



Genomic Insertions in BVDV and their Role in Non-Homologous Recombination

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DESCRIPTION

Bovine Viral Diarrhoea Virus (BVDV) is an important Ribonucleic Acid (RNA) virus belonging to the genus Pestivirus within the family Flaviviridae. It contains a positive-sense, single-stranded RNA genome that encodes structural and non-structural proteins required for replication, particle formation, and interactions with host cells. Although the viral genome has a compact organization and strong functional constraints, it can undergo different forms of genetic variation. Insertions are particularly important because they introduce additional nucleotide sequences into the existing genome and can influence protein structure, replication, genomic stability, and interactions between the virus and its host. BVDV insertions can vary in length, nucleotide composition, genomic position, and origin. Some may involve duplication of neighbouring viral sequences, whereas others can contain sequences related to cellular RNA or different regions of the viral genome. Their consequences depend strongly on their location. An insertion that preserves the reading frame may permit continued production of a functional protein, while an insertion that disrupts the frame can alter downstream amino acids or generate premature termination. Consequently, the molecular environment surrounding an insertion plays an important role in determining whether the altered viral genome remains viable.

The origin of inserted sequences provides important clues about the mechanisms responsible for genomic rearrangement. BVDV relies on an RNA-dependent RNA polymerase to produce new viral RNA molecules. During replication, this polymerase may encounter RNA secondary structures, damaged templates, unusual nucleotide arrangements, or other obstacles that interrupt normal synthesis. In some circumstances, the polymerase may detach from one template and resume synthesis using another RNA molecule. Such template switching can generate a new genomic arrangement in which an additional sequence becomes incorporated between previously connected viral regions. Non-homologous recombination is particularly relevant when an insertion has little or no extensive sequence

similarity with its surrounding regions. Homologous recombination generally involves alignment between related sequences, whereas non-homologous mechanisms can connect segments with limited sequence identity. During BVDV RNA replication, transient interactions between viral RNA molecules, cellular RNA, or rearranged RNA intermediates could provide opportunities for such events. If polymerase reassociation occurs at an alternative template, the resulting RNA may contain a sequence that was not originally present at that genomic position.

The boundaries of an insertion can provide valuable information about its possible formation. Clear transitions between unrelated nucleotide sequences may indicate a joining event involving limited homology. Short matching sequences near the junctions could facilitate temporary alignment between RNA molecules, although short similarities alone cannot establish a specific mechanism because they may occur randomly. A more reliable interpretation requires consideration of insertion length, nucleotide composition, reading-frame position, surrounding sequence characteristics, and similarity to potential donor sequences. RNA secondary structure may further influence the development of genomic insertions. Viral RNA can fold into hairpins, stem-loops, and other structures that affect polymerase movement. Strong structures may cause temporary polymerase pausing or dissociation, increasing the possibility of interaction with another RNA template. If synthesis resumes from an alternative template, the newly produced genome can contain an additional sequence. This mechanism is especially relevant to RNA viruses because their replication machinery operates directly on RNA molecules and can encounter multiple RNA species within an infected cell.

Insertions containing sequences resembling host-derived RNA are particularly noteworthy. Cellular transcripts are abundant in infected cells and may occasionally come into contact with viral replication complexes. A polymerase that switches from a viral RNA template to a cellular RNA and subsequently returns to the viral template could theoretically incorporate a portion of the

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Received: 30-Aug-2025, Manuscript No. JDMGP-25-32400; **Editor assigned:** 02-Sep-2025, PreQC No. JDMGP-25-32400; **Reviewed:** 16-Sep-2025, QC No. JDMGP-25-32400; **Revised:** 22-Sep-2025, Manuscript No. JDMGP-25-32400; **Published:** 30-Sep-2025, DOI: 10.35248/2153-0602.25.16.388

Citation: Hamaguchi Y (2025). Genomic Insertions in BVDV and their Role in Non-Homologous Recombination. J Data Mining Genomics Proteomics. 16:388.

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cellular sequence into the viral genome. For this altered genome to persist, the resulting RNA must retain enough functionality to support viral replication. Highly disruptive insertions are likely to be eliminated, whereas compatible additions may remain within viral populations and undergo further genetic modification. The biological consequences of insertions depend on the affected genomic region. Alterations within sequences encoding viral enzymes may influence catalytic activity, protein

stability, or interactions with replication components. Changes in structural-protein regions may affect protein processing, folding, particle assembly, or cellular interactions. An insertion can therefore produce effects that range from minimal structural changes to substantial modifications in viral properties. Insertions located in more tolerant regions may be accommodated more readily than additions within highly conserved functional domains.