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Canine Parvovirus in New Zealand

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ABSTRACT

Since the initial global emergence of canine parvovirus type 2 (CPV-2) in the early 1980s the virus has continued to evolve in its new host. As a result, the original CVP-2 was replaced by newly emerged subtypes designated CPV-2a and CPV-2b. Recently, a third antigenic subtype CPV-2c has emerged in several countries. In New Zealand the evolution of CVP-2 has not been monitored since its emergence in the early 1980s, largely because of the high efficacy of the vaccines available on the market. This lack of monitoring of CPV-2 has left a dearth of knowledge regarding the epidemiological features of CPV-2 in New Zealand. Hence, the aim of this study was to determine what subtypes of CPV-2 circulate in New Zealand and to investigate the phylogenetic relationships between CPV-2 from New Zealand and from other parts of the world.

As part of this project, a virological survey was conducted across New Zealand. A total of 79 faecal samples were collected from dogs suspected to be infected with CPV-2, as judged by submitting veterinarians. Of those, 70 tested positive for CPV-2 DNA. All but one of the CPV-2 sequences were subtyped as CPV-2a. The remaining sequence was subtyped as CPV-2, and most likely represented a vaccine strain of the virus. The majority (74.3%) of CPV-2 positive samples originated from dogs six months of age and younger, with 70% of samples collected from dogs considered not fully vaccinated (unvaccinated dogs or those with only single vaccination), a further 17% of samples originated from dogs with an unknown vaccination history.

Two separate phylogenetic analyses were performed. Seventy one CPV-2 positive sequences originated from New Zealand (61 survey samples, six historic samples, two vaccine sequences and one parvovirus sequence obtained from a cat) and the reference sequence were trimmed to produce contiguous sequences of equal length. These 72 sequences were used to investigate the genetic structure of CPV-2 within New Zealand. Haplotype network analyses revealed that Cook-strait is not an effective geographical barrier to CVP-2 gene flow with an equal distribution of genotypes in the North and South Islands. Translocation of the virus between the islands is likely occurring by transportation of sub-clinically infected animals and fomites.

Additional CPV-2 VP2 sequences (n=95) originating from various countries were obtained from the National Centre for Biotechnology Information (NCBI) database. The selection of 27 samples originating from New Zealand for which a full length contiguous sequence of VP-2

gene was available were aligned with sequences obtained from the NCBI database. The resulting dataset of 123 CPV-2 sequences was used to assess the New Zealand CPV-2 sequences in the context of the worldwide radiation of CPV-2. Phylogenetic analyses of this dataset revealed that New Zealand has a closed monophyletic population of CPV-2 sequences. This suggests that CPV-2 is not being continuously introduced to New Zealand from overseas, but has evolved following a limited number of introductions in the past. Phylogenetic analysis also revealed that CPV-2 subtypes from around the world have emerged independently of one another.

This work has contributed to our understanding of molecular epidemiology of CPV-2 in New Zealand. The knowledge of predominant CPV-2 subtypes circulating in this country is important for evidence driven recommendations with regard to CPV-2 vaccination. Understanding of the genetic structure of the current CPV-2 circulating in New Zealand is also crucial for timely recognition, detection and management of any novel antigenic subtypes that may emerge in the future.

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ACRONYMS USED IN THIS THESIS

<i>Ala</i>	Alanine
<i>Asp</i>	Aspartate
bp	base pair
CPV-1	Canine parvovirus type 1
CPV-2	Canine parvovirus type 2
DNA	Deoxyribonucleic acid
ELISA	Enzyme-Linked Immunosorbent Assay
FPLV	Feline panleukopenia virus
<i>Glu</i>	Glutamate
<i>Gly</i>	Glycine
HI	Haemagglutination inhibition
<i>Ile</i>	Isoleucine
<i>Leu</i>	Leucine
MAF	Ministry of Agriculture and Fisheries (AKA: MPI – Ministry of Primary Industries)
<i>Met</i>	Methionine
MVC	Minute virus of canines
NCBI	National Centre for Biotechnology Information
NLFK	Northern Line Feline Kidney (cells)
NS1	Non-structural protein 1
NS2	Non-structural protein 2
NZ	New Zealand
OD	Optical density
ORF	Open reading frame
PCR	Polymerase chain reaction
RNA	Ribonucleic acid
<i>Ser</i>	Serine

ssDNA	Single stranded deoxyribonucleic acid
S.T.A.R	Stool Transport and Recovery (system)
TfR	Transferrin receptor
<i>Thr</i>	Threonine
<i>Tyr</i>	Tyrosine
<i>Val</i>	Valine
VP	Viral protein