



Fig. 3. Phylogenetic analysis of the deduced amino acid sequences of CDV hemagglutinin gene fragments from local and worldwide strains. Arg 1–24: Argentine strains. Branch lengths indicate phylogenetic distances calculated from distance matrices of deduced amino acid sequences. Sequences accession numbers are listed in Section 2.

Please cite this article in press as: Calderon, M.G. et al., Detection by RT-PCR and genetic characterization of canine distemper virus from vaccinated and non-vaccinated dogs in Argentina, Vet. Microbiol. (2007), doi:10.1016/j.vetmic.2007.05.020