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Canine circovirus and Canine adenovirus type 1 and 2 in dogs with parvoviral enteritis

Andrea Balboni, Alessia Terrusi, Lorenza Urbani, Roberta Troia, Silvia A M Stefanelli, Massimo Giunti, Mara Battilani*.

* Corresponding author:

Mara Battilani

Department of Veterinary Medical Sciences, *Alma Mater Studiorum* – University of Bologna, Ozzano dell'Emilia (BO),

Italy

E-mail address: mara.battilani@unibo.it

Online Resource 4 Unrooted phylogenetic tree constructed with nucleotide sequences of partial E3 gene and flanking regions obtained in this study and 71 reference strains retrieved from the GenBank database (**Online Resource 2**).

Phylogeny was carried out using the software MEGA X version 10.1.7 (Kumar et al. 2018b) and the Neighbor-Joining method. The best-fit model of nucleotide substitution was determined using the Find Best DNA/Protein Model function implemented in MEGA X. The Kimura 2-parameter model with gamma distribution and invariable sites resulted optimal for the sequence data. Statistical support was provided by bootstrapping with 1000 replicates. Bootstrap values greater than 70% are indicated on the respective branches. The scale bars indicate the estimated numbers of nucleotide substitutions. Highlighted in black: Sequences generated in this study. In bold: Italian sequence of CADV type 1 and 2 isolated from dogs, foxes and wolves

