

TITLE: MOLECULAR CHARACTERIZATION OF CANINE PARVOVIRUS TYPE 2 DETECTED IN DOGS WITH GASTROENTERITIS FROM PARANÁ WEST REGION

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ABSTRACT:

Canine parvovirus type 2 (CPV-2) is one of the most important enteric pathogen in dogs with high morbidity and mortality on susceptible populations. Since its emergence in late 70s, CPV-2 has undergone mutations gaining adaptive advantages with its evolution. Currently three antigenic variants of CPV-2 are circulating, called CPV 2a, 2b and 2c. The frequency distribution of these variants vary according to geographical location and the time reference period of the studies. The objective of this study was to diagnose and molecularly characterize CPV-2 circulating in the dog population residing in the western region of Paraná between 2012 and 2016. Ninety three fecal samples from dogs with gastroenteritis were evaluated. DNA was extracted using a combination of the techniques phenol/chloroform/isoamyl alcohol and silica/guanidiniumisothiocyanate, being amplified by PCR a fragment of 583 bp VP2 gene and subsequent sequencing. From the 93 samples analyzed, 73 (78.5%) were positive for CPV-2. Sequencing and molecular characterization were performed on 41 samples, which resulted in 5 samples as CPV-2b and 36 as CPV-2c. CPV-2c was the predominant variant until 2015, being replaced in 2016 by the CPV-2b. Thirteen samples, characterized as CPV-2c, were identical to the reference CPV-2c strain originally isolated from Italy and other European, North American and South American countries, including Brazil. One sample showed a Thr440Ala mutation, which is the main antigenic site on VP2. Four samples had a silent mutation on residue 447 and 18 samples had a silent mutation on residue 500. Constant CPV-2 strains monitoring is necessary to subsidize epidemiological, pathogenic and evolutionary studies of CPV-2 in Brazil.

Keywords: canine parvovirus, PCR, molecular characterization

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