKGYVFGNDEMLTKLLNV
AGJ83652.1  KVVLVRMPGYVFGNDELMTKLLNV
AGJ83612.1  RVL L L K F S G H V F G N D E M L T K L L N V
ABB71694.1  DIVL L L K F H G H V F G N D E M L T K L L N V
AKV60674.1  QI L L L K F S G H V F G N D E M L T K L L N V
AAB30550.1  KVILVRMPGYVFGNDELMTKLLNV
AGW27481.1  DIVL L K F S G H V F G N D E M L T K L L N V
ABB71700.1  KVVLVRMPGHVFGNDELMTKLLNV
AGC83563.1  DVVLFKFSGYVFGNDEMLTKLLNV
AGJ83472.1  KVVLVKVKGYVFGHDEMLTKLLNV
AGJ83512.1  KVVLVKMPGYVFGNDELMTKLLNV
AEP22601.1  DVILIQTPGYVFGNDELLTKLLNI
CAE51109.1  KVILTKFAGLVYGNIELTKLANL
AKV60616.1  DVILLQTPGYVFGNDELLTKLLNI
AKV60677.1  KVVLTKFAGLVYGNIELTKLANL
AGJ83462.1  QI L L L K F S G H V F G N D E M L T K L L N V
AGJ83592.1  KVVLKVKGHVFGHDEMLTKLLNV
AKV60678.1  QVALLKVKGYVFGNDEMLIKLLNV
ALI51285.1  KVVLVRMPGHVFGNDELMTKLLNV
AMD77980.1  DVILFKFSGHVFGNDEMLTKLLNV
AGJ83582.1  DVILFKFSGYVFGNDEMLTKLLNV
AKV60675.1  KVILSRLCGLVYGNIELMTKLTNI
AGW27457.1  DVILIQIPGYVFGNDELLTKLLNI
    
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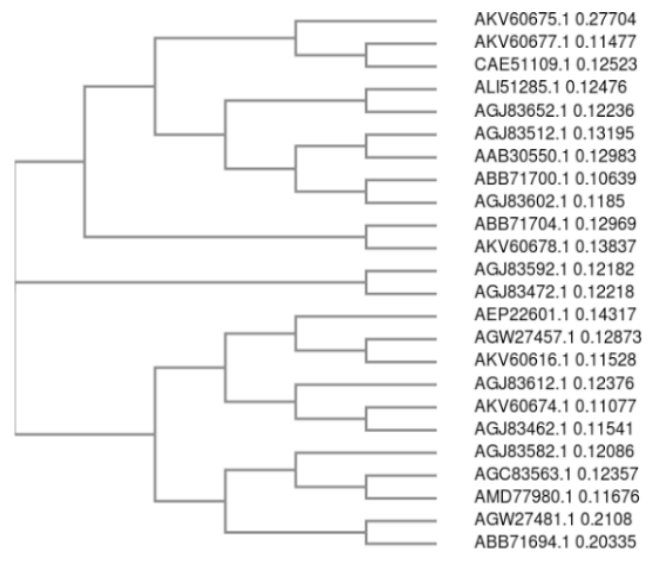
RESULTS

Sequence alignment produced by CLUSTAL X program of above Protein sequences is a key denoting: conserved sequences (*), Conservative mutation (:), semi-conserved mutation (.), and non conservative mutation (()).

Following are the Screen shots of multiple sequence alignment of 24 serotypes of VP2 Bluetongue virus.

Tree Construction in CLUSTAL Omega

Phylogenetic Tree construction was carried out in clustal omega.



Phylogenetic tree in CLUSTAL Omega

Discussion:The study in CLUSTAL X for multiple sequence alignment, of 24 serotypes of viral Protein 2 of Bluetongue virus, and CLUSTAL Omega for phylogenetic tree construction to review the Relation between different serotypes(1 to 24) of Bluetongue virus having same Protein (Viral protein 2), and from result of multiple sequence alignment, it is shown the conserved sequence, semiconservative mutation, conservative mutation and non conservative mutations among 24 different sequences.

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