

Presence and genetic characterization of canine parvovirus and distemper in domestic dogs and endemic and invasive mustelids in south-central Chile.



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A detrimental effect of the introduction of invasive species is the transmission of pathologies to native fauna. In central and southern Chile, the native mustelids *Lontra felina* and *L. provocax* are sympatric and syntopic with mink (*Neogale vison*) and domestic dogs (*Canis lupus familiaris*), both invasive species responsible for the spread of canine parvovirus (CPV) and canine distemper (CDV) viruses. We serologically detect the prevalence of CPV and CDV in *Canis lupus familiaris*, *Neogale vison*, *Lontra felina* and *Lontra provocax*, and estimate variations in the structure of the molecular of the markers used in both pathologies

Methodology: In three sectors of the temperate rain forest Pilolcura/valdivian Ecoregion (Toltén and Trumao), we obtained serum samples and conjunctival, nasal and tonsillar tissue of these four species. CDV and CPV were detected serologically (IgG Inmuno Comb Canine) and molecularly characterized by qPCR-HRM.

Nº	Localidad	<i>Canis lupus familiaris</i>	<i>Neogale vison</i>	<i>Lontra</i> ---	<i>Lontra</i> 5
1	Toltén	11	9		
2	Pilolcura	1	28	1	--
3	Trumao	0	9	4	--
		1		--	--
		1			

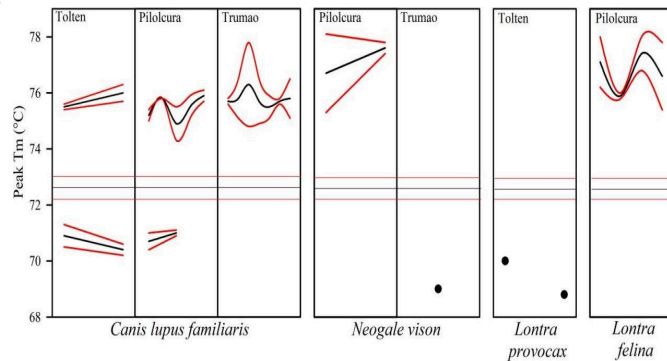
The study is carried out in three locations in the temperate rainforest ecoregion of south-central Chile.

Results: All studied species presented parvovirus. The serological presence of parvovirus was detected in approximately 79% of the *L. felina* individuals analyzed.

We found with two genetic variant of parvovirus in *N. vison* from the same locality and from domestic dogs, but which differed from the genetic variant observed in *L. felina*. Furthermore, parvovirus variants similar to those observed in *L. provocax* were also detected in *N. vison*. On the other hand, CDV was only found in dogs that had parvovirus.

Number samples extracted per location and species. Seropositivity for canine parvovirus (PVC), canine distemper (VDC) and both diseases simultaneously (PVC/VDC). Number of samples positive or negative for the serological examination and for the conventional PCR (PCR- and PCR+ respectively). (-: the species was not captured in that locality).

Localidad	<i>L. provocax</i>	<i>L. felina</i>	<i>N. vison</i>	<i>C.l. familiaris</i>
Río Toltén	5	-	9	11
Seropositivdad:				
- PVC	0	-	0	9
-VDC	0	-	0	0
-PVC/VDC	0	-	0	2
PVC(S+//PCR+)	0	-	0	7
PVC(S-//PCR+)	2	-	0	0
VDC (S-//PCR-)	0	-	0	2
Pilolcura	-	14	28	10
Seropositivdad: -				
PVC	-	11	1	4
-VDC	-	0	0	0
-PVC/VDC	-	0	0	6
PVC(S+//PCR+)	-	2	1	0
PVC(S+//PCR-)	-	11	3	3
PVC(S-//PCR+)	-	2	2	0
VDC (S-//PCR-)	-	0	0	6
Trumao	-	-	9	11
Seropositivdad: -				
PVC	-	-	0	7
-VDC	-	-	0	0
-PVC/VDC	-	-	0	1
PVC(S+//PCR+)	-	-	0	7
PVC(S-//PCR+)	-	-	1	0
VDC (S-//PCR-)	-	-	0	1



Ranges of peak melting temperature (Tm) values obtained by qPCR-HRM for the species analyzed within the three locations of the study area. Average values (black lines) and lower and upper ranges (red lines) of Tm are included. Horizontal lines show the average and standard deviation interval of the control sample.

Conclusions: For the first time, canine parvovirus infection was reported in *Lontra felina* individuals. The results support that *N. vison* acts as a bridge host of CDV and CPV between the domestic dog and the native fauna, and that this species together with the domestic dog also constitutes a reservoir of multiple genetic variants of parvovirus. Therefore, population control and mitigation of interactions between the American mink and the domestic dog may reduce the effects that the current range expansion of *N. vison* may have on CPV genotypic diversification.

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