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Bovine viral diarrhea virus type 1 current taxonomy according to palindromic nucleotide substitutions method

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Highlights

- BVDV-1 is a widely distributed pathogen affecting cattle and causing economic impact.
- Heterogeneity of BVDV has the potential to cause diagnostic and prophylactic difficulties, therefore, recognition of the molecular characteristics of BVDV field strains is a fundamental element.
- Palindromic nucleotide substitution method, based on the exclusive consideration of strategic genomic sequences corresponding to the 5'-UTR IRES, identified twenty-two genotypes in the species, applying a nomenclature based on divergence in the genus.

Abstract

Pestivirus bovine viral diarrhea virus type 1 species is responsible for cosmopolitan diseases affecting cattle and other ruminants, presenting a wide range of clinical manifestations, with relevant impact on zootechnic production. Understanding genomic characteristic and virus taxonomy is fundamental in order to sustain control and prophylactic programs. Given the recent various studies reporting a relatively high number of new strains, in particular from Asian countries, in the present study, four hundred-eighty-two genomic sequences have been evaluated applying the palindromic nucleotide substitutions method for genotyping. Based on the secondary structure alignment and computing genetic distance among strains in the 5' untranslated region of *Pestivirus* RNA, the current taxonomy of the species was reviewed. Twenty-two genotypes have been identified, applying a nomenclature based on divergence in the genus.

Key words: Bovine viral diarrhea virus type 1, genotypes, nomenclature, palindromic nucleotide substitutions, *Pestivirus*, secondary structure, taxonomy

Introduction

Bovine viral diarrhea virus type 1 (BVDV-1) is an established species of the genus *Pestivirus* of the family *Flaviviridae* (King *et al*., 2012), responsible for cosmopolitan disease affecting cattle and other ruminants, presenting a wide range of clinical manifestations, with relevant impact on zootechnic production. Heterogeneity of the species has been described by different authors based on primary sequence analysis of the 5' untranslated region (UTR) and Npro genomic regions (Vilcek *et al*., 2001; Stalder *et al*., 2005; Xu *et al*., 2006). The observation of nucleotide variations among virus strains at the level of the three specific variable loci in the secondary structure of the 5'-UTR of *Pestivirus* RNA has been conceived as a simple and practical procedure for genotyping (Harasawa and Giangaspero, 1998), since