# Canine Parvovirus in New Zealand

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**Sylvia Anna Ohneiser**

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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-straight 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

| | |
|---|---|
| *Ala* | Alanine |
| *Asp* | 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 |
| *Glu* | Glutamate |
| *Gly* | Glycine |
| HI | Haemagglutination inhibition |
| *Ile* | Isoleucine |
| *Leu* | Leucine |
| MAF | Ministry of Agriculture and Fisheries (AKA: MPI – Ministry of Primary Industries) |
| *Met* | 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 |
| *Ser* | Serine |

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