

Molecular Interactions of Bovine Viral Diarrhea Virus with Host Factors during its replication

Muhammad Atif Zahoor and Hiroomi Akashi

Department of Veterinary Microbiology, Graduate School of Agriculture and Life Sciences,
The University of Tokyo, 1-1-1, YAYOI, BUNKYO, TOKYO 113-8657, Japan

ABSTRACT

Livestock is important sector of Agriculture in Pakistan, which accounts for 46.8 percent of agriculture value added and about 10.8 percent of the GDP. It is estimated that the country produces 28 billion liter of milk a year whose value is more than that of the combined value of wheat and cotton. Despite good genetic potential among animals, low production is due to poor nutrition, mis-management, failure to control diseases, and lack of proper marketing of this highly perishable commodity.



Infectious diseases are the real threat to the flourishing dairy industry in Pakistan. Among these the most important one is the bovine viral diarrhea (BVD) which causes a wide variety of clinical disease syndromes in cattle including infertility, abortion, and congenital defects in calves. It is a small enveloped RNA virus, which belongs to the genus *Pestivirus* within the family *Flaviviridae*. Pestiviruses are widespread among the cloven-footed animals (Artiodactyla), causing disease in ruminants (*Bos*, *ovis*, and *Camelidae*) and non-ruminants (*Suidae*).

Bovine viral diarrhea virus was isolated and characterized as KS86-1 ncp (AB078950). The interaction of virus proteins with the host factors was investigated and some are being under trial. Interaction of BVDV-NS5A (1487 bp) with cellular proteins i.e. NS5A mediated Cellular signaling mechanism. NS5A Fragment 1, 2 and 3 i.e. 500 bp, 554 bp and 512 bp respectively were fused separately in frame with Δ c-Myc epitope tag into the pGBKT7 plasmid vector at *EcoRI*/*SaII* restriction sites and transformed into DH5 α *E.coli* strain. The bait plasmid were confirmed through DNA sequencing and then retransformed in to yeast *Saccharomyces cerevicea* strain AH109. The MDBK as well as BFM cell cDNA library was constructed and currently screening is in process. It is hoped that the present studies will help to elucidate the understanding of BVDV life cycle that would thus lead to the development of better BVDV control strategies.