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Complete genome sequence analyses of an Indian cattle strain of bovine viral diarrhoea virus 2 (BVDV-2)

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Bovine viral diarrhea virus (BVDV) is a pestivirus which infects cattle worldwide causing substantial economic losses in cattle farming. BVDV is divided into two recognized species, BVDV-1 and BVDV-2 and one tentative species, BVDV-3. Since, complete genome sequence analysis can provide better insights into molecular epidemiology of BVD, we report here the first complete genome sequence analyses of an Indian BVDV-2 strain isolated from cattle. The full-genome of strain Ind 141353 contains 12285 nucleotides (nt) with a single large open reading frame which codes for 3898 amino acids. Phylogenetic analysis indicated that this strain belongs to the BVDV-2a subtype and has highest (93%) level of genetic identity with the Chinese cattle strain JZ05-1. It was inferred that although introduction from China is possible, introduction of BVDV-2 into Indian and Chinese cattle from a common trade source cannot be ruled out completely. The results in this study extend the spectrum of pestivirus molecular data and provide important insights into BVDV molecular epidemiology.

Keywords: Cattle, Pestivirus, Phylogenetic analysis